

GenCore version 5.1.9
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File: nucleic search, using sw model

June 12, 2006, 07:37:54 ; Search time 5 Seconds
(without alignments)
3.589 Million cell updates/sec

US-09-930-503a-6

1766

1 aatcagagccacccgsgc.....cgagtcctcatcagatg 1766

IDENTITY: NUC

Gapop 10.0 , Gapext 0.5

264 seqs, 5081 residues

number of hits satisfying chosen parameters: 528

DB seq length: 8

DB seq length: 30

processing: Minimum Match 0%

Maximum Match 100%

Listing first 272 summaries

us-09-930-503a-6.sl.rn14.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Score	Query Match	Length	ID	Description
30	1.7	30	1	US-08-513-974B-133
25.2	1.4	30	1	US-08-513-974B-132
25	1.4	25	1	US-09-396-196G-67915
25	1.4	25	1	US-09-396-196G-67925
24.8	1.4	30	1	US-08-444-581B-6
24.8	1.4	30	1	US-08-446-088A-6
24.8	1.4	30	1	US-08-513-974B-139
24.2	1.4	30	1	US-08-513-974B-232
24	1.4	24	1	PCT-US92-06532-6
24	1.4	24	1	US-08-513-974B-61
24	1.4	29	1	US-08-776-971-32
24	1.4	29	1	US-09-461-436B-61
24	1.4	29	1	US-09-576-290-32
24	1.4	29	1	US-09-716-147-32
24	1.4	27	1	US-08-513-974B-85
23.8	1.3	25	1	US-09-396-196G-67914
23.4	1.3	25	1	US-09-396-196G-67926
23	1.3	24	1	US-07-701-935-4
23	1.3	24	1	US-08-117-965-4
22.4	1.3	24	1	US-07-701-935-5
22.4	1.3	24	1	US-08-117-965-5
22.2	1.3	27	1	US-08-513-974B-82
22.2	1.3	27	1	US-08-513-974B-84
22	1.2	25	1	US-09-396-196G-67908
21.8	1.2	25	1	US-09-396-196G-67912
21.8	1.2	27	1	US-08-513-974B-2
21.8	1.2	27	1	US-08-513-974B-76
21.8	1.2	27	1	US-08-776-971-30
21.8	1.2	27	1	US-08-540-650B-8
21.8	1.2	27	1	US-09-255-518C-6
21.8	1.2	27	1	US-09-461-436B-2

C 34	21.8	1.2	27	1	US-09-576-290-30	Sequence 30, App1
C 35	21.8	1.2	27	1	US-09-716-147-30	Sequence 30, App1
C 36	21	1.2	21	1	US-07-701-935-10	Sequence 13, App1
C 37	21	1.2	21	1	US-07-701-935-13	Sequence 13, App1
C 38	21	1.2	21	1	US-07-701-935-15	Sequence 15, App1
C 39	21	1.2	21	1	US-07-701-935-17	Sequence 17, App1
C 40	21	1.2	21	1	US-07-701-935-18	Sequence 18, App1
C 41	21	1.2	21	1	US-08-117-965-10	Sequence 10, App1
C 42	21	1.2	21	1	US-08-117-965-13	Sequence 13, App1
C 43	21	1.2	21	1	US-08-117-965-15	Sequence 15, App1
C 44	21	1.2	21	1	US-08-117-965-17	Sequence 17, App1
C 45	21	1.2	21	1	US-08-117-965-18	Sequence 18, App1
C 46	21	1.2	21	1	US-08-117-965-22	Sequence 22, App1
C 47	21	1.2	21	1	US-08-513-974B-263	Sequence 263, App
C 48	21	1.2	21	1	US-08-513-974B-264	Sequence 264, App
C 49	21	1.2	21	1	PCT-US92-06532-5	Sequence 6, App1
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C 51	20.8	1.2	24	1	US-08-117-965-6	Sequence 231, App
C 52	20.8	1.2	24	1	US-08-513-974B-231	Sequence 231, App
C 53	20.8	1.2	24	1	US-08-513-974B-233	Sequence 233, App
C 54	20.8	1.2	24	1	US-08-513-974B-237	Sequence 237, App
C 55	20.8	1.2	25	1	US-09-396-196G-67919	Sequence 15, App1
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C 57	20.6	1.2	24	1	US-08-513-974B-230	Sequence 230, App
C 58	20.6	1.2	24	1	US-09-461-436B-15	Sequence 15, App1
C 59	20.4	1.2	23	1	US-08-513-974B-235	Sequence 235, App
C 60	20.2	1.1	25	1	US-09-396-196G-67918	Sequence 67918, A
C 61	20.2	1.1	25	1	US-09-396-196G-67927	Sequence 67927, A
C 62	20.2	1.1	25	1	US-09-396-196G-67930	Sequence 67930, A
C 63	20.2	1.1	25	1	US-09-396-196G-67931	Sequence 67931, A
C 64	20	1.1	20	1	US-07-701-935-11	Sequence 11, App1
C 65	20	1.1	20	1	US-07-701-935-12	Sequence 12, App1
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C 68	20	1.1	20	1	US-07-701-935-19	Sequence 19, App1
C 69	20	1.1	20	1	US-07-701-935-20	Sequence 20, App1
C 70	20	1.1	20	1	US-08-117-965-11	Sequence 11, App1
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C 77	20	1.1	21	1	US-08-117-965-9	Sequence 9, App1
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C 79	19.4	1.1	21	1	US-08-513-974B-257	Sequence 257, App
C 80	19.2	1.1	24	1	US-08-125-012-7	Sequence 7, App1
C 81	19.2	1.1	24	1	US-08-221-579A-7	Sequence 7, App1
C 82	19.2	1.1	24	1	US-08-783-818-7	Sequence 7, App1
C 83	19.2	1.1	24	1	US-08-453-349-7	Sequence 7, App1
C 84	19.2	1.1	24	1	US-08-704-701-7	Sequence 7, App1
C 85	19.2	1.1	24	1	US-08-979-385B-7	Sequence 7, App1
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C 87	19.2	1.1	24	1	US-09-011-922A-13	Sequence 13, App1
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C 90	19	1.1	19	1	US-07-701-935-25	Sequence 25, App1
C 91	19	1.1	19	1	US-08-117-965-23	Sequence 23, App1
C 92	19	1.1	19	1	US-08-117-965-25	Sequence 25, App1
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C 94	18.4	1.0	20	1	US-08-287-075-9	Sequence 9, App1
C 95	18.2	1.0	20	1	US-07-915-966C-12	Sequence 12, App1
C 96	18.2	1.0	20	1	US-08-771-182-12	Sequence 12, App1
C 97	18.2	1.0	20	1	US-08-853-194-12	Sequence 12, App1
C 98	18	1.0	18	1	US-07-701-935-21	Sequence 21, App1
C 99	18	1.0	18	1	US-08-117-965-21	Sequence 21, App1
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C 101	17.8	1.0	21	1	US-08-513-974B-267	Sequence 267, App
C 102	17.8	1.0	21	1	US-08-513-974B-267	Sequence 267, App
C 103	17.8	1.0	21	1	US-08-513-974B-269	Sequence 269, App
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C 105	17.8	1.0	22	1	US-07-974-409C-5	Sequence 5, App1
C 106	17	1.0	21	1	US-08-182-175A-17	Sequence 17, App1

17	1.0	21	1	US-08-182-175A-19	Sequence 19, Appl	C 180	13.8	0.8	17	1	US-09-401-063-243	Sequence 243, App
17	1.0	21	1	US-08-182-175A-21	Sequence 21, Appl	C 181	13.8	0.8	17	1	US-09-866-108A-2756	Sequence 2756, Ap
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17	1.0	21	1	US-08-474-633A-41	Sequence 41, Appl	C 183	13.8	0.8	17	1	US-09-685-664B-1774	Sequence 1774, Ap
17	1.0	21	1	US-08-474-633A-43	Sequence 43, Appl	C 184	13.8	0.8	17	1	US-09-685-664B-1886	Sequence 1886, Ap
17	1.0	21	1	US-08-823-771-25	Sequence 25, Appl	C 185	13.8	0.8	17	1	US-10-156-306B-6951	Sequence 6951, Ap
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17	1.0	21	1	US-08-823-771-43	Sequence 43, Appl	C 187	13.8	0.8	17	1	US-10-138-674B-1866	Sequence 1866, Ap
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16.8	1.0	21	1	US-08-936-534-7	Sequence 7, Appl	C 192	13.4	0.8	15	1	US-09-038-073-2101	Sequence 2101, Ap
16.8	1.0	21	1	US-09-345-294-7	Sequence 7, Appl	C 193	13.4	0.8	15	1	US-08-502-185-16	Sequence 16, Appl
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16.4	0.9	18	1	US-08-117-965-2	Sequence 2, Appl	C 195	13	0.7	15	1	US-08-501-779-16	Sequence 16, Appl
16.4	0.9	18	1	US-08-584-040-6209	Sequence 6209, Ap	C 196	13	0.7	15	1	US-08-501-713-16	Sequence 16, Appl
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14.4	0.8	18	1	US-09-106-038A-9	Sequence 9, Appl	C 219	12.4	0.7	14	1	US-08-785-750-2	Sequence 2, Appl
14.4	0.8	18	1	US-09-289-376-17	Sequence 17, Appl	C 220	12.4	0.7	14	1	US-08-588-355-1	Sequence 1, Appl
14.4	0.8	18	1	US-09-344-520-9	Sequence 9, Appl	C 221	12.4	0.7	14	1	US-09-116-780-5	Sequence 5, Appl
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7	12.4	0.7	29	1	US-09-576-290-32	Sequence 32, Appl
8	12.4	0.7	29	1	US-09-716-147-32	Sequence 32, Appl
9	12.4	0.7	29	1	US-08-173-489C-232	Sequence 32, Appl
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14	12.4	0.7	15	1	US-09-180-437-143	Sequence 143, Appl
15	12.4	0.7	15	1	US-09-275-850-31	Sequence 31, Appl
16	12.4	0.7	15	1	US-09-081-646-49	Sequence 49, Appl
17	12.4	0.7	15	1	US-09-081-646-560	Sequence 560, Appl
18	12.4	0.7	15	1	US-09-015-188-6	Sequence 6, Appl
19	12.4	0.7	15	1	US-09-720-435A-39	Sequence 39, Appl
20	12.4	0.7	15	1	US-09-907-111-31	Sequence 31, Appl

ALIGNMENTS

513-974B-133
 Invention 133, Application US/08513974B
 Inventor No. 6114139

GENERAL INFORMATION:
 APPLICANT: Hinuma, Shuji
 APPLICANT: Hosoya, Masaki
 APPLICANT: Fujii, Ryo
 APPLICANT: Onitaki, Tetsuya
 APPLICANT: Fukusumi, Shoji
 APPLICANT: Onogi, Kazuhiko
 TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
 TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
 NUMBER OF SEQUENCES: 380
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/513,974B
 FILING DATE: 14-SEP-1995
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP95/01599
 FILING DATE: 10-AUG-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-093989
 FILING DATE: 19-AUG-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-057186
 FILING DATE: 16-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-007177
 FILING DATE: 20-JAN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-326611
 FILING DATE: 28-DEC-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-270017
 FILING DATE: 02-NOV-1994

```

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 133:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-513-974B-133

Query Match
Best Local Similarity 1.7%; Score 30; DB 1; Length 30;
Matches 30; Conservative 0; Pred. No. 2.7;
Matches 0; Indels 0; Gaps 0;

QY 979 TTGGCCATCTGCTGCTGCTGCTTCCACATC 1008
DB 1 TTGGCATCTGCTGCTGCTTCCACATC 30

RESULT 2
US-08-513-974B-132
Sequence 132, Application US/08513974B
Patent No. 6114139
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Onitaki, Tetsuya
APPLICANT: Fukusumi, Shoji
APPLICANT: Onogi, Kazuhiko
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
  
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R10R APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
R10R APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
R10R APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
R10R APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
R10R APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
R10R APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
R10R APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
R10R APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
R10R APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1945
R10R APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
FAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 132:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
513-974B-132

Y Match 1.4%; Score 25.2; DB 1; Length 30;
Local Similarity 90.0%; Pred. No. 12;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

979 TTGGCATCTGCTGGCTGCCCTTCACATC 1008
|||||
1 TTGGCATCTGCTGGCTGCCCTTCACATC 30

3
396-196G-67915
ence 67915, Application US/09396196G
nt No. 6821724
RAL INFORMATION:
LICANT: Michael Miltmann
LICANT: David Mack
LICANT: David Lockhart
LICANT: Affymetrix, Inc.
IE OF INVENTION: Methods of Genetic Analysis
E REFERENCE: 3101.1
RENT APPLICATION NUMBER: US/09/396,196G
RENT FILING DATE: 1999-09-15
OR APPLICATION NUMBER: 60/100,678
OR FILING DATE: 1998-09-17
BER OF SEQ ID NOS: 127806
TWARE: FastSeq for Windows Version 4.0
ID NO 67915

LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-67915

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1261 GTGACCGCCTGGAGACCACCATCT 1285
|||||
DB 1 GTGACCGCCTGGAGACCACCATCT 25

RESULT 4
US-09-396-196G-67925
Sequence 67925, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 67925
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-67925

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1123 TACTGCTGCTCATGACAGGTTCC 1147
|||||
DB 1 TACTGCTGCTCATGACAGGTTCC 25

RESULT 5
US-08-442-134A-6/c
Sequence 6, Application US/08442134A
Patent No. 5596088
GENERAL INFORMATION:
APPLICANT: Boucher, Richard C.
APPLICANT: Weisman, Gary A.
APPLICANT: Turner, John T.
APPLICANT: Harden, Thomas K.
APPLICANT: Parr, Claude E.
APPLICANT: Sullivan, Daniel M.
APPLICANT: Erb, Laura
APPLICANT: Lustig, Kevin D.
TITLE OF INVENTION: DNA Encoding the Human P2U Receptor and
TITLE OF INVENTION: Null Cells Expressing P2U Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Seltzer, Park & Gibson
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: No. 5596088th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,134A
FILING DATE: 16-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sidley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-71A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
SEQUENCE CHARACTERISTICS:
FORMATION FOR SEQ ID NO: 6:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
-442-134A-6

C Match 1.4%; Score 24.8; DB 1; Length 30;
Local Similarity 76.7%; Pred. No. 14;
Ches 23; Conservative 5; Mismatches 2; Indels 0; Gaps 0

979 TTGGCATCTGCTGGCTGCGCTTTCACATC 1008
|||||:||||:||||:||||:||||:
30 TTGGCCTCWCCTKCTGCTGCTTSCACGTC 1

T 6
-444-581B-6/C
ence 6, Application US/08444581B
ent No. 5607836
HERAL INFORMATION:
APPLICANT: Boucher, Richard C.
APPLICANT: Weisman, Gary A.
APPLICANT: Turner, John T.
APPLICANT: Harden, Thomas K.
APPLICANT: Parr, Claude E.
APPLICANT: Sullivan, Daniel M.
APPLICANT: Erb, Laura
APPLICANT: Lustig, Kevin D.
TITLE OF INVENTION: DNA Encoding the Human P2U Receptor and
TITLE OF INVENTION: Null Cells Expressing P2U Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Bell, Selzer, Park & Gibson
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: No. 5607836ch Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,581B
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/442,134
FILING DATE: 16-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Sidley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-71A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
FORMATION FOR SEQ ID NO: 6:

```

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: SEQUENCE CHARACTERISTICS:
: LENGTH: 30 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
:
US-08-444-581B-6
:
Query Match 1.4%; Score 24.8; DB 1; Length 30;
Best Local Similarity 76.7%; Pred. No. 14;
Matches 23; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
:
QY 979 TTGGCATTGCTGCTGCTGCCTTCACATC 1008
: ||||| :|||:|||||:|||||:|||||
Db 30 TTGGCCTTGWGCTKCTGCTGCTTSCAGTC 1
:
RESULT 7
US-08-446-088A-6/c
: Sequence 6, Application US/08446088A
: Patent No. 5691156
: GENERAL INFORMATION:
: APPLICANT: Boucher, Richard C.
: APPLICANT: Weisman, Gary A.
: APPLICANT: Turner, John T.
: APPLICANT: Harden, Thomas K.
: APPLICANT: Parr, Claude E.
: APPLICANT: Sullivan, Daniel M.
: APPLICANT: Erb, Laura
: APPLICANT: Lustig, Kevin D.
: TITLE OF INVENTION: DNA Encoding the Human P2U Receptor and
: TITLE OF INVENTION: Null Cells Expressing P2U Receptors
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Bell, Seltzer, Park & Gibson
: STREET: Post Office Drawer 34009
: CITY: Charlotte
: STATE: No. 5691156th Carolina
: COUNTRY: USA
: ZIP: 28234
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/446, 088A
: FILING DATE: 19-MAY-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Kenneth D. Sibley
: REGISTRATION NUMBER: 31,665
: REFERENCE/DOCKET NUMBER: 5470-71C
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 919-420-2200
: TELEFAX: 919-881-3175
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 30 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
:
US-08-446-088A-6
:
Query Match 1.4%; Score 24.8; DB 1; Length 30;
Best Local Similarity 76.7%; Pred. No. 14;
Matches 23; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
:
QY 979 TTGGCATTGCTGCTGCTGCCTTCACATC 1008
: ||||| :|||:|||||:|||||:|||||
Db 30 TTGGCCTTGWGCTKCTGCTGCTTSCAGTC 1

```

8
513-974B-139
ence 139, Application US/08513974B
te No. 6114139
ERAL INFORMATION:
PLICANT: Hinuma, Shuji
PLICANT: Hosoya, Masaki
PLICANT: Fujii, Ryo
PLICANT: Ohaki, Tetsuya
PLICANT: Fukusumi, Shoji
PLICANT: Ohgi, Kazuhiko
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
ORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
OMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
URRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
RIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
TORNEX/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
ELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
ORMATION FOR SEQ ID NO: 139:
EQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-513-974B-139
Query Match 1.4%; Score 24.2; DB 1; Length 30;
Best local similarity 89.7%; Pred. No. 17;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 979 TTGGCATCTGCTGCTGCCTTCCACAT 1007
Db 1 TTGGCATCTGCTGCTGCCTTCCACAT 29
RESULT 9
US-08-513-974B-232
Sequence 232, Application US/08513974B
Patent No. 6114139
GENERAL INFORMATION:
PLICANT: Hinuma, Shuji
PLICANT: Hosoya, Masaki
PLICANT: Fujii, Ryo
PLICANT: Ohaki, Tetsuya
PLICANT: Fukusumi, Shoji
PLICANT: Ohgi, Kazuhiko
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
RIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189273
 FILING DATE: 11-AUG-1945
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189272
 FILING DATE: 11-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Resnick, David S.
 REGISTRATION NUMBER: 34,235
 REFERENCE/DOCKET NUMBER: 45753
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 FORMATION FOR SEQ ID NO: 232:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 513-974B-232

cy Match 1.4%; Score 24; DB 1; Length 24;
 Local Similarity 100.0%; Pred. No. 12;
 ches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

979 TTGGCATCTGCTGGCTGCCTTC 1002
 1 TTGGCATCTGCTGGCTGCCTTC 24

10
 392-06532-6/C
 jence 6; Application PC/TUS9206532
 NERAL INFORMATION:
 APPLICANT: Krause, James E.
 TITLE OF INVENTION: Human Substance P Receptor
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Scott J Meyer, Monsanto Co., ASD
 STREET: 800 N. Lindbergh Blvd.
 CITY: St. Louis
 STATE: Missouri
 COUNTRY: U.S.A
 ZIP: 63167

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/06532
 FILING DATE: 19920805

CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Meyer, Scott J.
 REGISTRATION NUMBER: 25,275
 REFERENCE/DOCKET NUMBER: 07-24(776)A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (314)694-3117
 FORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ANTI-SENSE: YES
 392-06532-6

cy Match 1.4%; Score 24; DB 1; Length 24;
 Local Similarity 100.0%; Pred. No. 12;
 ches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1411 TTCTCTCCATGTCCTCTCTAG 1434
 DB 24 TTCTCTCCATGTCCTCTCTAG 1

RESULT 11
 US-08-513-974B-61/C
 Sequence 61, Application US/08513974B
 Patent No. 6114139
 GENERAL INFORMATION:
 APPLICANT: Hinuma, Shuji
 APPLICANT: Hosoya, Masaki
 APPLICANT: Fujii, Ryo
 APPLICANT: Ohtaki, Tetsuya
 APPLICANT: Fukushima, Shoji
 APPLICANT: Ohgi, Kazuhiro
 TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
 TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
 NUMBER OF SEQUENCES: 380
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/513,974B
 FILING DATE: 14-SEP-1995

CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP95/01599
 FILING DATE: 10-AUG-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-093989
 FILING DATE: 19-AUG-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-057186
 FILING DATE: 16-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-007177
 FILING DATE: 20-JAN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-326611
 FILING DATE: 28-DEC-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-270017
 FILING DATE: 02-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-236357
 FILING DATE: 30-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-236356
 FILING DATE: 30-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189274
 FILING DATE: 11-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189273
 FILING DATE: 11-AUG-1945
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189272
 FILING DATE: 11-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Resnick, David S.
 REGISTRATION NUMBER: 34,235
 REFERENCE/DOCKET NUMBER: 45753

REGISTRATION NUMBER: <Unknown>
REFERENCE/DOCKET NUMBER: 45753 DIV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-439-4444
TELEFAX: 617-439-4170
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
FEATURE:
OTHER INFORMATION: /note = N is inosine; S is G or C; W is A or T;
R is A or G; K is G or T; Y is C or T."
SEQUENCE DESCRIPTION: SEQ ID NO: 61:
-461-436B-61
Query Match 1.4%; Score 24; DB 1; Length 29;
c Local Similarity 72.4%; Pred. No. 17;
Matches 21; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
979 TTCGCCATCTGCTGGCTGCCCTTCCACAT 1007
||||:|||||||||||||||||:
29 TTCRYSNCTGCTGGCTGCCCTWCTWCMWT 1
F 14
-576-290-32/c
Jence 32, Application US/09576290
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Habata, Yugo
APPLICANT: Kawamata, Yuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Fukusumi, Shoji
APPLICANT: Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESSES:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/576,290
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/776,971
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996

ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
US-09-576-290-32
Query Match 1.4%; Score 24; DB 1; Length 29;
Best Local Similarity 72.4%; Pred. No. 17;
Matches 21; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
979 TTCGCCATCTGCTGGCTGCCCTTCCACAT 1007
||||:|||||||||||||||||:
29 TTCRYSNCTGCTGGCTGCCCTWCTWCMWT 1
Db
RESULT 15
US-09-716-147-32/c
Jence 32, Application US/09716147
Patent No. 6881545
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Habata, Yugo
APPLICANT: Kawamata, Yuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Fukusumi, Shoji
APPLICANT: Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESSES:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/716,147
FILING DATE: 17-NOV-6881545-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-FEB-1997
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176

ent No. 6821724
 SERIAL INFORMATION:
 APPLICANT: Michael Miltmann
 APPLICANT: David Mack
 APPLICANT: David Lockhart
 APPLICANT: Affymetrix, Inc.
 TITLE OF INVENTION: Methods of Genetic Analysis
 FILE REFERENCE: 3101.1
 CURRENT APPLICATION NUMBER: US/09/396,196G
 CURRENT FILING DATE: 1999-09-15
 FOR APPLICATION NUMBER: 60/100,678
 FOR FILING DATE: 1998-09-17
 NUMBER OF SEQ ID NOS: 127806
 SOFTWARE: FastSeq for Windows Version 4.0
 ID NO: 67926
 LENGTH: 25
 TYPE: DNA
 ORGANISM: mus musculus
 -396-196G-67926

cy Match 1.3%; Score 23.4; DB 1; Length 25;
 Local Similarity 96.0%; Pred. No. 15;
 Mismatches 1; Indels 0; Gaps 0;

1147 CGCTGGGCTTCAGCATGCTTCC 1171
 1 CGCTGGGCTTCAGCATGCTTTC 25

19
 -701-935-4/c
 Sequence 4, Application US/07701935
 ent No. 5336595
 SERIAL INFORMATION:
 APPLICANT: Strader, C. D.
 APPLICANT: Fong, T. M.
 TITLE OF INVENTION: Method of Using Human Neurokinin-1
 TITLE OF INVENTION: Receptor Short Form
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Merck & Co., Inc.
 STREET: P.O. Box 2000
 CITY: Rahway
 STATE: New Jersey
 COUNTRY: US
 ZIP: 07065-0907
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/701,935
 FILING DATE: 19910517
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Nicholson, William H.
 REGISTRATION NUMBER: 25,147
 REFERENCE/DOCKET NUMBER: 18409
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 594-5315
 TELEFAX: (908) 594-4720
 FORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE:
 -701-935-4

cy Match 1.3%; Score 23; DB 1; Length 24;
 Local Similarity 100.0%; Pred. No. 16;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1105 ATGTACACCCCATCATCTACTG 1127
 Db 24 ATGTACACCCCATCATCTACTG 2

RESULT 20
 US-08-117-965-4/c
 Sequence 4, Application US/08117965
 Patent No. 5484886
 GENERAL INFORMATION:
 APPLICANT: Tung, Fong M.
 APPLICANT: Cathrine, Strader D.
 TITLE OF INVENTION: Human Neurokinin-1 Receptor
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Merck & Co., Inc.
 STREET: P.O. Box 2000
 CITY: Rahway
 STATE: New Jersey
 COUNTRY: US
 ZIP: 07065-0907
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/117,965
 FILING DATE:
 CLASSIFICATION: 514
 PRIOR APPLICATION NUMBER:
 APPLICATION NUMBER: US 691,197
 FILING DATE: 25-APR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Nicholson, William H.
 REGISTRATION NUMBER: 25,147
 REFERENCE/DOCKET NUMBER: 18387
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 594-5315
 TELEFAX: (908) 594-4720
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE:
 US-08-117-965-4

Query Match 1.3%; Score 23; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1105 ATGTACACCCCATCATCTACTG 1127
 Db 24 ATGTACACCCCATCATCTACTG 2

RESULT 21
 US-07-701-935-5/c
 Sequence 5, Application US/07701935
 Patent No. 5336595
 GENERAL INFORMATION:
 APPLICANT: Strader, C. D.
 APPLICANT: Fong, T. M.
 TITLE OF INVENTION: Method of Using Human Neurokinin-1
 TITLE OF INVENTION: Receptor Short Form
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Merck & Co., Inc.
 STREET: P.O. Box 2000

CITY: Rahway
STATE: New Jersey
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/701,935
FILING DATE: 19910517
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nicholson, William H.
REGISTRATION NUMBER: 25,147
REFERENCE/DOCKET NUMBER: 18409
TELEPHONE: (908) 594-5315
TELEFAX: (908) 594-4720
FORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
701-935-5
Y Match 1.3%; Score 22.4; DB 1; Length 24;
Local Similarity 95.8%; Pred. No. 19;
hes 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1051 AAGTTATCCAGCAGGCTCTACTG 1074
|||||
24 AAGTTCATCCAGCAGGCTCTACTG 1

22
117-965-5/c
ence 5, Application US/08117965
nt No. 5484886
ERAL INFORMATION:
PLICANT: Tung, Fong M.
PLICANT: Cathline, Strader D.
TITLE OF INVENTION: Human Neurokinin-1 Receptor
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P. O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,965
FILING DATE:
CLASSIFICATION: 514
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 691,197
FILING DATE: 25-APR-1991
TTORNEY/AGENT INFORMATION:
NAME: Nicholson, William H.
REGISTRATION NUMBER: 25,147
REFERENCE/DOCKET NUMBER: 18387
TELEPHONE: (908) 594-5315
TELEFAX: (908) 594-4720

;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 24 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE:
US-08-117-965-5
Query Match 1.3%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 19;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1051 AAGTTATCCAGCAGGCTCTACTG 1074
|||||
Db 24 AAGTTCATCCAGCAGGCTCTACTG 1

RESULT 23
US-08-513-974B-82
Sequence 82, Application US/08513974B
Patent No. 6114139
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Fukusumi, Shoji
APPLICANT: Ohgi, Kazuhiko
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 6-189274
 FILING DATE: 11-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189273
 FILING DATE: 11-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189272
 FILING DATE: 11-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Resnick, David S.
 REGISTRATION NUMBER: 34,235
 REFERENCE/DOCKET NUMBER: 45753
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 FORMATION FOR SEQ ID NO: 82:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 27 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 -513-974B-82

Query Match 1.3%; Score 22.2; DB 1; Length 27;
 Local Similarity 88.9%; Pred. No. 26;
 Cons 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

979 TTGGCATTCTGCTGGCTGCCCTTCCAC 1005
 1 TTGGCATTCTGCTGGCTGCCCTATCAC 27

1 24
 -513-974B-84
 ence 84, Application US/08513974B
 ent No. 6114139
 ERAL INFORMATION:
 APPLICANT: Hinuma, Shuji
 APPLICANT: Hosoya, Masaki
 APPLICANT: Fujii, Ryo
 APPLICANT: Ontaka, Tetsuya
 APPLICANT: Fukusumi, Shoji
 APPLICANT: Ohgi, Kazuhiro
 TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
 TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
 NUMBER OF SEQUENCES: 380
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/513,974B
 FILING DATE: 14-SEP-1995
 CLASSIFICATION: 516
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP95/01599
 FILING DATE: 10-AUG-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-093989
 FILING DATE: 19-AUG-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-057186
 FILING DATE: 16-MAR-1995
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 7-007177
 FILING DATE: 20-JAN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-326611
 FILING DATE: 28-DEC-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-270017
 FILING DATE: 02-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-236357
 FILING DATE: 30-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-236356
 FILING DATE: 30-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189274
 FILING DATE: 11-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189273
 FILING DATE: 11-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189272
 FILING DATE: 11-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Resnick, David S.
 REGISTRATION NUMBER: 34,235
 REFERENCE/DOCKET NUMBER: 45753
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 84:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 27 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 US-08-513-974B-84

Query Match 1.3%; Score 22.2; DB 1; Length 27;
 Best Local Similarity 88.9%; Pred. No. 26;
 Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 979 TTGGCATTCTGCTGGCTGCCCTTCCAC 1005
 Db 1 TTGGCATTCTGCTGGCTGCCCTATCAC 27

RESULT 25
 US-09-396-196G-67908
 Sequence 67908, Application US/09396196G
 Patent No. 6821724
 GENERAL INFORMATION:
 APPLICANT: Michael Miltmann
 APPLICANT: David Mack
 APPLICANT: David Lockhart
 APPLICANT: Affymetrix, Inc.
 TITLE OF INVENTION: Methods of Genetic Analysis
 FILE REFERENCE: 3101.1
 CURRENT APPLICATION NUMBER: US/09/396,196G
 CURRENT FILING DATE: 1999-09-15
 PRIOR APPLICATION NUMBER: 60/100,678
 PRIOR FILING DATE: 1998-09-17
 NUMBER OF SEQ ID NOS: 127806
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 67908
 LENGTH: 25
 TYPE: DNA
 ORGANISM: mus musculus
 US-09-396-196G-67908

Query Match 1.2%; Score 22; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 24;

hes 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1051 AAGTTATCCAGAGGTCTACC 1072
|||||
4 AAGTTATCCAGAGGTCTACC 25

26
396-196G-67912
ence 67912, Application US/09396196G
nt No. 6821724
RAL INFORMATION:
LICANT: Michael Miltmann
LICANT: David Mack
LICANT: David Lockhart
LICANT: Affymetrix, Inc.
LE OF INVENTION: Methods of Genetic Analysis
E REFERENCE: 3101.1
RENT APPLICATION NUMBER: US/09/396.196G
RENT FILING DATE: 1999-09-15
OR APPLICATION NUMBER: 60/100,678
OR FILING DATE: 1998-09-17
BER OF SEQ ID NOS: 127806
TWARE: FastSeq for Windows Version 4.0
ID NO 67912
NGTH: 25
PE: DNA
GANISM: mus musculus
396-196G-67912

Y March 1.2%; Score 21.8; DB 1; Length 25;
Local Similarity 92.0%; Pred. No. 25;
hes 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

907 TCTGACCGCTACACGAGCAAGTCT 931
|||||
1 TCTGACCGCTACACGAGCAAGTCT 25

27
396-196G-67913
ence 67913, Application US/09396196G
nt No. 6821724
RAL INFORMATION:
LICANT: Michael Miltmann
LICANT: David Mack
LICANT: David Lockhart
LICANT: Affymetrix, Inc.
LE OF INVENTION: Methods of Genetic Analysis
E REFERENCE: 3101.1
RENT APPLICATION NUMBER: US/09/396.196G
RENT FILING DATE: 1999-09-15
OR APPLICATION NUMBER: 60/100,678
OR FILING DATE: 1998-09-17
BER OF SEQ ID NOS: 127806
TWARE: FastSeq for Windows Version 4.0
ID NO 67913
NGTH: 25
PE: DNA
GANISM: mus musculus
396-196G-67913

Y Match 1.2%; Score 21.8; DB 1; Length 25;
Local Similarity 92.0%; Pred. No. 25;
hes 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

913 CGCTACCGAGCAAGTCTCGCCA 937
|||||
1 CGTTACCATGAGCAAGTCTCGCCA 25

28
513-974B-2/c

Sequence 2, Application US/08513974B
Patent No. 6114139
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaaki
APPLICANT: Fujii, Ryo
APPLICANT: Ohaki, Tetsuya
APPLICANT: Fukusumi, Shoji
APPLICANT: Ohgi, Kazuhiko
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-226356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1945
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
FORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
776-971-30

1.2%; Score 21.8; DB 1; Length 27;
Local Similarity 74.1%; Pred. No. 30;
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

979 TTGGCATCTGCTGCTGCTGCTTCCAC 1005
|||:|||||:|||||:|||||:
27 TTGGCMTCTGCTGNTGCCYWCNAC 1

31
540-650B-8/c
ence 8, Application US/08540650B
nt No. 6399325

GENERAL INFORMATION:
APPLICANT: HINDMA, Shuji
APPLICANT: FUJII, Ryo
APPLICANT: FUKUSUMI, Shoji
APPLICANT: OHTAKI, Tetsuya
APPLICANT: HOSOYA, Masaki
APPLICANT: OHGI, Kazuhiro
APPLICANT: ONDA, Haruo
TITLE OF INVENTION: GALANIN RECEPTOR PROTEIN, PRODUCTION AND USE THEREOF
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/540,650B
FILING DATE: 11-OCT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 7-134412
FILING DATE: 31-MAY-1995
APPLICATION NUMBER: 6-326610
FILING DATE: 28-DEC-1994
APPLICATION NUMBER: 6-247599
FILING DATE: 13-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45901
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
FORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 27
TYPE: Nucleic acid
STRANDEDNESS: Single

TOPOLOGY: Linear
MOLECULE TYPE: Other nucleic acid
MOLECULE TYPE: Synthetic DNA
FEATURE: N is A, G, C, or T
US-08-540-650B-8

Query Match 1.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 30;
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 979 TTGGCATCTGCTGCTGCTTCCAC 1005
Db 27 TTGGCMTCTGCTGNTGCCYWCNAC 1

RESULT 32
US-09-255-518C-6/c
Sequence 6, Application US/09255518C
Patent No. 6492324
GENERAL INFORMATION:
APPLICANT: HINDMA, SHUJI
APPLICANT: TATEMOTO, KAZUHIKO
APPLICANT: HOSOYA, MASAKI
APPLICANT: HABATA, YUO
APPLICANT: FUJII, RYO
APPLICANT: KITADA, CHIEKO
TITLE OF INVENTION: POLYPEPTIDES, THEIR PRODUCTION AND USE
FILE REFERENCE: 48970(342)
CURRENT APPLICATION NUMBER: US/09/255,518C
CURRENT FILING DATE: 1999-02-22
PRIOR APPLICATION NUMBER: PCT/JP98/05805
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 9-353955
PRIOR FILING DATE: 1997-12-24
PRIOR APPLICATION NUMBER: 10-032577
PRIOR FILING DATE: 1998-02-16
PRIOR APPLICATION NUMBER: 10-220853
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 10-271645
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 27
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
NAME/key: modified base
LOCATION: (1)..(27)
OTHER INFORMATION: "n" may be a, t, c, g
US-09-255-518C-6

Query Match 1.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 30;
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 979 TTGGCATCTGCTGCTGCTTCCAC 1005
Db 27 TTGGCMTCTGCTGNTGCCYWCNAC 1

RESULT 33
US-09-461-436B-2/c
Sequence 2, Application US/09461436B
Patent No. 6538107
GENERAL INFORMATION:
APPLICANT: Shuji Hinuma
Yasuki Ito
Ryo Fujii
TITLE OF INVENTION: G Protein Coupled Receptor Protein,
Production, And Use Thereof
NUMBER OF SEQUENCES: 61

CORRESPONDENCE ADDRESS:

ADDRESSEE: Edwards & Angel, LLP
STREET: 101 Federal Street
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02209

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/461,436B
FILING DATE: 14-Dec-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/513,974
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
APPLICATION NUMBER: 7-093989
FILING DATE: 19-APR-1995
APPLICATION NUMBER: 7-057186
FILING DATE: 16-MAR-1995
APPLICATION NUMBER: 7-007177
FILING DATE: 20-JAN-1995
APPLICATION NUMBER: 6-326611
FILING DATE: 28-DEC-1994
APPLICATION NUMBER: 6-270017
FILING DATE: 02-NOV-1994
APPLICATION NUMBER: 6-236357
FILING DATE: 30-SEP-1994
APPLICATION NUMBER: 6-236356
FILING DATE: 30-SEP-1994
APPLICATION NUMBER: 6-189274
FILING DATE: 11-AUG-1994
APPLICATION NUMBER: 6-189273
FILING DATE: 11-AUG-1994
APPLICATION NUMBER: 6-189272
FILING DATE: 11-AUG-1994

ATTORNEY/AGENT INFORMATION:

NAME: CONLIN, DAVID G.
REGISTRATION NUMBER: <Unknown>
REFERENCE/DOCKET NUMBER: 45753 DIV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-439-4444
TELEFAX: 617-439-4170

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 27
TYPE: Nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
FEATURE:
OTHER INFORMATION: /note= N is A, G, C, or T; W is A or T;
R is A or G; K is G or T."

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
-461-436B-2

Query Match 1.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 30;
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

979 TTGGCCATCTGCTGCTGCCCTTCAC 1005
|||:|||||:|||||:|||||:|||||:
27 TTGGCCATCTGCTGCTGCCCTTCAC 1

1 34
-576-290-30/C

; Sequence 30, Application US/09576290
; Patent No. 6794491

GENERAL INFORMATION:

APPLICANT: Hanuma, Shuji
APPLICANT: Habata, Yugo
APPLICANT: Kawamata, Yoji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Fukusumi, Shoji
APPLICANT: Kikada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/576,290
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/776,971
FILING DATE:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
US-09-576-290-30

Query Match 1.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 30;
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

979 TTGGCCATCTGCTGCTGCCCTTCAC 1005
|||:|||||:|||||:|||||:|||||:
27 TTGGCCATCTGCTGCTGCCCTTCAC 1

RESULT 35

US-09-716-147-30/C
; Sequence 30, Application US/09716147
; Patent No. 6881545

```

NEPAL INFORMATION:
APPLICANT: Hinuma, Shuji
            Habata, Yugo
            Kawamata, Taji
            Hosoya, Masaki
            Fujii, Ryo
            Fukushima, Shoji
            Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/716,147
FILING DATE: 17-NO. 6881545-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996

ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
716-147-30

Y Match 1.2%; Score 21.8; DB 1; Length 27;
Local Similarity 74.1%; Pred. No. 30;
hes 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

979 TTGGCATCTGCTGGTGGCCCTTCAC 1005
|||:||||:||||:||||:||||:
27 TTGGCMTCTGCTGGTGGCCCTTCAC 1

701-935-10/c
ence 10. Application US/07701935
re No. 533595
ERAL INFORMATION:
PLICANT: Strader, C. D.
PLICANT: Fong, T. M.

```

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1  TITLE OF INVENTION:  Method of Using Human Neurokinin-1
2  TITLE OF INVENTION:  Receptor Short Form
3  NUMBER OF SEQUENCES:  27
4  CORRESPONDENCE ADDRESS:
5  ADDRESSEE:  Merck & Co., Inc.
6  STREET:  P.O. Box 2000
7  CITY:  Rahway
8  STATE:  New Jersey
9  COUNTRY:  US
10 ZIP:  07065-0907
11
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE:  Floppy disk
14 COMPUTER:  IBM PC compatible
15 OPERATING SYSTEM:  PC-DOS/MS-DOS
16 SOFTWARE:  Patentin Release #1.0, Version #1.25
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER:  US/07/701,935
19 FILING DATE:  19910517
20
21 CLASSIFICATION:  435
22 ATTORNEY/AGENT INFORMATION:
23 NAME:  Nicholson, William H.
24 REGISTRATION NUMBER:  25,147
25 REFERENCE/DOCKET NUMBER:  18409
26 TELECOMMUNICATION INFORMATION:
27 TELEPHONE:  (908) 594-4720
28 TELEFAX:  (908) 594-5315
29
30 INFORMATION FOR SEQ ID NO:  10:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH:  21 base pairs
33 TYPE:  NUCLEIC ACID
34 STRANDEDNESS:  single
35 TOPOLOGY:  linear
36 MOLECULE TYPE:
37
38 US-07-701-935-10
39
40 Query Match          1.2%; Score 21; DB 1; Length 21;
41 Best Local Similarity 100.0%; Pred. No. 23;
42 Matches  21; Conservative  0; Mismatches  0; Indels  0; Gaps  0;
43
44 QY          559  TTGGCAGTATCTACTCCATG  579
45          |||||
46 Db          21  TTGGCAGTATCTACTCCATG  1
47
48 RESULT 37
49 US-07-701-935-13/c
50 ; Sequence 13, Application US/07701935
51 ; Patent No. 5336595
52 ; GENERAL INFORMATION:
53 ; APPLICANT:  Strader, C. D.
54 ; TITLE OF INVENTION:  Method of Using Human Neurokinin-1
55 ; TITLE OF INVENTION:  Receptor Short Form
56 ; NUMBER OF SEQUENCES:  27
57 ; CORRESPONDENCE ADDRESS:
58 ; ADDRESSEE:  Merck & Co., Inc.
59 ; STREET:  P.O. Box 2000
60 ; CITY:  Rahway
61 ; STATE:  New Jersey
62 ; COUNTRY:  US
63 ; ZIP:  07065-0907
64
65 COMPUTER READABLE FORM:
66 MEDIUM TYPE:  Floppy disk
67 COMPUTER:  IBM PC compatible
68 OPERATING SYSTEM:  PC-DOS/MS-DOS
69 SOFTWARE:  Patentin Release #1.0, Version #1.25
70 CURRENT APPLICATION DATA:
71 APPLICATION NUMBER:  US/07/701,935
72 FILING DATE:  19910517
73
74 CLASSIFICATION:  435
75 ATTORNEY/AGENT INFORMATION:
76 NAME:  Nicholson, William H.
77 REGISTRATION NUMBER:  25,147
78 REFERENCE/DOCKET NUMBER:  18409
79 TELECOMMUNICATION INFORMATION:
80 TELEPHONE:  (908) 594-4720
81 TELEFAX:  (908) 594-5315
82
83 INFORMATION FOR SEQ ID NO:  10:
84 SEQUENCE CHARACTERISTICS:
85 LENGTH:  21 base pairs
86 TYPE:  NUCLEIC ACID
87 STRANDEDNESS:  single
88 TOPOLOGY:  linear
89 MOLECULE TYPE:
90
91 US-07-701-935-10

```


URGENT APPLICATION DATA:
APPLICATION NUMBER: US/07/701,935
FILING DATE: 19910517
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nicholson, William H.
REGISTRATION NUMBER: 25,147
REFERENCE/DOCKET NUMBER: 18409
ELECTRONIC INFORMATION:
TELEPHONE: (908) 594-5315
TELEFAX: (908) 594-4720
ORAMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
701-935-18

Y Match 1.2%; Score 21; DB 1; Length 21;
Local Similarity 100.0%; Pred. No. 23;
hes 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

956 TGATGATTGCTGCTGTGCA 976
|||||
1 TGATGATTGCTGCTGTGCA 21

41
117-965-10/c
ence 10, Application US/08117965
nt No. 548486
ERAL INFORMATION:
.APPLICANT: Tung, Fong M.
PLICANT: Cathrine, Strader D.
TITLE OF INVENTION: Human Neurokinin-1 Receptor
UMBER OF SEQUENCES: 27
ORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: US
ZIP: 07065-0907
OMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
URGENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,965
FILING DATE:
CLASSIFICATION: 514
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 691,197
FILING DATE: 25-APR-1991
TTORNEY/AGENT INFORMATION:
NAME: Nicholson, William H.
REGISTRATION NUMBER: 25,147
REFERENCE/DOCKET NUMBER: 18387
ELECTRONIC INFORMATION:
TELEPHONE: (908) 594-5315
TELEFAX: (908) 594-4720
ORAMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
117-965-10

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 559 TTGGCAGTATCTATCTCATG 579
|||||
Db 21 TTGGCAGTATCTATCTCATG 1

RESULT 42
US-08-117-965-13/c
Sequence 13, Application US/08117965
Patent No. 548486
GENERAL INFORMATION:
APPLICANT: Tung, Fong M.
PLICANT: Cathrine, Strader D.
TITLE OF INVENTION: Human Neurokinin-1 Receptor
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,965
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 691,197
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Nicholson, William H.
REGISTRATION NUMBER: 25,147
REFERENCE/DOCKET NUMBER: 18387
ELECTRONIC INFORMATION:
TELEPHONE: (908) 594-5315
TELEFAX: (908) 594-4720
ORAMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
US-08-117-965-13

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 836 TGCTGTGATTGCTATGAT 856
|||||
Db 21 TGCTGTGATTGCTATGAT 1

RESULT 43
US-08-117-965-15/c
Sequence 15, Application US/08117965
Patent No. 548486
GENERAL INFORMATION:
APPLICANT: Tung, Fong M.
PLICANT: Cathrine, Strader D.
TITLE OF INVENTION: Human Neurokinin-1 Receptor
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.

REFERENCE/DOCKET NUMBER: 18409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-5315
TELEFAX: (908) 594-4720
FORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
-701-935-13

cy Match 1.2%; Score 21; DB 1; Length 21;
Local Similarity 100.0%; Pred. No. 23;
ches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

836 TGCTGTGATTGGCTATGTCAT 856
|||||
21 TGCTGTGATTGGCTATGTCAT 1

38
-701-935-15/c
ence 15, Application US/07701935
ant No. 5336595
GENERAL INFORMATION:
APPLICANT: Strader, C. D.
APPLICANT: Fong, T. M.
TITLE OF INVENTION: Method of Using Human Neurokinin-1
TITLE OF INVENTION: Receptor Short Form
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: US
ZIP: 07065-0907

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/701,935
FILING DATE: 19910517
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nicholson, William H.
REGISTRATION NUMBER: 25,147
REFERENCE/DOCKET NUMBER: 18409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-5315
TELEFAX: (908) 594-4720
FORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
-701-935-15

cy Match 1.2%; Score 21; DB 1; Length 21;
Local Similarity 100.0%; Pred. No. 23;
ches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

956 TGATGATTGCGTGGTGTGCA 976
|||||
21 TGATGATTGCGTGGTGTGCA 1

RESULT 39
US-07-701-935-17
Sequence 17, Application US/07701935
Patent No. 5336595
GENERAL INFORMATION:
APPLICANT: Strader, C. D.
APPLICANT: Fong, T. M.
TITLE OF INVENTION: Method of Using Human Neurokinin-1
TITLE OF INVENTION: Receptor Short Form
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: US
ZIP: 07065-0907

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/701,935
FILING DATE: 19910517
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nicholson, William H.
REGISTRATION NUMBER: 25,147
REFERENCE/DOCKET NUMBER: 18409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-5315
TELEFAX: (908) 594-4720
FORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
US-07-701-935-17

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 924 GCAAGTCTCTGCCAGCGCA 944
|||||
Db 1 GCAAGTCTCTGCCAGCGCA 21

RESULT 40
US-07-701-935-18
Sequence 18, Application US/07701935
Patent No. 5336595
GENERAL INFORMATION:
APPLICANT: Strader, C. D.
APPLICANT: Fong, T. M.
TITLE OF INVENTION: Method of Using Human Neurokinin-1
TITLE OF INVENTION: Receptor Short Form
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: US
ZIP: 07065-0907

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

STREET: P.O. Box 2000
 CITY: Rahway
 STATE: New Jersey
 COUNTRY: US
 ZIP: 07065-0907
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/117,965
 FILING DATE:
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 691,197
 FILING DATE: 25-APR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Nicholson, William H.
 REGISTRATION NUMBER: 25,147
 REFERENCE/DOCKET NUMBER: 18387
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 594-5315
 TELEFAX: (908) 594-4720
 FORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE:
 -117-965-15

Query Match 1.2%; Score 21; DB 1; Length 21;
 Local Similarity 100.0%; Pred. No. 23;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

956 TGATGATTGTCGTGTCGCA 976
 21 TGATGATTGTCGTGTCGCA 1

117-965-17
 Hence 17, Application US/08117965
 Patent No. 5484886
 GENERAL INFORMATION:
 APPLICANT: Tung, Fong M.
 ATTORNEY/AGENT INFORMATION:
 NAME: Cathrine, Strader D.
 REGISTRATION NUMBER: 25,147
 REFERENCE/DOCKET NUMBER: 18387
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 594-5315
 TELEFAX: (908) 594-4720
 FORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE:
 -117-965-17

Query Match 1.2%; Score 21; DB 1; Length 21;
 Local Similarity 100.0%; Pred. No. 23;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

956 TGATGATTGTCGTGTCGCA 976
 21 TGATGATTGTCGTGTCGCA 1

117-965-17
 Hence 17, Application US/08117965
 Patent No. 5484886
 GENERAL INFORMATION:
 APPLICANT: Tung, Fong M.
 ATTORNEY/AGENT INFORMATION:
 NAME: Cathrine, Strader D.
 REGISTRATION NUMBER: 25,147
 REFERENCE/DOCKET NUMBER: 18387
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 594-5315
 TELEFAX: (908) 594-4720
 FORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE:
 -117-965-17

Query Match 1.2%; Score 21; DB 1; Length 21;
 Local Similarity 100.0%; Pred. No. 23;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

956 TGATGATTGTCGTGTCGCA 976
 21 TGATGATTGTCGTGTCGCA 1

REFERENCE/DOCKET NUMBER: 18387
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 594-5315
 TELEFAX: (908) 594-4720
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE:
 -117-965-17

Query Match 1.2%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 924 GCAAGTCTCTGCCAAGCGCAA 944
 DB 1 GCAAGTCTCTGCCAAGCGCAA 21

RESULT 45
 US-08-117-965-18
 Sequence 18, Application US/08117965
 Patent No. 5484886
 GENERAL INFORMATION:
 APPLICANT: Tung, Fong M.
 ATTORNEY/AGENT INFORMATION:
 NAME: Cathrine, Strader D.
 REGISTRATION NUMBER: 25,147
 REFERENCE/DOCKET NUMBER: 18387
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 594-5315
 TELEFAX: (908) 594-4720
 FORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE:
 -117-965-18

Query Match 1.2%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 956 TGATGATTGTCGTGTCGCA 976
 DB 1 TGATGATTGTCGTGTCGCA 21

117-965-17
 Hence 17, Application US/08117965
 Patent No. 5484886
 GENERAL INFORMATION:
 APPLICANT: Tung, Fong M.
 ATTORNEY/AGENT INFORMATION:
 NAME: Cathrine, Strader D.
 REGISTRATION NUMBER: 25,147
 REFERENCE/DOCKET NUMBER: 18387
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 594-5315
 TELEFAX: (908) 594-4720
 FORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE:
 -117-965-17

Query Match 1.2%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 956 TGATGATTGTCGTGTCGCA 976
 DB 1 TGATGATTGTCGTGTCGCA 21

46
117-965-22/c
ence 22, Application US/08117965
nt No. 548486
ERAL INFORMATION:
PLICANT: Tung, Fong M.
PLICANT: Cathline, Strader D.
TITLE OF INVENTION: Human Neurokinin-1 Receptor
UMBER OF SEQUENCES: 27
ORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: US
ZIP: 07065-0907
OMPUTER READABLE FORM:
EDIUM TYPE: Floppy disk
OMPUTER: IBM PC compatible
PERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
URRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,965
ILING DATE:
CLASSIFICATION: 514
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 691,197
ILING DATE: 25-APR-1991
TTOREY/AGENT INFORMATION:
NAME: Nicholson, William H.
EGISTRATION NUMBER: 25,147
EREFERENCE/DOCKET NUMBER: 18387
ELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-5315
TELEFAX: (908) 594-4720
ORMATION FOR SEQ ID NO: 22:
EQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
OLECULE TYPE:
117-965-22
Y Match 1.2%; Score 21; DB 1; Length 21;
Local Similarity 100.0%; Pred. No. 23;
hes 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1567 AGGAAACATTCATCCTTG 1587
21 AGGAAACATTCATCCTTG 1
47
513-974B-263
ence 263, Application US/08513974B
nt No. 6114139
ERAL INFORMATION:
PLICANT: Hinuma, Shuji
PLICANT: Hosoya, Masaki
PLICANT: Fujii, Ryo
PLICANT: Ohtaki, Tetsuya
PLICANT: Fukusumi, Shoji
PLICANT: Ohgi, Kazuhito
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
UMBER OF SEQUENCES: 380
ORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston

STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
EDIUM TYPE: Floppy disk
OMPUTER: IBM PC compatible
PERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
ILING DATE: 14-SEP-1995
CLASSIFICATION: 536
RIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
ILING DATE: 10-AUG-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
ILING DATE: 19-AUG-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
ILING DATE: 16-MAR-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
ILING DATE: 20-JAN-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
ILING DATE: 28-DEC-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
ILING DATE: 02-NOV-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
ILING DATE: 30-SEP-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
ILING DATE: 30-SEP-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
ILING DATE: 11-AUG-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
ILING DATE: 11-AUG-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
ILING DATE: 11-AUG-1994
TTOREY/AGENT INFORMATION:
NAME: Resnick, David S.
EGISTRATION NUMBER: 34,235
EREFERENCE/DOCKET NUMBER: 45753
ELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
FORMATION FOR SEQ ID NO: 263:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
OLECULE TYPE: CDNA
US-08-513-974B-263
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
979 TTGCGCATCTGCTGCTGCC 999
1 TTGCGCATCTGCTGCTGCC 21
RESULT 48
US-08-513-974B-264
; Sequence 264, Application US/08513974B

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ENT No. 6114139
VERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Ontaki, Tetsuya
APPLICANT: Fukushima, Shoji
APPLICANT: Ohji, Kazuhiko
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
FORMATION FOR SEQ ID NO: 264:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

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STATE: New Jersey
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
URGENT APPLICATION DATA:
APPLICATION NUMBER: US/07/701,935
FILING DATE: 19910517
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nicholson, William H.
REGISTRATION NUMBER: 25,147
REFERENCE/DOCKET NUMBER: 18409
ELECTRONIC INFORMATION:
TELEPHONE: (908) 594-5315
TELEFAX: (908) 594-4720
ORAMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
701-935-6
Y Match 1.2%; Score 20.8; DB 1; Length 24;
Local Similarity 91.7%; Pred. No. 32;
hes 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
1051 AAGTTATCCAGCAGGTCTACTG 1074
24 AAGTTCATCCAGCAGGTGTAAGTCTG 1
51
117-965-6/c
ence 6, Application US/08117965
nt No. 5484886
BRAL INFORMATION:
PLICANT: Tung, Pong M.
PLICANT: Cathrine, Strader D.
TITLE OF INVENTION: Human Neurokinin-1 Receptor
UMBER OF SEQUENCES: 27
ORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
URGENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,965
FILING DATE:
CLASSIFICATION: 514
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 691,197
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Nicholson, William H.
REGISTRATION NUMBER: 25,147
REFERENCE/DOCKET NUMBER: 18387
ELECTRONIC INFORMATION:
TELEPHONE: (908) 594-5315
TELEFAX: (908) 594-4720
ORAMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
US-08-117-965-6
Query Match 1.2%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 32;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1051 AAGTTATCCAGCAGGTCTACTG 1074
Db 24 AAGTTCATCCAGCAGGTGTAAGTCTG 1
RESULT 52
US-08-513-974B-231
Sequence 231, Application US/08513974B
Patent No. 6114139
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Fukusumi, Shoji
APPLICANT: Ohgi, Kazuhito
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274

FILING DATE: 11-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189273
 FILING DATE: 11-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189272
 FILING DATE: 11-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Resnick, David S.
 REGISTRATION NUMBER: 34,235
 REFERENCE/DOCKET NUMBER: 45753
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 FORMATION FOR SEQ ID NO: 231:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 513-974B-231
 Match 1.2%; Score 20.8; DB 1; Length 24;
 Local Similarity 91.7%; Pred. No. 32;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 979 TTGGCATCTGCTGGCTGCCCTTC 1002
 1 TTGGCATCTGCTGGCTGCCCTAC 24
 F 53
 513-974B-233
 Invention 233, Application US/08513974B
 Patent No. 6114139
 GENERAL INFORMATION:
 APPLICANT: Hinuma, Shuji
 APPLICANT: Hosoya, Masaki
 APPLICANT: Fujii, Ryo
 APPLICANT: Ontaki, Tetsuya
 APPLICANT: Fukusumi, Shoji
 APPLICANT: Ohgi, Kazuhiro
 TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
 TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
 NUMBER OF SEQUENCES: 380
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/513,974B
 FILING DATE: 14-SEP-1995
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP95/01599
 FILING DATE: 10-AUG-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-093989
 FILING DATE: 19-AUG-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-057186
 FILING DATE: 16-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-007177

FILING DATE: 20-JAN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-326611
 FILING DATE: 28-DEC-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-270017
 FILING DATE: 02-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-236357
 FILING DATE: 30-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-236356
 FILING DATE: 30-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189274
 FILING DATE: 11-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189273
 FILING DATE: 11-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189272
 FILING DATE: 11-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Resnick, David S.
 REGISTRATION NUMBER: 34,235
 REFERENCE/DOCKET NUMBER: 45753
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 233:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-513-974B-233
 Query Match 1.2%; Score 20.8; DB 1; Length 24;
 Best Local Similarity 91.7%; Pred. No. 32;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 979 TTGGCATCTGCTGGCTGCCCTTC 1002
 Db 1 TTGGCATCTGCTGGCTGCCCTAC 24
 RESULT 54
 US-08-513-974B-237
 Invention 237, Application US/08513974B
 Patent No. 6114139
 GENERAL INFORMATION:
 APPLICANT: Hinuma, Shuji
 APPLICANT: Hosoya, Masaki
 APPLICANT: Fujii, Ryo
 APPLICANT: Ontaki, Tetsuya
 APPLICANT: Fukusumi, Shoji
 APPLICANT: Ohgi, Kazuhiro
 TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
 TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
 NUMBER OF SEQUENCES: 380
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
RIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
ELECTRONIC COMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
ORAMATION FOR SEQ ID NO: 237:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
OLBECUL TYPE: CDNA
513-974B-237

Y Match 1.2%; Score 20.8; DB 1; Length 24;
Local Similarity 91.7%; Pred. No. 32;
hes 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

979 TTGCGCATCTGCTGCTGCCCTTC 1002
|||||
1 TTCACCCCTCTGCTGCTGCCCTTC 24

55
396-196G-67919
ence 67919, Application US/09396196G
nt No. 6821724
RAL INFORMATION:
LICANT: Michael Miltmann
LICANT: David Mack
LICANT: David Lockhart
LICANT: Affymetrix, Inc.
LE OF INVENTION: Methods of Genetic Analysis
E REFERENCE: 3101.1

CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 67919
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-67919

Query Match 1.2%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 35;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1382 ACTCGAGACCATGACGAGAGCT 1405
|||||
Db 2 ACTCGAGACCATGACGAGAGCT 25

RESULT 56
US-08-513-974B-15/c
Sequence 15, Application US/08513974B
Patent No. 6114139
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Fukusumi, Shoji
APPLICANT: Ohgi, Kazuhiko
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 6-226356
 FILING DATE: 30-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189274
 FILING DATE: 11-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189273
 FILING DATE: 11-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189272
 FILING DATE: 11-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Resnick, David S.
 REGISTRATION NUMBER: 34,235
 REFERENCE/DOCKET NUMBER: 45753
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "synthetic DNA"
 FEATURE: OTHER INFORMATION: N = inosine
 -513-974B-15

Query Match 1.2%; Score 20.6; DB 1; Length 24;
 Local Similarity 70.8%; Pred. No. 34;
 Matches 17; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

979 TTGGCCATCTGCTGCTGCCCTTC 1002
 ||:||||:||||:||||:||||:|
 24 TTYGCCNTSTGCTGCTGNTSCCWC 1

57
 -513-974B-230
 Invention 230, Application US/08513974B
 Patent No. 6114139
 GENERAL INFORMATION:
 APPLICANT: Hinuma, Shuji
 APPLICANT: Hosoya, Masaki
 APPLICANT: Fujii, Ryo
 APPLICANT: Ohtaki, Tetsuya
 APPLICANT: Fukusumi, Shoji
 APPLICANT: Ohgi, Kazuhiko
 TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
 TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
 NUMBER OF SEQUENCES: 380
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/513,974B
 FILING DATE: 14-SEP-1995
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP95/01599
 FILING DATE: 10-AUG-1995
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 7-093989
 FILING DATE: 19-AUG-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-057186
 FILING DATE: 16-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-007177
 FILING DATE: 20-JAN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-326611
 FILING DATE: 28-DEC-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-270017
 FILING DATE: 02-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-236357
 FILING DATE: 30-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-226356
 FILING DATE: 30-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189274
 FILING DATE: 11-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189273
 FILING DATE: 11-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189272
 FILING DATE: 11-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Resnick, David S.
 REGISTRATION NUMBER: 34,235
 REFERENCE/DOCKET NUMBER: 45753
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 230:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: unknown
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 -US-08-513-974B-230

Query Match 1.2%; Score 20.6; DB 1; Length 24;
 Best Local Similarity 70.8%; Pred. No. 34;
 Matches 17; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 979 TTGGCCATCTGCTGCTGCCCTTC 1002
 ||:||||:||||:||||:||||:|
 Db 1 TTYGCCNTSTGCTGCTGNTSCCWC 24

RESULT 58
 US-09-461-436B-15/c
 Sequence 15, Application US/09461436B
 Patent No. 6538107
 GENERAL INFORMATION:
 APPLICANT: Shuji Hinuma
 APPLICANT: Yasuaki Ito
 APPLICANT: Ryo Fujii
 TITLE OF INVENTION: G Protein Coupled Receptor Protein,
 PRODUCTION, AND USE THEREOF
 NUMBER OF SEQUENCES: 61
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Edwards & Angell, LLP
 STREET: 101 Federal Street
 CITY: BOSTON
 STATE: MA
 COUNTRY: USA
 ZIP: 02209
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/461,436B
FILING DATE: 14-Dec-1999
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/513,974
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
APPLICATION NUMBER: 7-093989
FILING DATE: 19-APR-1995
APPLICATION NUMBER: 7-057186
FILING DATE: 16-MAR-1995
APPLICATION NUMBER: 7-007177
FILING DATE: 20-JAN-1995
APPLICATION NUMBER: 6-326611
FILING DATE: 28-DEC-1994
APPLICATION NUMBER: 6-270017
FILING DATE: 02-NOV-1994
APPLICATION NUMBER: 6-236357
FILING DATE: 30-SEP-1994
APPLICATION NUMBER: 6-236356
FILING DATE: 30-SEP-1994
APPLICATION NUMBER: 6-189274
FILING DATE: 11-AUG-1994
APPLICATION NUMBER: 6-189273
FILING DATE: 11-AUG-1994
APPLICATION NUMBER: 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: COMLIN, DAVID G.
REGISTRATION NUMBER: <unknown>
REFERENCE/DOCKET NUMBER: 45753 DIV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-439-4444
TELEFAX: 617-439-4170
FORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 24
TYPE: Nucleic acid
STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
FEATURE:
OTHER INFORMATION: /note= N is inosine; W is A or T;
S is G or C; K is G or T; R is A or G."
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
461-436B-15
v Match 1.2%; Score 20.6; DB 1; Length 24;
Local Similarity 70.8%; Pred. No. 34;
hes 17; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
979 TTGGCCATCTGCTGCTGCTCCCTTC 1002
|||||:|||||:|||||:
24 TTGGCCTGTGCTGCTGCCCMWC 1
59
513-974B-235
ence 235, Application US/08513974B
nt No. 6114139
ERAL INFORMATION:
.PLICANT: Hinuma, Shuji
.PLICANT: Hosoya, Masaki
.PLICANT: Fujii, Ryo
.PLICANT: Ohtaki, Tetsuya
.PLICANT: Fukusumi, Shoji

APPLICANT: Ohgi, Kazuhiro
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1945
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
FORMATION FOR SEQ ID NO: 235:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-513-974B-235
Query Match 1.2%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 33;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

979 TTGGCATCTGCTGCTGCT 1000
 |||||
 1 TTGGCATCTGCTGCTGCT 22

60
 -396-196G-67918
 ence 67918, Application US/09396196G
 nt No. 6821724

GENERAL INFORMATION:

PLICANT: Michael Miltmann

PLICANT: David Mack

PLICANT: David Lockhart

PLICANT: Affymetrix, Inc.

FILE OF INVENTION: Methods of Genetic Analysis

REFERENCE: 3101.1

RENT APPLICATION NUMBER: US/09/396,196G

RENT FILING DATE: 1999-09-15

OR APPLICATION NUMBER: 60/100,678

OR FILING DATE: 1998-09-17

BER OF SEQ ID NOS: 127806

FTWARE: FastSeq for Windows Version 4.0

ID NO 67918

LENGTH: 25

TYPE: DNA

ORGANISM: mus musculus

-396-196G-67918

Match 1.1%; Score 20.2; DB 1; Length 25;
 Local Similarity 88.0%; Pred. No. 42;
 hes 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1375 CGAAGTACTCCAGACCATGACAG 1399
 |||||
 1 CGAAGCACTCGAAGCATGACAG 25

61
 -396-196G-67927
 ence 67927, Application US/09396196G
 nt No. 6821724

GENERAL INFORMATION:

PLICANT: Michael Miltmann

PLICANT: David Mack

PLICANT: David Lockhart

PLICANT: Affymetrix, Inc.

FILE OF INVENTION: Methods of Genetic Analysis

REFERENCE: 3101.1

RENT APPLICATION NUMBER: US/09/396,196G

RENT FILING DATE: 1999-09-15

OR APPLICATION NUMBER: 60/100,678

OR FILING DATE: 1998-09-17

BER OF SEQ ID NOS: 127806

FTWARE: FastSeq for Windows Version 4.0

ID NO 67927

LENGTH: 25

TYPE: DNA

ORGANISM: mus musculus

-396-196G-67927

Match 1.1%; Score 20.2; DB 1; Length 25;
 Local Similarity 88.0%; Pred. No. 42;
 hes 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1165 GCCTTCGGTGTGCTGCTGCT 1189
 |||||
 1 GCCTTCGGTGTGCTGCTGCT 25

62
 -396-196G-67930
 ence 67930, Application US/09396196G
 nt No. 6821724

GENERAL INFORMATION:
 APPLICANT: Michael Miltmann
 APPLICANT: David Mack
 APPLICANT: David Lockhart
 APPLICANT: Affymetrix, Inc.
 TITLE OF INVENTION: Methods of Genetic Analysis
 FILE REFERENCE: 3101.1
 CURRENT APPLICATION NUMBER: US/09/396,196G
 CURRENT FILING DATE: 1999-09-15
 PRIOR APPLICATION NUMBER: 60/100,678
 PRIOR FILING DATE: 1998-09-17
 NUMBER OF SEQ ID NOS: 127806
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 67930
 LENGTH: 25
 TYPE: DNA
 ORGANISM: mus musculus
 US-09-396-196G-67930

Query Match 1.1%; Score 20.2; DB 1; Length 25;
 Best Local Similarity 88.0%; Pred. No. 42;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1231 TATCTCCAGACCGGCGAGTGT 1255
 |||||
 Db 1 TACTTCAGACCGGCGAGTGT 25

RESULT 63

US-09-396-196G-67931

Sequence 67931, Application US/09396196G

Patent No. 6821724

GENERAL INFORMATION:

APPLICANT: Michael Miltmann

APPLICANT: David Mack

APPLICANT: David Lockhart

APPLICANT: Affymetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis

FILE REFERENCE: 3101.1

CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: 60/100,678

PRIOR FILING DATE: 1998-09-17

NUMBER OF SEQ ID NOS: 127806

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 67931

LENGTH: 25

TYPE: DNA

ORGANISM: mus musculus

US-09-396-196G-67931

Query Match 1.1%; Score 20.2; DB 1; Length 25;
 Best Local Similarity 88.0%; Pred. No. 42;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1237 CAGACCCAGGCGAGTGTACAAAG 1261
 |||||
 Db 1 CAGACCCAGGCGAGTGTACAAAG 25

RESULT 64

US-07-701-935-11/C

Sequence 11, Application US/07701935

Patent No. 5336595

GENERAL INFORMATION:

APPLICANT: Strader, C. D.

APPLICANT: Fong, T. M.

TITLE OF INVENTION: Method of Using Human Neurokinin-1

TITLE OF INVENTION: Receptor Short Form

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merck & Co., Inc.

STREET: P.O. Box 2000

CITY: Rahway
STATE: New Jersey
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/701,935
FILING DATE: 19910517
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nicholson, William H.
REGISTRATION NUMBER: 25,147
REFERENCE/DOCKET NUMBER: 18409
TELEPHONE: (908) 594-4720
TELEFAX: (908) 594-5315
ORAMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
701-935-11

Y Match 1.1%; Score 20; DB 1; Length 20;
Local Similarity 100.0%; Pred. No. 29;
hes 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

601 TACATGCCATCATCATCC 620
20 TACATGCCATCATCATCC 1

701-935-12/C
ence 12, Application US/07701935
nt No. 5336595
ERAL INFORMATION:
PLICANT: Strader, C. D.
PLICANT: Fong, T. M.
TITLE OF INVENTION: Method of Using Human Neurokinin-1
TITLE OF INVENTION: Receptor Short Form
UMBER OF SEQUENCES: 27
ORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/701,935
FILING DATE: 19910517
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nicholson, William H.
REGISTRATION NUMBER: 25,147
REFERENCE/DOCKET NUMBER: 18409
TELEPHONE: (908) 594-4720
TELEFAX: (908) 594-5315
ORAMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
US-07-701-935-12

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 637 TCAGCCACAGCCCAAGT 656
Db 20 TCAGCCACAGCCCAAGT 1

RESULT 66
US-07-701-935-14/C
Sequence 14, Application US/07701935
Patent No. 5336595
GENERAL INFORMATION:
APPLICANT: Strader, C. D.
APPLICANT: Fong, T. M.
TITLE OF INVENTION: Method of Using Human Neurokinin-1
TITLE OF INVENTION: Receptor Short Form
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/701,935
FILING DATE: 19910517
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nicholson, William H.
REGISTRATION NUMBER: 25,147
REFERENCE/DOCKET NUMBER: 18409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-5315
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
US-07-701-935-14

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 862 GTAGTGGAAATCAGCTATG 881
Db 20 GTAGTGGAAATCAGCTATG 1

RESULT 67
US-07-701-935-16/C
Sequence 16, Application US/07701935
Patent No. 5336595
GENERAL INFORMATION:
APPLICANT: Strader, C. D.

APPLICANT: Fong, T. M.
 TITLE OF INVENTION: Method of Using Human Neurokinin-1
 TITLE OF INVENTION: Receptor Short Form
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Merck & Co., Inc.
 STREET: P. O. Box 2000
 CITY: Rahway
 STATE: New Jersey
 COUNTRY: US
 ZIP: 07065-0907
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/701,935
 FILING DATE: 19910517
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Nicholson, William H.
 REGISTRATION NUMBER: 25,147
 REFERENCE/DOCKET NUMBER: 18409
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 594-5315
 TELEFAX: (908) 594-4720
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE:
 -701-935-16
 Local Similarity 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1012 TTCCTCTGCGCTACATCAA 1031
 |||||
 20 TTCCTCTGCGCTACATCAA 1

168
 -701-935-19
 ence 19, Application US/07701935
 ant No. 5336595
 VERAL INFORMATION:
 APPLICANT: Strader, C. D.
 APPLICANT: Fong, T. M.
 TITLE OF INVENTION: Method of Using Human Neurokinin-1
 TITLE OF INVENTION: Receptor Short Form
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Merck & Co., Inc.
 STREET: P. O. Box 2000
 CITY: Rahway
 STATE: New Jersey
 COUNTRY: US
 ZIP: 07065-0907
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/701,935
 FILING DATE: 19910517
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Nicholson, William H.

REGISTRATION NUMBER: 25,147
 REFERENCE/DOCKET NUMBER: 18409
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 594-5315
 TELEFAX: (908) 594-4720
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE:
 US-07-701-935-19
 Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1000 TTCACATCTTCTCTCTCT 1019
 |||||
 Db 1 TTCACATCTTCTCTCTCT 20

RESULT 69
 US-07-701-935-20
 Sequence 20, Application US/07701935
 Patent No. 5336595
 GENERAL INFORMATION:
 APPLICANT: Strader, C. D.
 APPLICANT: Fong, T. M.
 TITLE OF INVENTION: Method of Using Human Neurokinin-1
 TITLE OF INVENTION: Receptor Short Form
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Merck & Co., Inc.
 STREET: P. O. Box 2000
 CITY: Rahway
 STATE: New Jersey
 COUNTRY: US
 ZIP: 07065-0907
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/701,935
 FILING DATE: 19910517
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Nicholson, William H.
 REGISTRATION NUMBER: 25,147
 REFERENCE/DOCKET NUMBER: 18409
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 594-5315
 TELEFAX: (908) 594-4720
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE:
 US-07-701-935-20
 Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1023 CTACATCAACCCAGATCTCT 1042
 |||||
 Db 1 CTACATCAACCCAGATCTCT 20

70
117-965-11/c
ence 11, Application US/08117965
nt No. 548486
ERAL INFORMATION:
PLICANT: Tung, Fong M.
PLICANT: Cathrine, Strader D.
TITLE OF INVENTION: Human Neurokinin-1 Receptor
UMBER OF SEQUENCES: 27
ORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: US
ZIP: 07065-0907
OMPUTER READABLE FORM:
EDIUM TYPE: Floppy disk
OMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
URRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,965
ILING DATE:
CLASSIFICATION: 514
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 691,197
ILING DATE: 25-APR-1991
TTORENEY/AGENT INFORMATION:
NAME: Nicholson, William H.
REGISTRATION NUMBER: 25,147
REFERENCE/DOCKET NUMBER: 18387
ELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-5315
TELEFAX: (908) 594-4720
ORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
OLECULE TYPE:
117-965-11
Y Match 1.1%; Score 20; DB 1; Length 20;
Local Similarity 100.0%; Pred. No. 29;
hes 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
601 TACATGCCATCATACATCC 620
|||||
20 TACATGCCATCATACATCC 1
71
117-965-12/c
ence 12, Application US/08117965
nt No. 548486
ERAL INFORMATION:
PLICANT: Tung, Fong M.
PLICANT: Cathrine, Strader D.
TITLE OF INVENTION: Human Neurokinin-1 Receptor
UMBER OF SEQUENCES: 27
ORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: US
ZIP: 07065-0907
OMPUTER READABLE FORM:
EDIUM TYPE: Floppy disk
OMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,965
ILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 691,197
ILING DATE: 25-APR-1991
TTORENEY/AGENT INFORMATION:
NAME: Nicholson, William H.
REGISTRATION NUMBER: 25,147
REFERENCE/DOCKET NUMBER: 18387
ELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-5315
TELEFAX: (908) 594-4720
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
OLECULE TYPE:
US-08-117-965-12
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 637 TCAGCACAGCCACCAAGT 656
|||||
Db 20 TCAGCACAGCCACCAAGT 1
RESULT 72
US-08-117-965-14/c
Sequence 14, Application US/08117965
Patent No. 548486
GENERAL INFORMATION:
PLICANT: Tung, Fong M.
PLICANT: Cathrine, Strader D.
TITLE OF INVENTION: Human Neurokinin-1 Receptor
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: US
ZIP: 07065-0907
OMPUTER READABLE FORM:
EDIUM TYPE: Floppy disk
OMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,965
ILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 691,197
ILING DATE: 25-APR-1991
TTORENEY/AGENT INFORMATION:
NAME: Nicholson, William H.
REGISTRATION NUMBER: 25,147
REFERENCE/DOCKET NUMBER: 18387
ELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-5315
TELEFAX: (908) 594-4720
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
-117-965-14

Query Match 1.1%; Score 20; DB 1; Length 20;
Local Similarity 100.0%; Pred. No. 29;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

862 GTACGTGGATCATCATG 881
|||||
20 GTAGTGGATCATCATG 1

r 73
-117-965-16/C
ence 16, Application US/08117965
ent No. 5484886
GENERAL INFORMATION:
APPLICANT: Tung, Fong M.
TITLE OF INVENTION: Human Neurokinin-1 Receptor
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,965
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 691,197
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Nicholson, William H.
REGISTRATION NUMBER: 25,147
REFERENCE/DOCKET NUMBER: 18387
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-5315
TELEFAX: (908) 594-4720
FORMATION FOR SEQ. ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
-117-965-16

Query Match 1.1%; Score 20; DB 1; Length 20;
Local Similarity 100.0%; Pred. No. 29;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1012 TTCCTCTGCTCATCA 1031
|||||
20 TTCCTCTGCTCATCA 1

r 74
-117-965-19
ence 19, Application US/08117965
ent No. 5484886
GENERAL INFORMATION:
APPLICANT: Tung, Fong M.

APPLICANT: Cathrine, Strader D.
TITLE OF INVENTION: Human Neurokinin-1 Receptor
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,965
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 691,197
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Nicholson, William H.
REGISTRATION NUMBER: 25,147
REFERENCE/DOCKET NUMBER: 18387
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-5315
TELEFAX: (908) 594-4720
FORMATION FOR SEQ. ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
US-08-117-965-19

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1000 TTCACATCTTCTCTCT 1019
|||||
Db 1 TTCACATCTTCTCTCT 20

RESULT 75
US-08-117-965-20
Sequence 20, Application US/08117965
Patent No. 5484886
GENERAL INFORMATION:
APPLICANT: Tung, Fong M.
TITLE OF INVENTION: Human Neurokinin-1 Receptor
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,965
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 691,197
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Nicholson, William H.
REGISTRATION NUMBER: 25,147
ELECTRONIC/DOCKET NUMBER: 18387
TELEPHONE: (908) 594-5315
TELEFAX: (908) 594-4720
ORAMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
117-965-20

Y Match 1.1%; Score 20; DB 1; Length 20;
Local Similarity 100.0%; Pred. No. 29;
hes 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1023 CTACATCAACCCAGATCTCT 1042
|||||
1 CTACATCAACCCAGATCTCT 20

76
701-935-9/c
since 9, Application US/07701935
nt No. 5336595
ERAL INFORMATION:
PLICANT: Strader, C. D.
PLICANT: Fong, T. M.
TITLE OF INVENTION: Method of Using Human Neurokinin-1
TITLE OF INVENTION: Receptor Short Form
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/701,935
FILING DATE: 19910517
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nicholson, William H.
REGISTRATION NUMBER: 25,147
REFERENCE/DOCKET NUMBER: 18409
ELECTRONIC/DOCKET NUMBER:
TELEPHONE: (908) 594-5315
TELEFAX: (908) 594-4720
ORAMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
701-935-9

Y Match 1.1%; Score 20; DB 1; Length 21;
Local Similarity 100.0%; Pred. No. 32;
hes 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 523 TGCAAGTTCACAACTTCTT 542
|||
Db 21 TGCAAGTTCACAACTTCTT 2

RESULT 77
US-08-117-965-9/c
Sequence 9, Application US/08117965
Patent No. 548486
GENERAL INFORMATION:
APPLICANT: Tung, Fong M.
APPLICANT: Cathrine, Strader D.
TITLE OF INVENTION: Human Neurokinin-1 Receptor
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,965
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 691,197
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Nicholson, William H.
REGISTRATION NUMBER: 25,147
REFERENCE/DOCKET NUMBER: 18387
ELECTRONIC/DOCKET NUMBER:
TELEPHONE: (908) 594-5315
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
US-08-117-965-9

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 523 TGCAAGTTCACAACTTCTT 542
|||
Db 21 TGCAAGTTCACAACTTCTT 2

RESULT 78
US-08-513-974B-240
Sequence 240, Application US/08513974B
Patent No. 6114139
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Fukusumi, Shoji
APPLICANT: Ohgi, Kazuhiro
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
FORMATION FOR SEQ ID NO: 240:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
-513-974B-240

979 TTGGCCTGCTGGCTGCTT 1001
|||||
1 TTGGCCTGCTGGCTGCTT 23

979 Match 1.1%; Score 19.8; DB 1; Length 23;
: Local Similarity 91.3%; Pred. No. 40;
:hes 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 79
US-08-513-974B-257
; Sequence 257, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukushima, Shoji
; APPLICANT: Ohgi, Kazuhiro
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-057186
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-270017
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236357
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236356
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189274
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189273
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 45753
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 257:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
VECTUE TYPE: CDNA
513-974B-257

Y Match 1.1%; Score 19.4; DB 1; Length 21;
Local Similarity 95.2%; Pred. No. 38;
hes 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

979 TTGGCCATCTGCTGCTGCC 999

1 TTGGCCATCTGCTGCTGCC 21

125-012-7
ence 7, Application US/08125012

nt No. 5593972

ERAL INFORMATION:

PLICANT: Weiner, David B.

PLICANT: Williams, William V.

PLICANT: Wang, Bin

PLICANT: Coney, Leslie R.

TITLE OF INVENTION: Genetic Immunization

UMBER OF SEQUENCES: 34

ORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5593972ris

STREET: One Liberty Place 46th Floor

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19103

OMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 mb-MD/JAF

URRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/125,012

FILING DATE:

CLASSIFICATION: 435

RIOR APPLICATION DATA:

APPLICATION NUMBER: 08/029,336

FILING DATE: 11-MAR-1993

NAME:

RIOR APPLICATION DATA:

APPLICATION NUMBER: 08/008,342

FILING DATE: 26-JAN-1993

NAME:

ITORNEY/AGENT INFORMATION:

NAME: Deluca, Mark

REGISTRATION NUMBER: 33,229

REFERENCE/DOCKET NUMBER: APOL-0013

ELCOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

TELEFAX: 215-568-3429

ORMATION FOR SEQ ID NO: 7:

BOUNCE CHARACTERISTICS:

LENGTH: 24 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

OLECUE TYPE: DNA

125-012-7

Y Match 1.1%; Score 19.2; DB 1; Length 24;
Local Similarity 87.5%; Pred. No. 52;
hes 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

885 CAGTGAGATCCCCGGGAGACTCCTC 908

1 CAGTGATATCCCCGGGAGACTCCTC 24

RESULT 81

US-08-221-579A-7

; Sequence 7, Application US/08221579A

; Patent No. 5739118

; GENERAL INFORMATION:

; APPLICANT: Carrano, Richard A.

; TITLE OF INVENTION: Compositions and Methods for

; TITLE OF INVENTION: Delivery of Genetic Material

; NUMBER OF SEQUENCES: 48

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz

; ADDRESSEE: and No. 573918ris

; STREET: One Liberty Place - 46th Floor

; CITY: Philadelphia

; STATE: PA

; COUNTRY: U.S.A.

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch disk, 720 Kb

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WordPerfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/221,579A

; FILING DATE: 01-APR-1994

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Deluca, Mark

; REGISTRATION NUMBER: 33,229

; REFERENCE/DOCKET NUMBER: APOL-0186

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 215-568-3100

; TELEFAX: 215-568-3429

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 24 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-221-579A-7

Query Match 1.1%; Score 19.2; DB 1; Length 24;

Best Local Similarity 87.5%; Pred. No. 52;

Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 885 CAGTGAGATCCCCGGGAGACTCCTC 908

DB 1 CAGTGATATCCCCGGGAGACTCCTC 24

RESULT 82

US-08-783-818-7

; Sequence 7, Application US/08783818

; Patent No. 5817637

; GENERAL INFORMATION:

; APPLICANT: Weiner, David B.

; APPLICANT: Williams, William V.

; APPLICANT: Wang, Bin

; APPLICANT: Coney, Leslie R.

; TITLE OF INVENTION: Genetic Immunization

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5817637ris

; STREET: One Liberty Place 46th Floor

; CITY: Philadelphia

; STATE: Pennsylvania

; COUNTRY: USA

; ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 mb-MD/JAF
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/783,818
FILING DATE: 13-JAN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/125,012
FILING DATE: 21-SEP-1993
APPLICATION NUMBER: 08/029,336
FILING DATE: 11-MAR-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/008,342
FILING DATE: 26-JAN-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: APOL-0013
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3429
FORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
-783-818-7

Query Match 1.1%; Score 19.2; DB 1; Length 24;
Local Similarity 87.5%; Pred. No. 52;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

885 CAGTGAATCCCCGGGAGACTCTC 908
|||||
1 CAGTGATATCCCGGAGACTCTC 24
|||||

83
-453-349-7
ence 7, Application US/08453349
nt No. 5830876
ERAL INFORMATION:
PLICANT: Weiner, David B.
PLICANT: Williams, William V.
PLICANT: Wang, Bin
TTL OF INVENTION: Genetic Immunization
NUMBER OF SEQUENCES: 34
ORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5830876ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 mb-MD/JAF
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,349
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/029,336
FILING DATE: March 11, 1993

APPLICATION NUMBER: 08/008,342
FILING DATE: January 26, 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: APOL-0013
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3429
FORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-453-349-7

Query Match 1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 52;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 885 CAGTGAATCCCCGGGAGACTCTC 908
|||||
Db 1 CAGTGATATCCCGGAGACTCTC 24
|||||

RESULT 84
US-08-704-701-7
Sequence 7, Application US/08704701
Patent No. 5962428
GENERAL INFORMATION:
APPLICANT: Carrano, Richard A.
TITLE OF INVENTION: Compositions and Methods for
TITLE OF INVENTION: Delivery of Genetic Material
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
STREET: and No. 5962428ris
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,701
FILING DATE: 16-SEP-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/221,579
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: APOL-0186
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
FORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-704-701-7

Query Match 1.1%; Score 19.2; DB 1; Length 24;

Local Similarity 87.5%; Pred. No. 52;
hes 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

885 CAGTGAGATCCCGGAGACTCTC 908
|||||

1 CAGTGATATCCCGGAGACTCTC 24

85
979-385B-7
ence 7, Application US/08979385B
nt No. 5981505
ERAL INFORMATION:
PLICANT: Weiner, David B.
PLICANT: Williams, William V.
TITLE OF INVENTION: Compositions and Methods for Delivery of
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESS: Woodcock Washburn Kurtz Mackiewicz & No. 5981505ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 mb-MD/JAF
URGENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,385B
FILING DATE: 26-NOV-1997
CLASSIFICATION: 514
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/495,684
FILING DATE: 28-SEP-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00899
FILING DATE: 26-JAN-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: 08/125,012
FILING DATE: 21-SEP-1993
RIOR APPLICATION DATA:
APPLICATION NUMBER: 08/124,962
FILING DATE: 21-SEP-1993
RIOR APPLICATION DATA:
APPLICATION NUMBER: 08/093,235
FILING DATE: 15-JUL-1993
RIOR APPLICATION DATA:
APPLICATION NUMBER: 08/029,336
FILING DATE: 11-MAR-1993
RIOR APPLICATION DATA:
APPLICATION NUMBER: 08/008,342
FILING DATE: 26-JAN-1993
ITORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPAW-0253
ELECTRONIC INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3429
ORINATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
OLECULE TYPE: DNA
979-385B-7

Y Match 1.1%; Score 19.2; DB 1; Length 24;
Local Similarity 87.5%; Pred. No. 52;

Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 885 CAGTGAGATCCCGGAGACTCTC 908
|||||

Db 1 CAGTGATATCCCGGAGACTCTC 24

RESULT 86
US-09-321-461-7
; Sequence 7, Application US/09321461
; Patent No. 6197755
; GENERAL INFORMATION:
; APPLICANT: Carrano, Richard A.
; TITLE OF INVENTION: Compositions and Methods for
; Delivery of Genetic Material
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESS: Woodcock Washburn Kurtz Mackiewicz
; and No. 6197755ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 KB
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/321,461
; FILING DATE: 27-May-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,701
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: APOL-0186
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-321-461-7
Query Match 1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 52;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 885 CAGTGAGATCCCGGAGACTCTC 908
|||||

Db 1 CAGTGATATCCCGGAGACTCTC 24

RESULT 87
US-09-011-922A-13/C
; Sequence 13, Application US/09011922A
; Patent No. 6320022
; GENERAL INFORMATION:
; APPLICANT: Cuttitta, Frank; Martinez,
; APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
; APPLICANT: U.; Hook, William; Walsh, Thomas; Grey,
; APPLICANT: Karen; Macri, Charles
; TITLE OF INVENTION: Functional Role of
; TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
; TITLE OF INVENTION: Product (PAMP) in Human Pathology and

Page 39

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CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 mb-MD/JAF
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,576
FILING DATE: 23-JUN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/125,012
FILING DATE: 21-SEP-1993
APPLICATION NUMBER: 08/029,336
FILING DATE: 11-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/008,342
FILING DATE: 26-JAN-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: APOL-0013
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3429
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-880-576-7

Query Match 1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 52;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      885 CAGTGAGATCCCGGAGACTCTC 908
DB      1 CAGTGATATCCCGGAGACTCTC 24
|||||
|||||

RESULT 89
US-09-359-975-7
Sequence 7, Application US/09359975
Patent No. 7001759
GENERAL INFORMATION:
APPLICANT: Weiner, David B.
           Williams, William V.
           Wand, Bin
TITLE OF INVENTION: Compositions and Methods for Delivery of
Genetic Material
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 7001759aris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 mb-MD/JAF
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/359,975
FILING DATE: 23-Jul-1999

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CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/979,385B
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: US 08/495,684
FILING DATE: 28-SEP-1995
APPLICATION NUMBER: PCT/US94/00899
FILING DATE: 26-JUN-1994
APPLICATION NUMBER: 08/125,012
FILING DATE: 21-SEP-1993
APPLICATION NUMBER: 08/124,962
FILING DATE: 21-SEP-1993
APPLICATION NUMBER: 08/093,235
FILING DATE: 15-JUL-1993
APPLICATION NUMBER: 08/029,336
FILING DATE: 11-MAR-1993
APPLICATION NUMBER: 08/008,342
FILING DATE: 26-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPAP-0253
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3429
FORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
359-975-7
Y Match 1.1%; Score 19.2; DB 1; Length 24;
Local Similarity 87.5%; Pred. No. 52;
hes 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
885 CAGTGAGATCCCGGGGAGACTCTC 908
|||||
1 CAGTATATCCCGGAGACTCTC 24
90
701-935-25
ence 25, Application US/07701935
nt No. 5336595
ERAL INFORMATION:
PLICANT: Strader, C. D.
PLICANT: Fong, T. M.
TITLE OF INVENTION: Method of Using Human Neurokinin-1
TITLE OF INVENTION: Receptor Short Form
UMBER OF SEQUENCES: 27
ORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: US
ZIP: 07065-0907
OMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
URRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/701,935
FILING DATE: 19910517
CLASSIFICATION: 435
TTORNEY/AGENT INFORMATION:
NAME: Nicholson, William H.
REGISTRATION NUMBER: 25,147

REFERENCE/DOCKET NUMBER: 18409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-5315
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
US-07-701-935-25
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 176 GTGTACGATGATGAGGCTT 194
|||||
Db 1 GTGTACGATGATGAGGCTT 19
RESULT 91
US-08-117-965-23/C
Sequence 23, Application US/08117965
Patent No. 548486
GENERAL INFORMATION:
APPLICANT: Tung, Fong M.
APPLICANT: Cathrine, Strader D.
TITLE OF INVENTION: Human Neurokinin-1 Receptor
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,965
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 691,197
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Nicholson, William H.
REGISTRATION NUMBER: 25,147
REFERENCE/DOCKET NUMBER: 18387
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-5315
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
US-08-117-965-23
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1548 AAAAGGTCAGTATGCGTT 1566
|||||
Db 19 AAAAGGTCAGTATGCGTT 1

nt No. 5656462
 BRAL INFORMATION:
 PPLICANT: Keller, Cylla
 PPLICANT: Mitsuhashi, Masato
 PPLICANT: Akitaya, Tatsuo
 TITLE OF INVENTION: POLYNUCLEOTIDE IMMOBILIZED SUPPORT
 UMBER OF SEQUENCES: 12
 ORRESPONDENCE ADDRESS:
 ADDRESS: KNOBBE, MARTENS, OLSON, AND BEAR
 STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR
 CITY: NEWPORT BEACH
 STATE: CA
 COUNTRY: USA
 ZIP: 92660
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 URGENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/287,075
 FILING DATE:
 CLASSIFICATION: 435
 RIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/827,975
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Altman, Daniel E
 REGISTRATION NUMBER: 34,115
 REFERENCE/DOCKET NUMBER: HITACHI.002A
 TELEPHONE: 714-760-9502
 TELEFAX: 714-760-9502
 CRAMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 HYPOTHETICAL: NO
 NTI-SENSE: NO
 RIGINAL SOURCE:
 ORGANISM: TAC-S OLIGONUCLEOTIDE PRIMER
 287-075-9

Y Match 1.0%; Score 18.4; DB 1; Length 20;
 Local Similarity 95.0%; Pred. No. 47;
 hes 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

562 GCCAGTCTACTCCATGAC 581
 1 GCCAGCTCTACTCCATGAC 20

95
 915-966C-12
 nt No. 5668006
 BRAL INFORMATION:
 PPLICANT: Hadcock Dr., John R.
 PPLICANT: Ozenberger Dr., Bradley A.
 PPLICANT: Pausch Dr., Mark H.
 TITLE OF INVENTION: Receptor Identification Method
 UMBER OF SEQUENCES: 19
 ORRESPONDENCE ADDRESS:
 ADDRESS: American Home Products Corporation
 STREET: One Campus Drive
 CITY: Parsippany
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07054
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/915,966C
 FILING DATE: 17-JUL-1992
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Matthews, Gale M.
 REGISTRATION NUMBER: 32,269
 REFERENCE/DOCKET NUMBER: 31,829-00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-683-4117
 TELEFAX: 201-683-2134
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Synthetic
 FEATURE:
 NAME/KEY: modified_base
 LOCATION: 16
 PUBLICATION INFORMATION:
 AUTHORS: Hadcock Dr., John R.
 AUTHORS: Dr. Ozenberger, Bradley A.
 AUTHORS: Dr. Pausch, Mark H.
 TITLE: Receptor Identification Method
 DATE: 17-JUL-1992
 US-07-915-966C-12

Query Match 1.0%; Score 18.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 50;
 Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 979 TTGGCAGCTGCTGCTGCC 998
 DB 1 TTTCGATCTGCTGNTGCC 20

RESULT 96
 US-08-771-182-12
 Sequence 12, Application US/08771182
 Patent No. 5929209
 GENERAL INFORMATION:
 APPLICANT: Hadcock Dr., John R.
 APPLICANT: Ozenberger Dr., Bradley A.
 APPLICANT: Pausch Dr., Mark H.
 TITLE OF INVENTION: Receptor Identification Method
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESS: American Home Products Corporation
 STREET: One Campus Drive
 CITY: Parsippany
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07054
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/771,182
 FILING DATE: 20-DEC-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:

NAME: Mathews, Gale F.
 REGISTRATION NUMBER: 32,269
 REFERENCE/DOCKET NUMBER: 31,829-D1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-683-2134
 TELEFAX: 201-683-4117
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHEetical: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Synthetic
 FEATURE:
 NAME/KEY: modified_base
 LOCATION: 16
 PUBLICATION INFORMATION:
 AUTHORS: Hadcock Dr., John R.
 AUTHORS: Dr. Ozenberger, Bradley A.
 AUTHORS: Dr. Pausch, Mark H.
 TITLE: Receptor Identification Method
 DATE: 20-DEC-1996
 -771-182-12

Query Match 1.0%; Score 18.2; DB 1; Length 20;
 : Local Similarity 85.0%; Pred. No. 50;
 : 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

979 TTGGCATCTGCTGCTGCC 998
 ||:|||||||||
 1 TTGYCATCTGCTGANTGCC 20

-853-194-12
 Inence 12, Application US/08853194
 ent No. 6077666
 GENERAL INFORMATION:
 APPLICANT: Hadcock Dr., John R.
 APPLICANT: Ozenberger Dr., Bradley A.
 APPLICANT: Pausch Dr., Mark H.
 TITLE OF INVENTION: Receptor Identification Method
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: American Cyanamid Company
 STREET: One Cyanamid Plaza
 CITY: Wayne
 STATE: NJ
 COUNTRY: United States of America
 ZIP: 06904-0060
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/853,194
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/915,966
 FILING DATE: 17-JUL-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Tsevdos Dr., Estelle J.
 REGISTRATION NUMBER: 31,145
 REFERENCE/DOCKET NUMBER: 31829-00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 203-321-2361
 TELEFAX: 203-321-2971

TELEX: 710-474-4059
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHEtical: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Synthetic
 FEATURE:
 NAME/KEY: modified_base
 LOCATION: 16
 OTHER INFORMATION: /mod_base=1
 PUBLICATION INFORMATION:
 AUTHORS: Hadcock Dr., John R.
 AUTHORS: Dr. Ozenberger, Bradley A.
 AUTHORS: Dr. Pausch, Mark
 TITLE: Receptor Identification Method
 DATE: 17-JUL-1992
 US-08-853-194-12

Query Match 1.0%; Score 18.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 50;
 Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 979 TTGGCATCTGCTGCTGCC 998
 ||:|||||||||
 Db 1 TTGYCATCTGCTGANTGCC 20

RESULT 98
 US-07-701-935-21
 Sequence 21, Application US/07701935
 Patent No. 5336595
 GENERAL INFORMATION:
 APPLICANT: Strader, C. D.
 APPLICANT: Fong, T. M.
 TITLE OF INVENTION: Method of Using Human Neurokinin-1
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Merck & Co., Inc.
 STREET: P. O. Box 2000
 CITY: Rahway
 STATE: New Jersey
 COUNTRY: US
 ZIP: 07065-0907
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/701,935
 FILING DATE: 19910517
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Nicholson, William H.
 REGISTRATION NUMBER: 25,147
 REFERENCE/DOCKET NUMBER: 18409
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 594-5315
 TELEFAX: (908) 594-4720
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE:

701-935-21

Y Match 1.0%; Score 18; DB 1; Length 18;
Local Similarity 100.0%; Pred. No. 43;
hes 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1038 TCTCTACCTGAAGAAGTT 1055

1 TCTCTACCTGAAGAAGTT 18

99 117-965-21

ence 21, Application US/08117965
nt No. 548486

ERAL INFORMATION:

PLICANT: Tung, Fong M.

TITLE OF INVENTION: Human Neutrokinin-1 Receptor

UMBER OF SEQUENCES: 27

ORRESPONDENCE ADDRESS:

ADDRESSEE: Merck & Co., Inc.

STREET: P.O. Box 2000

CITY: Rahway

STATE: New Jersey

COUNTRY: US

ZIP: 07065-0907

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

URRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/117,965

FILING DATE:

CLASSIFICATION: 514

RIOR APPLICATION DATA:

APPLICATION NUMBER: US 691,197

FILING DATE: 25-APR-1991

TJORNEY/AGENT INFORMATION:

NAME: Nicholson, William H.

REGISTRATION NUMBER: 25,147

REFERENCE/DOCKET NUMBER: 18387

ELECTRONIC COMMUNICATION INFORMATION:

TELEPHONE: (908) 594-5315

TELEFAX: (908) 594-4720

ORAMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

OLECULE TYPE:

117-965-21

Y Match 1.0%; Score 18; DB 1; Length 18;
Local Similarity 100.0%; Pred. No. 43;
hes 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1038 TCTCTACCTGAAGAAGTT 1055

1 TCTCTACCTGAAGAAGTT 18

100

543-679A-1372/C

ence 1372, Application US/09543679A

nt No. 7034007

ERAL INFORMATION:

APPLICANT: NYCE, Jonathan W.

TITLE OF INVENTION: LOW ADEOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT

OF AIRWAY DISORDERS ASSOCIATED WITH

BRONCHOCONSTRICITION, LUNG INFLAMMATION,

NUMBER OF SEQUENCES: 3111

CORRESPONDENCE ADDRESS:

ADDRESSEE: EPIDEMIS PHARMACEUTICALS, INC.

STREET: 7 Clarke Drive

CITY: Cranbury

STATE: NJ

COUNTRY: USA

ZIP: 08512

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-R

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: N/A

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/543,679A

FILING DATE: 13-APR-2000

CLASSIFICATION: UNKNOWN

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/127,958

FILING DATE: 1998-08-03

ATTORNEY/AGENT INFORMATION:

NAME: Amzel, Viviana

REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: EPI-0067191b

TELECOMMUNICATION INFORMATION:

TELEPHONE: 609-409-3035

TELEFAX: 413-254-9245

TELEX: <unknown>

INFORMATION FOR SEQ ID NO: 1372:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1372:

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 638 CAGCCACAGCCACCAAG 655

Db 18 CAGCCACAGCCACCAAG 1

RESULT 101
US-08-513-974B-256
Sequence 256, Application US/08513974B
Patent No. 6114139

GENERAL INFORMATION:

APPLICANT: Hinuma, Shuji

APPLICANT: Hosoya, Masaki

APPLICANT: Fujii, Ryo

APPLICANT: Ohtaki, Tetsuya

APPLICANT: Fukushima, Shoji

APPLICANT: Ohgi, Kazuhito

TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
NUMBER OF SEQUENCES: 380

TITLE OF INVENTION: PRODUCTION, AND USE THEREOF

CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/513,974B
 FILING DATE: 14-SEP-1995
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP95/01599
 FILING DATE: 10-AUG-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-093989
 FILING DATE: 19-AUG-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-057186
 FILING DATE: 16-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-007177
 FILING DATE: 20-JAN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-326611
 FILING DATE: 28-DEC-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-270017
 FILING DATE: 02-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-236357
 FILING DATE: 30-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-236356
 FILING DATE: 30-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189274
 FILING DATE: 11-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189273
 FILING DATE: 11-AUG-1945
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189272
 FILING DATE: 11-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Resnick, David S.
 REGISTRATION/DOCKET NUMBER: 34,235
 REFERENCE/DOCKET NUMBER: 45753
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 256:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 513-974B-256
 Local Similarity 1.0%; Score 17.8; DB 1; Length 21;
 : Local Similarity 90.5%; Pred. No. 62;
 : Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
 TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
 NUMBER OF SEQUENCES: 380
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/513,974B
 FILING DATE: 14-SEP-1995
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP95/01599
 FILING DATE: 10-AUG-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-093989
 FILING DATE: 19-AUG-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-057186
 FILING DATE: 16-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-007177
 FILING DATE: 20-JAN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-326611
 FILING DATE: 28-DEC-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-270017
 FILING DATE: 02-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-236357
 FILING DATE: 30-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-236356
 FILING DATE: 30-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189274
 FILING DATE: 11-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189273
 FILING DATE: 11-AUG-1945
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189272
 FILING DATE: 11-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Resnick, David S.
 REGISTRATION/DOCKET NUMBER: 34,235
 REFERENCE/DOCKET NUMBER: 45753
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 267:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 513-974B-267
 Local Similarity 1.0%; Score 17.8; DB 1; Length 21;
 : Local Similarity 90.5%; Pred. No. 62;
 : Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 TTTCATCTCTGCTGCTGCC 21

103
513-974B-269
ence 269, Application US/08513974B
nt No. 6114139
ERAL INFORMATION:
PLICANT: Hinuma, Shuji
PLICANT: Hosoya, Masaki
PLICANT: Fujii, Ryo
PLICANT: Ohtaki, Tetsuya
PLICANT: Fukusumi, Shoji
PLICANT: Ohgi, Kazuhiro
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
UMBER OF SEQUENCES: 380
ORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
OMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
URRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
RIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1945
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
TORN/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
ELECTRONIC INFORMATION:
TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 269:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-513-974B-269

Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 62;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 979 TTGCCATCTGCTGCTGCC 999
Db 1 TTTCCTCTGCTGCTGCC 21

RESULT 104
US-08-513-974B-270
Sequence 270, Application US/08513974B
Patent No. 6114139
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Fukusumi, Shoji
APPLICANT: Ohgi, Kazuhiro
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
RIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 02-NOV-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 11-AUG-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
FORMATION FOR SEQ ID NO: 270:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
-513-974B-270

Match 1.0%; Score 17.8; DB 1; Length 21;
Local Similarity 90.5%; Pred. No. 62;
Indels 2; Mismatches 0; Gaps 0;

979 TTGCGCATCTGCTGGCTGCC 999
1 TTGATCATCTGCTGGCTGCC 21

974-409C-5
ence 5, Application US/07974409C
ent No. 6300058
GENERAL INFORMATION:
APPLICANT: Akitaya, Tatsuo
APPLICANT: Mitsuhashi, Masato
APPLICANT: Cooper, Allan
TITLE OF INVENTION: METHOD AND REAGENT
TITLE OF INVENTION: FOR MEASURING MESSENGER RNA
NUMBER OF SEQUENCES: 457
CORRESPONDENCE ADDRESS:
ADDRESSER: Knobbe, Martens, Olson, and Bear
STREET: 620 Newport Center Dr. Sixteenth Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/974,409C
FILING DATE: 12-NOV-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel R.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: HITACHI.006CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
FORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 bases
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: SUBSTANCE P RECEPTOR mRNA PROBE
US-07-974-409C-5

Query Match 1.0%; Score 17.8; DB 1; Length 22;
Best Local Similarity 90.5%; Pred. No. 68;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 780 GATTATGAGAAAGTGTAACA 800
Db 2 GACTTATGAGAAAGCGTACCA 22

RESULT 106
US-08-182-175A-17/C
Sequence 17, Application US/08182175A
Patent No. 5559223
GENERAL INFORMATION:
APPLICANT: Saverio Carl Falco
APPLICANT: Sharon J. Keeler
APPLICANT: Janet A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSER: E.I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,175A
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 August 1991
ATTORNEY/AGENT INFORMATION:
NAME: Linda Axemethy Floyd
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 992-4929
TELEFAX: (302) 892-7949
TELEX: 835420
FORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..21
OTHER INFORMATION: /product= "synthetic oligonucleotide"
OTHER INFORMATION: /strand_name= "SM 82"
US-08-182-175A-17

Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1404 CTTGAGCTTCTCTCCA 1420

|||||
19 CTTGAGCTTCTCTCA 3

107
182-175A-19/c
ence 19, Application US/08182175A
nt No. 5559223
ERAL INFORMATION:
PLICANT: Saverio Carl Falco
PLICANT: Sharon J. Keeler
PLICANT: Janet A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing F
UMBER OF SEQUENCES: 113
ORRESPONDENCE ADDRESS:
ADDRESSEE: E.I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,175A
FILING DATE:
CLASSIFICATION: 800
RIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 August 1991
TTORNEY/AGENT INFORMATION:
NAME: Linda Akamehy Floyd
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1031
ELECTRONIC COMMUNICATION INFORMATION:
TELEPHONE: (302) 992-4929
TELEFAX: (302) 892-7949
TELEX: 835420

ORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
OLBUCE TYPE: DNA (genomic)
ATURE:
NAME/KEY: misc_feature
LOCATION: 1..21
OTHER INFORMATION: /product= "synthetic oligonucleotide"
OTHER INFORMATION: /standard_name= "SM 86"
182-175A-19

Y Match 1.0%; Score 17; DB 1; Length 21;
Local Similarity 100.0%; Pred. No. 79;
hes 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1404 CTTGAGCTTCTCTCA 1420
|||||
19 CTTGAGCTTCTCTCA 3

108
182-175A-21/c
ence 21, Application US/08182175A
nt No. 5559223
ERAL INFORMATION:
PLICANT: Saverio Carl Falco
PLICANT: Sharon J. Keeler
PLICANT: Janet A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing F

NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: E.I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,175A
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 August 1991
ATTORNEY/AGENT INFORMATION:
NAME: Linda Akamehy Floyd
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 992-4929
TELEFAX: (302) 892-7949
TELEX: 835420

INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..21
OTHER INFORMATION: /product= "synthetic oligonucleotide"
OTHER INFORMATION: /standard_name= "SM 88"
US-08-182-175A-21

Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1404 CTTGAGCTTCTCTCA 1420
|||||
DB 19 CTTGAGCTTCTCTCA 3

RESULT 109
US-08-474-633A-25/c
Sequence 25, Application US/08474633A
Patent No. 5773691
GENERAL INFORMATION:
APPLICANT: E. I. DU PONT DE NEMOURS AND
APPLICANT: COMPANY
TITLE OF INVENTION: CHIMERIC GENES AND
TITLE OF INVENTION: METHODS FOR INCREASING
TITLE OF INVENTION: INCREASING THE LYSINE
TITLE OF INVENTION: AND THREONINE CONTENT
TITLE OF INVENTION: OF THE SEEDS OF PLANTS
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS
ADDRESSEE: AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: MICROSOFT WORD VERSION 2.0C
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/474,633A
 FILING DATE:
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: BARBARA C. SIEGELL
 REGISTRATION NUMBER: 30,684
 REFERENCE/DOCKET NUMBER: BB-1037-C
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 302-992-4931
 TELEFAX: 302-773-0164
 TELEX: 835420
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: 1..21
 OTHER INFORMATION: /product="synthetic"
 OTHER INFORMATION: oligonucleotide
 OTHER INFORMATION: /standard_name="SM"
 OTHER INFORMATION: 82"
 -474-633A-25

Query Match 1.0%; Score 17; DB 1; Length 21;
 Local Similarity 100.0%; Pred. No. 79;
 Mismatches 0; Indels 0; Gaps 0;

1404 CTTGAGCTTCTCTCTCA 1420
 |||||
 19 CTTGAGCTTCTCTCTCA 3

110
 -474-633A-41/c
 Patent No. 5773691
 Application US/08474633A
 GENERAL INFORMATION:
 APPLICANT: E. I. DU PONT DE NEMOURS AND
 COMPANY
 TITLE OF INVENTION: CHIMERIC GENES AND
 METHODS FOR INCREASING
 TITLE OF INVENTION: INCREASING THE LYSINE
 TITLE OF INVENTION: AND THREONINE CONTENT
 TITLE OF INVENTION: OF THE SEEDS OF PLANTS
 NUMBER OF SEQUENCES: 107
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: E. I. DU PONT DE NEMOURS
 AND COMPANY
 STREET: 1007 MARKET STREET
 CITY: WILMINGTON
 STATE: DELAWARE
 COUNTRY: U.S.A.
 ZIP: 19898

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: MICROSOFT WORD VERSION 2.0C
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/474,633A
 FILING DATE:
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: BARBARA C. SIEGELL

REGISTRATION NUMBER: 30,684
 REFERENCE/DOCKET NUMBER: BB-1037-C
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 302-992-4931
 TELEFAX: 302-773-0164
 TELEX: 835420
 INFORMATION FOR SEQ ID NO: 41:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: 1..21
 OTHER INFORMATION: /product="synthetic"
 OTHER INFORMATION: oligonucleotide
 OTHER INFORMATION: /standard_name="SM"
 OTHER INFORMATION: 86"
 US-08-474-633A-41

Query Match 1.0%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 79;
 Mismatches 0; Indels 0; Gaps 0;

Qy 1404 CTTGAGCTTCTCTCTCA 1420
 |||||
 Db 19 CTTGAGCTTCTCTCTCA 3

RESULT 111
 US-08-474-633A-43/c
 Sequence 43, Application US/08474633A
 Patent No. 5773691
 GENERAL INFORMATION:
 APPLICANT: E. I. DU PONT DE NEMOURS AND
 COMPANY
 TITLE OF INVENTION: CHIMERIC GENES AND
 METHODS FOR INCREASING
 TITLE OF INVENTION: INCREASING THE LYSINE
 TITLE OF INVENTION: AND THREONINE CONTENT
 TITLE OF INVENTION: OF THE SEEDS OF PLANTS
 NUMBER OF SEQUENCES: 107
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: E. I. DU PONT DE NEMOURS
 AND COMPANY
 STREET: 1007 MARKET STREET
 CITY: WILMINGTON
 STATE: DELAWARE
 COUNTRY: U.S.A.
 ZIP: 19898

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: MICROSOFT WORD VERSION 2.0C
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/474,633A
 FILING DATE:
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: BARBARA C. SIEGELL
 REGISTRATION NUMBER: 30,684
 REFERENCE/DOCKET NUMBER: BB-1037-C
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 302-992-4931
 TELEFAX: 302-773-0164
 TELEX: 835420
 INFORMATION FOR SEQ ID NO: 43:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 base pairs
 TYPE: nucleic acid

STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: 1..21
 OTHER INFORMATION: /product= "synthetic
 OTHER INFORMATION: /standard_name= "SM
 OTHER INFORMATION: /standard_name= "SM
 OTHER INFORMATION: 88"
 474-633A-43

Y Match 1.0%; Score 17; DB 1; Length 21;
 Local Similarity 100.0%; Pred. No. 79;
 hes 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1404 CTTGAGCTTCTCTCCA 1420
 |||||
 19 CTTGAGCTTCTCTCCA 3

112
 823-771-25/c
 ence 25, Application US/08823771
 nt No. 6459019
 NERL INFORMATION:
 APPLICANT: E. I. DU PONT DE NEMOURS AND
 COMPANY
 TITLE OF INVENTION: CHIMERIC GENES AND
 METHODS FOR INCREASING
 INCREASING THE LYSINE
 AND THREONINE CONTENT
 NUMBER OF SEQUENCES: 107
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: E. I. DU PONT DE NEMOURS
 AND COMPANY
 STREET: 1007 MARKET STREET
 CITY: WILMINGTON
 STATE: DELAWARE
 COUNTRY: U.S.A.
 ZIP: 19898
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: MICROSOFT WORD VERSION 2.0C
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/823,771
 FILING DATE: 24-Mar-1997
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/474,633
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: BARBARA C. SIEGEL
 REGISTRATION NUMBER: 30,684
 REFERENCE/DOCKET NUMBER: BB-1037-C
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 302-992-4931
 TELEFAX: 302-773-0164
 TELEX: 835420
 FORMATION FOR SEQ ID NO: 25;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: 1..21
 OTHER INFORMATION: /product= "synthetic
 oligonucleotide"

; /standard_name= "SM
 ; 82"
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 25;
 ; US-08-823-771-25
 Query Match 1.0%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 79;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1404 CTTGAGCTTCTCTCCA 1420
 |||||
 Db 19 CTTGAGCTTCTCTCCA 3

RESULT 113
 US-08-823-771-41/c
 ; Sequence 41; Application US/08823771
 ; Patent No. 6459019
 ; GENERAL INFORMATION:
 ; APPLICANT: E. I. DU PONT DE NEMOURS AND
 ; COMPANY
 ; TITLE OF INVENTION: CHIMERIC GENES AND
 ; METHODS FOR INCREASING
 ; INCREASING THE LYSINE
 ; AND THREONINE CONTENT
 ; NUMBER OF SEQUENCES: 107
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: E. I. DU PONT DE NEMOURS
 ; AND COMPANY
 ; STREET: 1007 MARKET STREET
 ; CITY: WILMINGTON
 ; STATE: DELAWARE
 ; COUNTRY: U.S.A.
 ; ZIP: 19898
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY DISK
 ; COMPUTER: IBM PC COMPATIBLE
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: MICROSOFT WORD VERSION 2.0C
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/823,771
 ; FILING DATE: 24-Mar-1997
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/474,633
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BARBARA C. SIEGEL
 ; REGISTRATION NUMBER: 30,684
 ; REFERENCE/DOCKET NUMBER: BB-1037-C
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 302-992-4931
 ; TELEFAX: 302-773-0164
 ; TELEX: 835420
 ; INFORMATION FOR SEQ ID NO: 41:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 21 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 1..21
 ; OTHER INFORMATION: /product= "synthetic
 ; oligonucleotide"
 ; /standard_name= "SM
 ; 86"
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 41:
 ; US-08-823-771-41
 Query Match 1.0%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 79;

hes 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1404 CTTGAGCTTCTCTCCCA 1420
19 CTTGAGCTTCTCTCCCA 3

114
-823-771-43/c
ence 43, Application US/08823771
nt No. 6459019
GENERAL INFORMATION:
APPLICANT: E. I. DU PONT DE NEMOURS AND
COMPANY
TITLE OF INVENTION: CHIMERIC GENES AND
METHODS FOR INCREASING
INCREASING THE LYSINE
AND THREONINE CONTENT

NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS
AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/823,771
FILING DATE: 24-Mar-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/474,633
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4931
TELEFAX: 302-773-0164
TELEX: 835420

FORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..21
OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
88"

SEQUENCE DESCRIPTION: SEQ ID NO: 43:
-823-771-43

Match 1.0%; Score 17; DB 1; Length 21;
Local Similarity 100.0%; Pred. No. 79;
hes 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1404 CTTGAGCTTCTCTCCCA 1420
19 CTTGAGCTTCTCTCCCA 3

RESULT 115
PCT-US92-06412-17/c
Sequence 17, Application PC/TUS9206412
GENERAL INFORMATION:
APPLICANT: Saverio Carl Falco
APPLICANT: Sharon J. Keeler
APPLICANT: Janet A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06412
FILING DATE: 19920807
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 August 1991
ATTORNEY/AGENT INFORMATION:
NAME: Linda A. Amethy Floyd
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 992-4929
TELEFAX: (302) 892-7949
TELEX: 835420

INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..21
OTHER INFORMATION: /product= "synthetic oligonucleotide"
/standard_name= "SM 82"

PCT-US92-06412-17

Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1404 CTTGAGCTTCTCTCCCA 1420
Db 19 CTTGAGCTTCTCTCCCA 3

RESULT 116
PCT-US92-06412-19/c
Sequence 19, Application PC/TUS9206412
GENERAL INFORMATION:
APPLICANT: Saverio Carl Falco
APPLICANT: Sharon J. Keeler
APPLICANT: Janet A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware

COUNTRY: USA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06412
FILING DATE: 19920807
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 August 1991
TORNBY/AGENT INFORMATION:
NAME: Linda Axamechy Floyd
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1031
ELECTRONIC INFORMATION:
TELEPHONE: (302) 992-4929
TELEFAX: (302) 892-7949
TELEX: 835420
ORIGIN FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..21
OTHER INFORMATION: /product="synthetic oligonucleotide"
OTHER INFORMATION: /standard_name="SM 86"
92-06412-19
Y Match 1.0%; Score 17; DB 1; Length 21;
Local Similarity 100.0%; Pred. No. 79;
has 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1404 CTTGAGCTTCTCTCCA 1420
|||||
19 CTTGAGCTTCTCTCCA 3
117
92-06412-21/c
since 21, Application PC/TUS9206412
ERRA INFORMATION:
PLICANT: Saverio Carl Falco
PLICANT: Sharon J. Keele
PLICANT: Janet A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing F
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: E.I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06412
FILING DATE: 19920807
CLASSIFICATION: 530
RIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 August 1991

ATTORNEY/AGENT INFORMATION:
NAME: Linda Axamechy Floyd
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 992-4929
TELEFAX: (302) 892-7949
TELEX: 835420
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..21
OTHER INFORMATION: /product="synthetic oligonucleotide"
OTHER INFORMATION: /standard_name="SM 88"
PCT-US92-06412-21
Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1404 CTTGAGCTTCTCTCCA 1420
|||||
Db 19 CTTGAGCTTCTCTCCA 3
RESULT 118
US-08-431-080-7/c
Sequence 7, Application US/08431080
Patent No. 5698686
GENERAL INFORMATION:
APPLICANT: Gottschling, Daniel E.
APPLICANT: Singer, Miriam S.
TITLE OF INVENTION: Telomerase Compositions and Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TEXAS
COUNTRY: UNITED STATES OF AMERICA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,080
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SN 08/326,781
FILING DATE: October 20, 1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARCD:155/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear

431-080-7
y Match 1.0%; Score 16.8; DB 1; Length 21;
Local Similarity 90.0%; Pred. No. 84;
Indels 18; Conservative 0; Mismatches 2; Gaps 0;

921 CGAGCAAGTCTATGCGCAGC 940
21 CGAGCAAGTCTATGCGCAGC 2

938-534-7/c
ence 7, Application US/08938534
nt No. 5516752
GENERAL INFORMATION:
APPLICANT: Gottschling, Daniel E.
APPLICANT: Singer, Miriam S.
TITLE OF INVENTION: Telomerase Compositions and Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TEXAS
COUNTRY: UNITED STATES OF AMERICA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,534
FILING DATE: 26-SEP-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,080
FILING DATE:
APPLICATION NUMBER: SN 08/326,781
FILING DATE: October 20, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARCD:155/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
938-534-7
y Match 1.0%; Score 16.8; DB 1; Length 21;
Local Similarity 90.0%; Pred. No. 84;
Indels 18; Conservative 0; Mismatches 2; Gaps 0;

921 CGAGCAAGTCTGCGCAGC 940
21 CGAGCAAGTCTATGCGCAGC 2

938-534-7/c
ence 7, Application US/09345294
nt No. 6387619
GENERAL INFORMATION:
APPLICANT: Gottschling, Daniel E.

Singer, Miriam S.
TITLE OF INVENTION: Telomerase Compositions and Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TEXAS
COUNTRY: UNITED STATES OF AMERICA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/345,294
FILING DATE: 30-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,080
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARCD:155/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-345-294-7

Query Match 1.0%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 84;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 921 CGAGCAAGTCTGCGCAGC 940
db 21 CGAGCAAGTCTATGCGCAGC 2

RESULT 121
US-07-701-935-2
Sequence 2, Application US/07701935
Patent No. 5336595
GENERAL INFORMATION:
APPLICANT: Strader, C. D.
APPLICANT: Fong, T. M.
TITLE OF INVENTION: Method of Using Human Neurokinin-1
TITLE OF INVENTION: Receptor Short Form
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/701,935
FILING DATE: 19910517

CLASSIFICATION: 435
TTOURNEY/AGENT INFORMATION:
NAME: Nicholson, William H.
REGISTRATION NUMBER: 25,147
REFERENCE/DOCKET NUMBER: 18409
ELECTRONIC INFORMATION:
TELEPHONE: (908) 594-5315
TELEFAX: (908) 594-4720
ORAMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
OLECULE TYPE:
701-935-2

Y Match 0.9%; Score 16.4; DB 1; Length 18;
Local Similarity 94.4%; Pred. No. 71;
hes 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

448 TCCATGCTGCATTCAT 465
1 TGCATGCTGCATTCAT 18

117-965-2
ence 2, Application US/08117965
nt No. 5484886
ERAL INFORMATION:
PLICANT: Tung, Fong M.
TITLE OF INVENTION: Human Neurokinin-1 Receptor
UMBER OF SEQUENCES: 27
ORRESPONDENCE ADDRESSES:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: US
ZIP: 07065-0907
OMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
URRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,965
ILING DATE:
CLASSIFICATION: 514
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 691,197
ILING DATE: 25-APR-1991
TTOURNEY/AGENT INFORMATION:
NAME: Nicholson, William H.
REGISTRATION NUMBER: 25,147
REFERENCE/DOCKET NUMBER: 18387
ELECTRONIC INFORMATION:
TELEPHONE: (908) 594-5315
TELEFAX: (908) 594-4720
ORAMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
OLECULE TYPE:
117-965-2

Y Match 0.9%; Score 16.4; DB 1; Length 18;
Local Similarity 94.4%; Pred. No. 71;
hes 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 448 TCCATGCTGCATTCAT 465
Db 1 TGCATGCTGCATTCAT 18

RESULT 123
US-08-584-040-6209/c
Sequence 6209, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
ELECTRONIC INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 6209:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-6209

Query Match 0.9%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 624 CCAGCCCGGCTGTACG 641
Db 18 CCAGCCCGGCTGTACG 1

RESULT 124
US-09-371-772B-2971/c
Sequence 2971, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.

STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
ELECTRONIC INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
ORAMATION FOR SEQ ID NO: 5544:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
584-040-5544

Y Match 0.9%; Score 15.4; DB 1; Length 17;
Local Similarity 94.1%; Pred. No. 86;
hes 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

716 CAACCAAGAGAGCCATG 732
17 CAACCAAGAGAGCCATG 1

129
371-772B-2435/c
ence 2435, Application US/09371772B
nt No. 6566127

GENERAL INFORMATION:
LICANT: Ribozyme Pharmaceuticals, Inc.
LICANT: Pavco, Pam
LICANT: McSwigen, Jim
LICANT: Stinchcomb, Dan
LICANT: Escobedo, Jaime

LE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
E REFERENCE: MHB00,876-J (237/198)
RENT APPLICATION NUMBER: US/09/371,772B
RENT FILING DATE: 1999-08-10
OR APPLICATION NUMBER: US 60/005,974
OR FILING DATE: 1995-10-26
OR APPLICATION NUMBER: US 08/584,040
OR FILING DATE: 1996-01-08
BER OF SEQ ID NOS: 14225
TWARE: PatentIn version 3.0
ID NO 2435
NGTH: 17
PE: RNA
GANISM: Mus sp.
371-772B-2435

Y Match 0.9%; Score 15.4; DB 1; Length 17;
Local Similarity 94.1%; Pred. No. 86;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 716 CAACCAAGAGAGCCATG 732
Db 17 CAACCAAGAGAGCCATG 1

RESULT 130
US-09-685-664B-2435/c
; Sequence 2435, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
FILE REFERENCE: MHB00-876-K (400/021)
CURRENT APPLICATION NUMBER: US/09/685,664B
CURRENT FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
PRIOR APPLICATION NUMBER: US 09/371,772
PRIOR FILING DATE: 1999-08-10
NUMBER OF SEQ ID NOS: 8231
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2435
LENGTH: 17
TYPE: RNA
ORGANISM: Mus musculus
US-09-685-664B-2435

Query Match 0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 86;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 716 CAACCAAGAGAGCCATG 732
Db 17 CAACCAAGAGAGCCATG 1

RESULT 131
US-10-138-674B-2435/c
; Sequence 2435, Application US/10138674B
; Patent No. 7034009
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
FILE REFERENCE: MHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/138,674B
CURRENT FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 20829
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2435
LENGTH: 17
TYPE: RNA
ORGANISM: Mus musculus
US-10-138-674B-2435

Query Match 0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 86;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 716 CAACCAAGAGAGCCATG 732

APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
REFERENCE: MBH00,876-J (237/198)
CURRENT FILING DATE: 1999-08-10
FOR FILING DATE: 1995-10-26
FOR APPLICATION NUMBER: US 08/584,040
FOR FILING DATE: 1996-01-08
ABSTRACT OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
ID NO: 2971
LENGTH: 18
SEQUENCE: 18
ORGANISM: Mus sp.
-371-772B-2971

Query Match
Local Similarity 94.4%; Score 16.4; DB 1; Length 18;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

624 CCAGCCCGGCTGTGACG 641
18 CCAGCCCGGCTGTGACG 1

125
-685-664B-2971/C
Sequence 2971, Application US/09685664B
Patent No. 6818447
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
REFERENCE: MBH00-876-K (400/021)
CURRENT FILING DATE: 2000-10-10
FOR FILING DATE: 1995-10-26
FOR APPLICATION NUMBER: US 08/584,040
FOR FILING DATE: 1996-01-08
FOR APPLICATION NUMBER: US 09/371,772
FOR FILING DATE: 1999-08-10
ABSTRACT OF SEQ ID NOS: 8231
SOFTWARE: PatentIn version 3.0
ID NO: 2971
LENGTH: 18
SEQUENCE: 18
ORGANISM: Mus musculus
-685-664B-2971

Query Match
Local Similarity 94.4%; Score 16.4; DB 1; Length 18;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

624 CCAGCCCGGCTGTGACG 641
18 CCAGCCCGGCTGTGACG 1

126
-138-674B-2971/C
Sequence 2971, Application US/10138674B
Patent No. 7034009
GENERAL INFORMATION:

APPLICANT: Sirta Therapeutics, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
REFERENCE: MBH00-876-N (400/049)
CURRENT FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 20829
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 2971
LENGTH: 18
TYPE: RNA
ORGANISM: Mus musculus
US-10-138-674B-2971

Query Match
Local Similarity 94.4%; Score 16.4; DB 1; Length 18;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

624 CCAGCCCGGCTGTGACG 641
18 CCAGCCCGGCTGTGACG 1

RESULT 127
US-09-967-669-87/C
Sequence 87, Application US/09967669
Patent No. 6692960
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freiler
TITLE OF INVENTION: ANTISENSE MODULATION OF SPHINGOSINE-1-PHOSPHATE LYASE EXPRESSION
FILE REFERENCE: RTS-0259
CURRENT FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 90
SEQ ID NO: 87
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-967-669-87

Query Match
Local Similarity 94.4%; Score 16.4; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

624 CCAGCCCGGCTGTGACG 641
18 CCAGCCCGGCTGTGACG 1

RESULT 128
US-08-584-040-5544/C
Sequence 5544, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF DISEASES OR CONDITIONS RELATED TO LEVELS OF VASCULAR ENDOTHELIAL GROWTH FACTOR
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon

|||||
17 CAACGAGAGACCATG 1

1 132
-513-974B-243
ence 243, Application US/08513974B
nt No. 6114139
REAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Ontaki, Tetsuya
APPLICANT: Fukusumi, Shoji
APPLICANT: Ogi, Kazuhiro
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 243:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-513-974B-243

Query Match 0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 96;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 427 AACCTGGCCTTGGCGGA 443
|||||
DB 1 AACCTGGCCTTGGCGGA 17

RESULT 133
US-09-850-948-19/c
Sequence 19, Application US/09850948
Patent No. 6919176

GENERAL INFORMATION:
APPLICANT: Yang, Jianxin
APPLICANT: An, Songzhu
APPLICANT: Tularik Inc.
TITLE OF INVENTION: Polypeptides and Nucleic Acids Associated with Cancer
FILE REFERENCE: 018781-008300US
CURRENT APPLICATION NUMBER: US/09/850,948
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:quantitative
OTHER INFORMATION: RT-PCR primer OGR1 reverse
US-09-850-948-19

Query Match 0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 96;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 986 TCTGCTGGCTGCCTTC 1002
|||||
DB 18 TCTGCTGGCTGCCTTC 2

RESULT 134
US-09-543-679A-1373/C
Sequence 1373, Application US/09543679A
Patent No. 7034007
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICITION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: N/A
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/543,679A
 FILING DATE: 13-Apr-2000
 CLASSIFICATION: UNKNOWN
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/127,958
 FILING DATE: 1998-08-03
 ATTORNEY/AGENT INFORMATION:
 NAME: Amzel, Viviana
 REGISTRATION NUMBER: 30,930
 REFERENCE/DOCKET NUMBER: EPI-0067191b
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 609-409-3035
 TELEFAX: 413-254-9245
 TELE: <Unknown>
 FORMATION FOR SEQ ID NO: 1373:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 1373:
 543-679A-1373
 Y Match 0.8%; Score 15; DB 1; Length 15;
 Local Similarity 100.0%; Pred. No. 77;
 hes 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 716 CAACCAAGAGACCA 730
 |||||
 15 CAACCAAGAGACCA 1
 135
 543-679A-1374/C
 ence 1374, Application US/09543679A
 nt No. 7034007
 NERAL INFORMATION:
 APPLICANT: NICE, Jonathan W.
 TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
 COMPOSITIONS, KIT & METHOD FOR TREATMENT
 OF AIRWAY DISORDERS ASSOCIATED WITH
 BRONCHOCONSTRICTION, LUNG INFLAMMATION,
 NUMBER OF SEQUENCES: 3111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
 STREET: 7 Clarke Drive
 CITY: Cranbury
 STATE: NJ
 COUNTRY: USA
 ZIP: 08512
 COMPUTER READABLE FORM:
 MEDIUM TYPE: CD-R
 OPERATING SYSTEM: DOS
 SOFTWARE: N/A
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/543,679A
 FILING DATE: 13-Apr-2000
 CLASSIFICATION: UNKNOWN
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/127,958
 FILING DATE: 1998-08-03
 ATTORNEY/AGENT INFORMATION:
 NAME: Amzel, Viviana
 REGISTRATION NUMBER: 30,930
 REFERENCE/DOCKET NUMBER: EPI-0067191b
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 609-409-3035
 TELEFAX: 413-254-9245
 TELE: <Unknown>
 FORMATION FOR SEQ ID NO: 1374:

SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 1374:
 US-09-543-679A-1374
 Query Match 0.8%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 77;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1236 CCAGATCCAGGCGAG 1250
 |||||
 Db 15 CCAGATCCAGGCGAG 1
 RESULT 136
 US-09-866-108A-6966
 ; Sequence 6966, Application US/09866108A
 ; Patent No. 6686188
 ; GENERAL INFORMATION:
 ; APPLICANT: GU, Yizhong
 ; APPLICANT: PENN, Shatton G.
 ; APPLICANT: HANZEL, David K.
 ; APPLICANT: RANK, David R.
 ; APPLICANT: CHEN, Wensheng
 ; APPLICANT: SHANNON, Mark
 ; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
 ; FILE REFERENCE: ABOMICA-7
 ; CURRENT APPLICATION NUMBER: US/09/866,108A
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: GB 24263.6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663
 ; PRIOR FILING DATE: 2001-01-30
 ; Remaining Prior Application data removed - See file wrapper or PALM.
 ; NUMBER OF SBO ID NOS: 15755
 ; SOFTWARE: Acemica Sequence Listing Engine
 ; Patent No. 6686188
 ; SEQ ID NO 6966
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-866-108A-6966
 Query Match 0.8%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 97;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 28 CAGTGCATCCAGAG 42
 |||||
 Db 3 CAGTGCATCCAGAG 17
 RESULT 137


```

-866-108A-6967, Application US/09866108A
ence 6967, Application US/09866108A
ent No. 6686188
ERAL INFORMATION:
PLICANT: GU, Yizhong
PLICANT: JI, Yonggang
PLICANT: PENN, Sharon G.
PLICANT: HANZEL, David K.
PLICANT: RANK, David R.
PLICANT: CHEN, Wensheng
PLICANT: SHANNON, Mark
LE OF INVENTION: MOSIS-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
E REFERENCE: AEOMICA-7
RENT APPLICATION NUMBER: US/09/866,108A
RENT FILING DATE: 2001-05-25
OR APPLICATION NUMBER: US 60/207,456
OR FILING DATE: 2000-05-26
OR APPLICATION NUMBER: GB 24263.6
OR FILING DATE: 2000-10-04
OR APPLICATION NUMBER: US 60/236,359
OR FILING DATE: 2000-09-27
OR APPLICATION NUMBER: PCT/US01/00666
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00667
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00664
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00669
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00665
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00668
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00663
OR FILING DATE: 2001-01-30
aining Prior Application data removed - See File Wrapper or PALM.
BER OF SEQ ID NOS: 15755
TWARE: Aeomica Sequence Listing Engine
ent No. 6686188
ID NO. 6967
LENGTH: 17
GENE: DNA
GANISM: Homo sapiens
-866-108A-6967
CY Match 0.8%; Score 15; DB 1; Length 17;
: Local Similarity 100.0%; Pred. No. 97;
: Cons 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
28 CAGTGCATCCAGAG 42
|||||
2 CAGTGCATCCAGAG 16
f 138
-866-108A-6968
ence 6968, Application US/09866108A
ent No. 6686188
ERAL INFORMATION:
PLICANT: GU, Yizhong
PLICANT: JI, Yonggang
PLICANT: PENN, Sharon G.
PLICANT: HANZEL, David K.
PLICANT: RANK, David R.
PLICANT: CHEN, Wensheng
PLICANT: SHANNON, Mark
LE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
E REFERENCE: AEOMICA-7
RENT APPLICATION NUMBER: US/09/866,108A
RENT FILING DATE: 2001-05-25
OR APPLICATION NUMBER: US 60/207,456
OR FILING DATE: 2000-05-26
OR APPLICATION NUMBER: GB 24263.6

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Prior Filing Date: 2000-10-04
Prior Application Number: US 60/236,359
Prior Filing Date: 2000-09-27
Prior Application Number: PCT/US01/00666
Prior Filing Date: 2001-01-30
Prior Application Number: PCT/US01/00667
Prior Filing Date: 2001-01-30
Prior Application Number: PCT/US01/00664
Prior Filing Date: 2001-01-30
Prior Application Number: PCT/US01/00669
Prior Filing Date: 2001-01-30
Prior Application Number: PCT/US01/00665
Prior Filing Date: 2001-01-30
Prior Application Number: PCT/US01/00668
Prior Filing Date: 2001-01-30
Prior Application Number: PCT/US01/00663
Prior Filing Date: 2001-01-30
Prior Application Number: PCT/US01/00663
Remaining Prior Application data removed - See File Wrapper or PALM.
Number Of SEQ ID NOS: 15755
Software: Aeonica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 6968
LENGTH: 17
Type: DNA
ORGANISM: Homo sapiens
US-09-866-108A-6968

Query Match
Best Local Similarity 100.0%; Score 15; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      28 CAGTGCATCCAGAAG 42
      |||||
Db      1 CAGTGCATCCAGAAG 15

RESULT 139
US-08-475-742-5
Sequence 5, Application US/08475742
Patent No. 6121015
GENERAL INFORMATION:
APPLICANT: O'Malley, Karen L
APPLICANT: Todd, Richard D
TITLE OF INVENTION: Gene Encoding the Rat Dopamine D4 Receptor
FILE REFERENCE: WU 102 CON DIV
CURRENT APPLICATION NUMBER: US/08/475,742
CURRENT FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: US 08/261,293
EARLIER FILING DATE: 1994-06-16
EARLIER APPLICATION NUMBER: US 08/014,013
EARLIER FILING DATE: 1993-01-28
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 18
Type: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: primer-TM
OTHER INFORMATION: v1/vii primer set ord-403
PUBLICATION INFORMATION:
TITLE: The rat dopamine D4 receptor: sequence, gene structure
TITLE: and demonstration of expression in the cardiovascular
TITLE: system
JOURNAL: New Biol.
VOLUME: 4
PAGES: 1-9
DATE: 1992
US-08-475-742-5

0.8%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1,1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

988 TGCTGCTGCCCTTC 1002
|||||
1 TGCTGCTGCCCTTC 15

140
261-293-5
ence 5, Application US/08261293
nt No. 6486310
RRAL INFORMATION:
PLICANT: O'Malley, Karen L.
PLICANT: Todd, Richard D.
TITLE OF INVENTION: Gene Encoding the Rat Dopamine D4
TITLE OF INVENTION: Receptor
UMBER OF SEQUENCES: 16
ORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick & Cody
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30309-4530
OMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
URRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,293
ILING DATE:
CLASSIFICATION: 435
RIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/014,013
ILING DATE:
TTORNEY/AGENT INFORMATION:
NAME: Fabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: WU 102
ELECTRONIC INFORMATION:
TELEPHONE: (404) 815-6524
TELEFAX: (404) 815-6555
ORATION FOR SEQ ID NO: 5:
EQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
OLECULE TYPE: CDNA
YPOTHEICAL: NO
NTI-SENSE: NO
ATURE:
NAME/KEY: misc feature
LOCATION: 1..18
OTHER INFORMATION: /note="Synthetic oligonucleotide
OTHER INFORMATION: primer - Tm VI/VII primer set ord-403"
UBLICATION INFORMATION:
AUTHORS: O'Malley, K. L.
AUTHORS: Harmon, S.
AUTHORS: Tang, L.
AUTHORS: Todd, R. D.
TITLE: The rat dopamine D4 receptor: sequence, gene
TITLE: structure and demonstration of expression in the
TITLE: cardiovascular system.
JOURNAL: New Biol.
VOLUME: 4
PAGES: 1-9
DATE: 1992
RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 1 TO 18
261-293-5
Y Match 0.8%; Score 15; DB 1; length 18;
Local Similarity 100.0%; Pred. NO. 1.1e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 988 TGCTGCTGCCCTTC 1002
|||||
Db 1 TGCTGCTGCCCTTC 15

RESULT 141
US-08-210-762E-45/C
; Sequence 45, Application US/08210762E
; Patent No. 5837441
; GENERAL INFORMATION:
; APPLICANT: Hjelte, Brian
; APPLICANT: Jensen, Steve
; TITLE OF INVENTION: Molecular Clones Producing Recombinant DNA Antigens of
; TITLE OF INVENTION: the HARDS Virus.
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffman, Maason & Gitler
; STREET: 2361 Jefferson Davis Highway
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 500 Kb storage
; COMPUTER: Accel 486
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: Wordperfect 6.1 for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/210,762E
; FILING DATE: 22-MAR-94
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,035
; FILING DATE: 26-OCT-93
; APPLICATION NUMBER: 08/120,096
; FILING DATE: 13-SEP-93
; APPLICATION NUMBER: 08/111,519
; FILING DATE: 25-AUG-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Buttemi, Jean A.
; REGISTRATION NUMBER: 24,236
; REFERENCE/DOCKET NUMBER: A4710CIP3.SL3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)418-2768
; TELEFAX: (703)418-2768
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA viral
; HYPOTHEICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Four Corners Hantavirus
; INDIVIDUAL ISOLATE: 3H226
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; PUBLICATION INFORMATION:
; AUTHORS: Hjelte, Brian
; AUTHORS: Jensen, Steven
; AUTHORS: Torres-Martinez, No. 5837441ah
; AUTHORS: Yamada, Takashi
; AUTHORS: No. 5837441le, Kurt
; AUTHORS: Zumwalt, Ross
; AUTHORS: MacInnes, Kersti
; AUTHORS: Myers, Gerald
; TITLE: A No. 5837441el Hantavirus Associated with an Outbreak of Fatal Respirato
; TITLE: Disease in the Southwestern United States: Evolutionary Relationships to

TITLE: Hantaviruses-Running Title: Hantavirus-associated ARDS
JOURNAL: Journal of Virology
VOLUME: 68
PAGES: in press
DATE: 1994
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 18
210-762E-45

Match 0.8%; Score 14.8; DB 1; Length 18;
Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

129 CCTGAGCCCGAGCGCCA 146
18 CCTGAGCCCGATGCACCA 1

142
-071-433-50/c
ence 50, Application US/09071433A
ent No. 6197584
SERIAL INFORMATION:
PLICANT: Bennett, C. Frank
PLICANT: Cowsett, Lex M
FILE OF INVENTION: Antisense Modulation of CD40 Expression
E REFERENCE: RTS-0002
RENT APPLICATION NUMBER: US/09/071,433A
RENT FILING DATE: 1998-05-01
BER OF SEQ ID NOS: 91
FTWARE: PatentIn Ver. 2.0
ID NO 50
NGTH: 18
YPE: DNA
GANISM: Artificial Sequence
ATURE:
HER INFORMATION: Description of Artificial Sequence: Synthetic
-071-433-50

Match 0.8%; Score 14.8; DB 1; Length 18;
Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1406 TCAGCTTCTCTCCATG 1423
18 TCGCTTCTCTCCATG 1

143
-106-075A-45/c
ence 45, Application US/09106075A
ent No. 6316250
SERIAL INFORMATION:
PLICANT: Hjelle MD, Brian
PLICANT: Jentson, Steve
FILE OF INVENTION: Molecular Clones Producing Recombinant DNA Antigens of
E OF INVENTION: the HARDS Virus.
E REFERENCE: 10312-8U1, Hjelle et al. (210312.0009)
RENT APPLICATION NUMBER: US/09/106,075A
RENT FILING DATE: 1998-06-29
RENT APPLICATION NUMBER: 08/210,762
FOR FILING DATE: 1994-03-22
FOR APPLICATION NUMBER: 08/141,035
FOR FILING DATE: 1993-10-26
FOR APPLICATION NUMBER: 08/120,096
FOR FILING DATE: 1993-09-13
FOR APPLICATION NUMBER: 08/111,519
FOR FILING DATE: 1993-08-25
BER OF SEQ ID NOS: 90
FTWARE: PatentIn Ver. 2.1
ID NO 45
NGTH: 18
YPE: DNA
GANISM: Prospekt Hill Virus

US-09-106-075A-45

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 129 CCTGAGCCCGAGCGCCA 146
DB 18 CCTGAGCCCGATGCACCA 1

RESULT 144
US-09-341-587-9/c
Sequence 9, Application US/09341587
Patent No. 6346606
GENERAL INFORMATION:
APPLICANT: Mollenhauer, Jan
TITLE OF INVENTION: Protein Containing an SRCR Domain
FILE REFERENCE: 4121-108
CURRENT APPLICATION NUMBER: US/09/341,587
CURRENT FILING DATE: 1999-08-31
EARLIER APPLICATION NUMBER: PCT/DE98/00096
EARLIER FILING DATE: 1998-01-09
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 18
TYPE: DNA
ORGANISM: Homo sapiens
US-09-341-587-9

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1263 CAGCCGCTGAGACCA 1280
DB 18 CAGCTGCTGAGACCA 1

RESULT 145
US-08-411-020-44
Sequence 44, Application US/08411020
Patent No. 5712094
GENERAL INFORMATION:
APPLICANT: SEIDEL, H. MARTI
APPLICANT: LAMB, I. PETER
APPLICANT: CHAN, SHIN-SHAY TIAN
TITLE OF INVENTION: METHODS AND ASSOCIATED REAGENTS FOR
TITLE OF INVENTION: DETECTING MODULATORS OF CYTOKINE ACTION
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ligand Pharmaceuticals Incorporated
STREET: 9393 Towne Centre Drive
CITY: San Diego
STATE: California
COUNTRY: US
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/411,020
FILING DATE: 27-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jurgensen, Thomas E.
REGISTRATION NUMBER: 34,195
REFERENCE/DOCKET NUMBER: 016-0030.US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 550-7675

TELEFAX: (619) 535-3906
 ORAMATION FOR SEQ ID NO: 44:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 OLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
 DESCRIPTION: SYNTHETIC DNA"
 411-020-44

Y Match 0.8%; Score 14.4; DB 1; Length 18;
 Local Similarity 93.8%; Pred. No. 1.3e+02;
 hes 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1717 TCCATTCTCGAAGC 1732
 |||||
 3 TCCATTCTCGAAGC 18

146
 106-038A-9
 ence 9, Application US/09106038A
 nt No. 6007995
 ERAL INFORMATION:
 PPLICANT: Brenda F. Baker and Lex M. Cowsett
 TITLE OF INVENTION: ANTISENSE MODULATION OF TNFR1
 TITLE OF INVENTION: EXPRESSION
 UMBER OF SEQUENCES: 91
 ORRESPONDENCE ADDRESS:
 ADDRESSEE: Isis Pharmaceuticals, Inc.
 STREET: 2292 Faraday Avenue
 CITY: Carlebad
 STATE: CA
 COUNTRY: U.S.A.
 ZIP: 92008

OMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: Windows NT
 SOFTWARE: Microsoft Word 97
 URRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/106,038A
 FILING DATE: June 26, 1998

CLASSIFICATION: 514
 TTORNEY/AGENT INFORMATION:
 NAME: Laurel Spear Bernstein
 REGISTRATION NUMBER: 37,280
 REFERENCE/DOCKET NUMBER: RTS-0004
 ELECOMMUNICATION INFORMATION:
 TELEPHONE: (760) 931-9200
 TELEFAX: (760) 603-3820
 ORAMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 106-038A-9

Y Match 0.8%; Score 14.4; DB 1; Length 18;
 Local Similarity 93.8%; Pred. No. 1.3e+02;
 hes 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

105 CCTCTGCTGCTTT 120
 |||||
 3 CCTCTCTGCTTT 18

147
 289-376-17/c
 ence 17, Application US/09289376

Patent No. 6013788
 GENERAL INFORMATION:
 APPLICANT: Brett P. Monia
 APPLICANT: Lex M. Cowsett
 TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD3 EXPRESSION
 FILE REFERENCE: RTS-0043
 CURRENT APPLICATION NUMBER: US/09/289,376
 CURRENT FILING DATE: 1999-04-09
 NUMBER OF SEQ ID NOS: 47
 SEQ ID NO 17
 LENGTH: 18
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Antisense Oligonucleotide
 US-09-289-376-17

Query Match 0.8%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 1.3e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1118 TCATCTACTGCTGCTT 1133
 |||||
 Db 18 TCATCTACTGCGCGCT 3

RESULT 148
 US-09-344-520-9/c
 Sequence 9, Application US/09344520
 Patent No. 6037176
 GENERAL INFORMATION:
 APPLICANT: Frank Bennett
 APPLICANT: Brett P. Monia
 TITLE OF INVENTION: ANTISENSE MODULATION OF integrin beta 3 EXPRESSION
 FILE REFERENCE: RTS-0070
 CURRENT APPLICATION NUMBER: US/09/344,520
 CURRENT FILING DATE: 1999-06-25
 NUMBER OF SEQ ID NOS: 47
 SEQ ID NO 9
 LENGTH: 18
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Antisense Oligonucleotide
 US-09-344-520-9

Query Match 0.8%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 1.3e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 804 CTGTGTGACTGTGCTG 819
 |||||
 Db 18 CTGGGTGACTGTGCTG 3

RESULT 149
 US-08-584-040-6255/c
 Sequence 6255, Application US/08584040
 Patent No. 6346398
 GENERAL INFORMATION:
 APPLICANT: Pavco, Pamela
 APPLICANT: McSwiggen, James
 APPLICANT: Stinchcomb, Dan T.
 APPLICANT: Escobedo, Jaime
 TITLE OF INVENTION: METHOD AND REAGENT FOR THE
 TITLE OF INVENTION: TREATMENT OF DISEASES OR
 TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
 TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
 GROWTH FACTOR
 NUMBER OF SEQUENCES: 8502
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Storage
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996

CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440

TELEX: 67-3510

FORMATION FOR SEQ ID NO: 6255:

SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
584-040-6255

Query Match 0.8%; Score 14.4; DB 1; Length 18;
Local Similarity 93.8%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

662 TCTGTGTCATCTGGGT 677
18 TCTGTGTCATCTGAGT 3

F 150
422-978-10970
ence 10970, Application US/09422978
ent No. 6537751
RAL INFORMATION:

PLICANT: Cohen, Daniel
PLICANT: Blumenfeld, Marla
PLICANT: Chumakov, Ilya
FILE OF INVENTION: Biallelic markers for use in constructing a high density...

REFERENCE: GENSET.020CPI
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: US 09/298,850
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: US 60/109,732
PRIOR FILING DATE: 1998-11-23
PRIOR APPLICATION NUMBER: US 60/082,614
PRIOR FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
ID NO 10970

LENGTH: 18

TYPE: DNA
ORGANISM: Homo sapiens

NATURE:
NAME/KEY: primer:bind

LOCATION: 1..18
OTHER INFORMATION: downstream amplification primer 99-23427 for SEQ 3105, in complement
422-978-10970

Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1404 CTTGAGCTTCCTCC 1419
Db 2 CTTGATCTTCCTCC 17

RESULT 151

US-09-371-772B-3013/C
Sequence 3013, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Pavoce, Pam
APPLICANT: McSwiggan, Jim

APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
FILE REFERENCE: MBH00,876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B

CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3013

LENGTH: 18
TYPE: RNA
ORGANISM: Mus sp.
US-09-371-772B-3013

Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 662 TCTGTGTCATCTGGGT 677
Db 18 TCTGTGTCATCTGAGT 3

RESULT 152

US-09-747-391-42/C
Sequence 42, Application US/09747391
Patent No. 6670124
GENERAL INFORMATION:
APPLICANT: Chow, Robert
APPLICANT: Tonal, Richard
APPLICANT: Stemcyte, Inc.

TITLE OF INVENTION: High Throughput Methods of HLA Typing
FILE REFERENCE: 020035-000210US
CURRENT APPLICATION NUMBER: US/09/747,391
CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/172,768
PRIOR FILING DATE: 1999-12-20
NUMBER OF SEQ ID NOS: 278
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 42

LENGTH: 18
TYPE: DNA
ORGANISM: Homo sapiens
US-09-747-391-42

Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 438 CCGGAGCGCTCCATG 453
|||||

18 CGCGAGGACCTTCATG 3

153

685-664B-3013/c
ence 3013, Application US/09685664B
nt No. 6818447

RAL INFORMATION:

LICANT: Ribozyme Pharmaceuticals, Inc.

LICANT: Pavco, Pam

LICANT: McSwigen, Jim

LICANT: Stinchcomb, Dan

LICANT: Escobedo, Jaime

LE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate

E REFERENCE: MHB00-876-K (400/021)

RENT APPLICATION NUMBER: US/09/685,664B

RENT FILING DATE: 2000-10-10

OR APPLICATION NUMBER: US 60/005,974

OR FILING DATE: 1995-10-26

OR APPLICATION NUMBER: US 08/584,040

OR FILING DATE: 1996-01-08

OR APPLICATION NUMBER: US 09/371,772

OR FILING DATE: 1999-08-10

BER OF SEQ ID NOS: 8231

TWARE: PatentIn version 3.0

ID NO 3013

NGTH: 18

PE: RNA

GANISM: Mus musculus

685-664B-3013

Y Match 0.8%; Score 14.4; DB 1; Length 18;
Local Similarity 93.8%; Pred. No. 1.3e+02;
hes 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

662 TCTGTGTCATCTGGGT 677

18 TCTGTGTCATCTGAGT 3

154

138-674B-3013/c
ence 3013, Application US/10138674B
nt No. 7034009

RAL INFORMATION:

LICANT: Sirna Therapeutics, Inc.

LICANT: Pavco, Pam

LICANT: McSwigen, James

LICANT: Stinchcomb, Dan

LICANT: Escobedo, Jaime

LE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

E REFERENCE: MHB00-876-N (400/049)

RENT APPLICATION NUMBER: US/10/138,674B

RENT FILING DATE: 2002-05-03

BER OF SEQ ID NOS: 20829

TWARE: PatentIn version 3.0

ID NO 3013

NGTH: 18

PE: RNA

GANISM: Mus musculus

138-674B-3013

Y Match 0.8%; Score 14.4; DB 1; Length 18;
Local Similarity 93.8%; Pred. No. 1.3e+02;
hes 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

662 TCTGTGTCATCTGGGT 677

18 TCTGTGTCATCTGAGT 3

RESULT 155
US-09-874-601-5
; Sequence 5, Application US/09874601
; Patent No. 6632057

GENERAL INFORMATION:

APPLICANT: LEWIN, ALFRED S.

APPLICANT: SHAW, LYNN C.

APPLICANT: GRANT, MARIA B.

TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD.

TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES

FILE REFERENCE: 4300.014100

CURRENT APPLICATION NUMBER: US/09/874,601

CURRENT FILING DATE: 2001-05-01

PRIOR APPLICATION NUMBER: 09/063,667

PRIOR FILING DATE: 1998-04-21

PRIOR APPLICATION NUMBER: 60/046,147

PRIOR FILING DATE: 1997-05-09

PRIOR APPLICATION NUMBER: 60/044,492

PRIOR FILING DATE: 1997-04-21

NUMBER OF SEQ ID NOS: 182

SOFTWARE: PatentIn version 3.0

SEQ ID NO 5

LENGTH: 14

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:

NAME/KEY: misc feature

LOCATION: ()..()

OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE

US-09-874-601-5

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 71.4%; Pred. No. 92;
Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 689 TGCTGGCCTTCCCC 702

Db 1 UGCGGCGCCUCCCC 14

RESULT 156

US-09-543-679A-1371/c
; Sequence 1371, Application US/09543679A
; Patent No. 7034007

GENERAL INFORMATION:

APPLICANT: NYCE, Jonathan W.

TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,

COMPOSITIONS, KIT & METHOD FOR TREATMENT

OF AIRWAY DISORDERS ASSOCIATED WITH

BRONCHOCONSTRICTION, LUNG INFLAMMATION,

NUMBER OF SEQUENCES: 3111

CORRESPONDENCE ADDRESS:

ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.

STREET: 7 Clarke Drive

CITY: Cranbury

STATE: NJ

COUNTRY: USA

ZIP: 08512

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-R

OPERATING SYSTEM: DOS

SOFTWARE: N/A

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/543,679A

FILING DATE: 13-Apr-2000

CLASSIFICATION: UNKNOWN

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/127,958

FILING DATE: 1998-08-03

ATTORNEY/AGENT INFORMATION:

NAME: Amzel, Viviana

REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: EPI-0067191b
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 609-409-3035
 TELEFAX: 413-254-9245
 TELEX: <Unknown>
 INFORMATION FOR SEQ ID NO: 1371:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 1371:
 -543-679A-1371
 Match 0.8%; Score 14; DB 1; Length 14;
 Local Similarity 100.0%; Pred. No. 92;
 hes 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 384 AGCCCAAAAGAA 397
 14 AGCCCAAAAGAA 1
 157
 -588-821-84
 Ince 84, Application US/08588821
 In No. 5712097
 IERAL INFORMATION:
 APPLICANT: Kern, Scott E.
 APPLICANT: Hahn, Stephan A.
 TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE, DPC4
 NUMBER OF SEQUENCES: 91
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 4225 Executive Square, Suite 1400
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/588,821
 FILING DATE: 19-JAN-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Haile, Lisa A.
 REGISTRATION NUMBER: 38,347
 REFERENCE/DOCKET NUMBER: 07265/079001
 TELEPHONE: 619/678-5070
 TELEFAX: 619/678-5099
 INFORMATION FOR SEQ ID NO: 84:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 US-08-915-214-84
 Query Match 0.8%; Score 14; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 730 ATGCCGAGAGT 743
 DB 2 ATGCCGAGAGT 15
 RESULT 159
 US-09-005-532-84
 Sequence 84, Application US/09005532
 Patent No. 5955292
 GENERAL INFORMATION:
 APPLICANT: Kern, Scott E.
 APPLICANT: Hahn, Stephan A.
 TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE, DPC4
 NUMBER OF SEQUENCES: 91
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 4225 Executive Square, Suite 1400
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

RESULT 158
 US-08-915-214-84
 Sequence 84, Application US/08915214
 Patent No. 5814457
 GENERAL INFORMATION:
 APPLICANT: Kern, Scott E.
 APPLICANT: Hahn, Stephan A.
 TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE, DPC4
 NUMBER OF SEQUENCES: 91
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 4225 Executive Square, Suite 1400
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 US-08-915-214-84
 Query Match 0.8%; Score 14; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 730 ATGCCGAGAGT 743
 DB 2 ATGCCGAGAGT 15
 RESULT 159
 US-09-005-532-84
 Sequence 84, Application US/09005532
 Patent No. 5955292
 GENERAL INFORMATION:
 APPLICANT: Kern, Scott E.
 APPLICANT: Hahn, Stephan A.
 TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE, DPC4
 NUMBER OF SEQUENCES: 91
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 4225 Executive Square, Suite 1400
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
 URGENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/005,532
 FILING DATE:
 CLASSIFICATION:
 RIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/588,821
 FILING DATE: 19-JAN-1996
 TTORNEY/AGENT INFORMATION:
 NAME: Haile, Lisa A.
 REGISTRATION NUMBER: 39,347
 REFERENCE/DOCKET NUMBER: 07265/079001
 ELECOMMUNICATION INFORMATION:
 TELEPHONE: 619/678-5070
 TELEFAX: 619/678-5099
 ORAMATION FOR SEQ ID NO: 84:
 EQUENCE CHARACTERISTICS:
 LENGTH: 16 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 005-532-84

Y Match 0.8%; Score 14; DB 1; Length 16;
 Local Similarity 100.0%; Pred. No. 1.2e+02;
 hes 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

730 ATGCCCGACGAGT 743
 ||||||||||||
 2 ATGCCCGACGAGT 15

160
 897-340-14
 ence 14, Application US/08897340
 nt No. 5955306
 ERAL INFORMATION:
 PPLICANT: Gimeno, Carlos J. and Errada, Patrick, R.
 TITLE OF INVENTION: Weight Control Pathway Genes and Uses
 TITLE OF INVENTION: Therefor
 UMBER OF SEQUENCES: 36
 ORRESPONDENCE ADDRESS:
 ADDRESSSEE: LAHIVE & COCKFIELD, LLP
 STREET: 28 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109

OMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 URGENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/897,340
 FILING DATE:
 CLASSIFICATION: 435
 RIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/715,032
 FILING DATE: 17-SEP-1996
 TTORNEY/AGENT INFORMATION:
 NAME: Silveri, Jean M.
 REGISTRATION NUMBER: 39,030
 REFERENCE/DOCKET NUMBER: MNI-005CP
 ELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)227-5941
 ORAMATION FOR SEQ ID NO: 14:
 EQUENCE CHARACTERISTICS:
 LENGTH: 17 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single

TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-897-340-14

Query Match 0.8%; Score 14; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 571 TACTCCATGACGCG 584
 ||||||||||||
 Db 3 TACTCCATGACGCG 16

RESULT 161
 US-09-252-329-14
 Sequence 14, Application US/09252329
 Patent No. 6147192
 GENERAL INFORMATION:
 APPLICANT: Gimeno, Carlos J. and Errada, Patrick, R.
 TITLE OF INVENTION: Weight Control Pathway Genes and Uses
 TITLE OF INVENTION: Therefor
 NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESS:
 ADDRESSSEE: LAHIVE & COCKFIELD, LLP
 STREET: 28 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/252,329
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/897,340
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Silveri, Jean M.
 REGISTRATION NUMBER: 39,030
 REFERENCE/DOCKET NUMBER: MNI-005CP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)227-5941
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 17 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-09-252-329-14

Query Match 0.8%; Score 14; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 571 TACTCCATGACGCG 584
 ||||||||||||
 Db 3 TACTCCATGACGCG 16

RESULT 162
 US-09-724-566A-22
 Sequence 22, Application US/09724566A
 Patent No. 6627739
 GENERAL INFORMATION:
 APPLICANT: Anderson, John P.
 APPLICANT: Basi, Gurigbal

PLICANT: Doane, Minh Tam
PLICANT: Frigon, No. 6627739mand
PLICANT: John, Varghese
PLICANT: Power, Michael
PLICANT: Sinha, Sukanto
PLICANT: Tatsuno, Gwen
PLICANT: Tung, Jay
PLICANT: Wang, Shuwen
PLICANT: McConlogue, Lisa
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
METHOD OF INVENTION: Methods
SEQUENCE REFERENCE: 228-US-NEWC2
CURRENT APPLICATION NUMBER: US/09/724,566A
PENDING FILING DATE: 2000-11-28
FOR APPLICATION NUMBER: US 09/501,708
FOR FILING DATE: 2000-02-10
FOR APPLICATION NUMBER: 60/119,571
FOR FILING DATE: 1999-02-10
FOR APPLICATION NUMBER: 60/139,172
FOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 104
SOFTWARE: FastSeq for Windows Version 4.0
ID NO: 22
LENGTH: 17
SPECIES: DNA
ORGANISM: Artificial Sequence
NATURE: Degenerate oligonucleotide primer
FEATURE: misc_feature
LOCATION: (1)...(17)
OTHER INFORMATION: n = A,T,C or G
-724-566A-22
y Match 0.8%; Score 14; DB 1; Length 17;
Local Similarity 82.4%; Pred. No. 1.3e+02;
Indels 1; Mismatches 2; Gaps 0;
1306 GAGGAGGAGCCAGAGGA 1322
1 GAGGAGGAGCCAGAGGA 17
-866-108A-6965
Sequence 6965, Application US/09866108A
Patent No. 6686188
GENERAL INFORMATION:
PLICANT: GU, Yizhong
PLICANT: JI, Yonggang
PLICANT: PENN, Sharon G.
PLICANT: HANZEL, David K.
PLICANT: RANK, David R.
PLICANT: CHEN, Wensheng
PLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
SEQUENCE REFERENCE: AECOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
PENDING FILING DATE: 2001-05-25
FOR APPLICATION NUMBER: US 60/207,456
FOR FILING DATE: 2000-05-26
FOR APPLICATION NUMBER: GB 24263.6
FOR FILING DATE: 2000-10-04
FOR APPLICATION NUMBER: US 60/236,359
FOR FILING DATE: 2000-09-27
FOR APPLICATION NUMBER: PCT/US01/00666
FOR FILING DATE: 2001-01-30
FOR APPLICATION NUMBER: PCT/US01/00667
FOR FILING DATE: 2001-01-30
FOR APPLICATION NUMBER: PCT/US01/00664
FOR FILING DATE: 2001-01-30
FOR APPLICATION NUMBER: PCT/US01/00669
FOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aecmica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO: 6965
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108A-6965
Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 28 CAGTGATCCAGAA 41
Db 4 CAGTGATCCAGAA 17
RESULT 164
US-09-866-108A-6969
Sequence 6969, Application US/09866108A
Patent No. 6686188
GENERAL INFORMATION:
PLICANT: GU, Yizhong
PLICANT: JI, Yonggang
PLICANT: PENN, Sharon G.
PLICANT: HANZEL, David K.
PLICANT: RANK, David R.
PLICANT: CHEN, Wensheng
PLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
SEQUENCE REFERENCE: AECOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
PENDING FILING DATE: 2001-05-25
FOR APPLICATION NUMBER: US 60/207,456
FOR FILING DATE: 2000-05-26
FOR APPLICATION NUMBER: GB 24263.6
FOR FILING DATE: 2000-10-04
FOR APPLICATION NUMBER: US 60/236,359
FOR FILING DATE: 2000-09-27
FOR APPLICATION NUMBER: PCT/US01/00666
FOR FILING DATE: 2001-01-30
FOR APPLICATION NUMBER: PCT/US01/00667
FOR FILING DATE: 2001-01-30
FOR APPLICATION NUMBER: PCT/US01/00664
FOR FILING DATE: 2001-01-30
FOR APPLICATION NUMBER: PCT/US01/00669
FOR FILING DATE: 2001-01-30
FOR APPLICATION NUMBER: PCT/US01/00665
FOR FILING DATE: 2001-01-30
FOR APPLICATION NUMBER: PCT/US01/00668
FOR FILING DATE: 2001-01-30
FOR APPLICATION NUMBER: PCT/US01/00663
FOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aecmica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO: 6969
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108A-6969
Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

hes 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

29 AGTCATCCAGAG 42
|||||
1 AGTCATCCAGAG 14

165
471-669A-22
ence 22, Application US/09471669A
nt No. 6830918
RAL INFORMATION:
LICANT: Anderson, John P.
LICANT: Basi, Guribai
LICANT: Doane, Minh Tam
LICANT: Frigon, No. 6830918mand
LICANT: John, Varghese
LICANT: Power, Michael
LICANT: Sinha, Sukanto
LICANT: Tatsuno, Gwen
LICANT: Tung, Jay
LICANT: Wang, Shuwen
LICANT: McConlogue, Lisa
LE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
E REFERENCE: 015270-006430US
RENT APPLICATION NUMBER: US/09/471,669A
OR FILING DATE: 1998-12-31
OR APPLICATION NUMBER: US 60/114,408
OR FILING DATE: 1999-02-10
OR APPLICATION NUMBER: US 60/139,172
OR FILING DATE: 1999-06-15
BER OF SEQ ID NOS: 108
TWARE: PatentIn Ver. 2.1
ID NO 22
NGTH: 17
PE: DNA
GANISM: Artificial Sequence
ATURE:
HER INFORMATION: Description of Artificial Sequence: Degenerate
HER INFORMATION: oligonucleotide primer
ATURE:
ME/KEY: misc feature
CATION: (...)
HER INFORMATION: n = a, c, g, or t.
471-669A-22

Y Match 0.8%; Score 14; DB 1; Length 17;
Local Similarity 82.4%; Pred. No. 1.3e+02;
hes 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

1306 GAGGAGGAGCCAGAGGA 1322
|||:|||||
1 GAYGARAGAGCCAGAGGA 17

166
701-935-3
ence 3, Application US/07701935
nt No. 5336595
ERAL INFORMATION:
PLICANT: Strader, C. D.
PLICANT: Fong, T. M.
TITLE OF INVENTION: Method of Using Human Neurokinin-1
TITLE OF INVENTION: Receptor Short Form
UMBER OF SEQUENCES: 27
ORRESPONDENCE ADDRESS:
ADDRESSER: Merck & Co., Inc.
STREET: P. O. Box 2000
CITY: Rahway
STATE: New Jersey

COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/701,935
FILING DATE: 19910517
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nicholson, William H.
REGISTRATION NUMBER: 25,147
REFERENCE/DOCKET NUMBER: 18409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-5315
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
US-07-701-935-3

Query March 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 448 TCCATGCTGCATTCAA 464
|||||
Db 1 TGCATGCTGCCTTCAA 17

RESULT 167
US-08-117-965-3
Sequence 3, Application US/08117965
Patent No. 548486
GENERAL INFORMATION:
APPLICANT: Tung, Fong M.
TITLE OF INVENTION: Human Neurokinin-1 Receptor
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P. O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,965
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 691,197
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Nicholson, William H.
REGISTRATION NUMBER: 25,147
REFERENCE/DOCKET NUMBER: 18387
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-5315
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
117-965-3

Match 0.8% Score 13.8; DB 1; Length 17;
Local Similarity 88.2% Pred. No. 1.4e+02;
Indels 15; Conservative 0; Mismatches 2; Gaps 0;

448 TCCATGCTGCTGCTCA 464
1 TGCATGGCTGCTTCA 17

168
-373-124A-1749
ence 1749, Application US/08373124A
nt No. 5646042
HERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwigen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

FORMATION FOR SEQ. ID NO: 1749:

SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
-373-124A-1749

Match 0.8% Score 13.8; DB 1; Length 17;
Local Similarity 70.6% Pred. No. 1.4e+02;

Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 441 GGAGGCTTCATGGCTG 457
1 GGAGGCTTCATGGCTG 17

RESULT 169

US-08-287-075-10/c
Sequence 10, Application US/08287075
Patent No. 5656462

GENERAL INFORMATION:

APPLICANT: Keller, Cy'ia
APPLICANT: Mitsuhashi, Masato
APPLICANT: Akitaya, Tatsuo
TITLE OF INVENTION: POLYNUCLEOTIDE IMMOBILIZED SUPPORT
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: KNOBBE, MARTENS, OLSON, AND BEAR
STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR
CITY: NEWPORT BEACH
STATE: CA
COUNTRY: USA

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/287,075
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/827,975
FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: HITACHI.002A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: TRC-AS OLIGONUCLEOTIDE PRIMER
US-08-287-075-10

Query Match

Best Local Similarity 0.8% Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 983 CCATCTGCTGCTGCTCC 999
Db 17 CCATCTGCTGCTGCTCC 1

RESULT 170

US-08-435-628-1749
Sequence 1749, Application US/08435628
Patent No. 5817796

GENERAL INFORMATION:

APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwigen, James

APPLICANT: Jarvis, Thale
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
 TREATMENT OF RESTENOSIS AND
 TITLE OF INVENTION: CANCER USING RIBOZYMES
 NUMBER OF SEQUENCES: 2627
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/435,628
 FILING DATE: 05-MAY-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/373,124
 FILING DATE: January 13, 1995
 APPLICATION NUMBER: 08/245,466
 FILING DATE: May 18, 1994
 APPLICATION NUMBER: 08/192,943
 FILING DATE: February 7, 1994
 APPLICATION NUMBER: 07/987,132
 FILING DATE: December 7, 1992
 APPLICATION NUMBER: 07/936,422
 FILING DATE: August 26, 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 209/035
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELETYPE: 67-3510
 ORAMATION FOR SEQ ID NO: 1749:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 17 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 435-628-1749
 Y Match 0.8%; Score 13.8; DB 1; Length 17;
 Local Similarity 70.6%; Pred. No. 1.4e+02;
 hes 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 441 GGAGCGCTTCATGGCTG 457
 |||||:|||||:
 1 GGAGCGCTTCATGGCTG 17
 171
 985-162-243/c
 ence 243, Application US/08985162
 nt No. 6057156
 ERAL INFORMATION:
 APPLICANT: Akhtar, Saghar
 APPLICANT: Fell, Patricia
 APPLICANT: McSwigen, James
 TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT
 TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
 TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
 NUMBER OF SEQUENCES: 1877
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSeq for Windows 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/985,162
 FILING DATE: 04 December 1997
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/036,476
 FILING DATE: 31 January 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 230/107
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELETYPE: 67-3510
 INFORMATION FOR SEQ ID NO: 243:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 17 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-985-162-243
 Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.4e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1313 AGCCAGAGAGAGGCCCC 1329
 DB 17 AGCAAGAGAGAGGCCCC 1
 RESULT 172
 US-08-584-040-3947/c
 ; Sequence 3947, Application US/08584040
 ; Patent No. 6346398
 ; GENERAL INFORMATION:
 APPLICANT: Pavco, Pamela
 APPLICANT: McSwigen, James
 APPLICANT: Stinchcomb, Dan T.
 APPLICANT: Escobedo, Jaime
 TITLE OF INVENTION: METHOD AND REAGENT FOR THE
 TITLE OF INVENTION: TREATMENT OF DISEASES OR
 TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
 TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
 TITLE OF INVENTION: GROWTH FACTOR
 NUMBER OF SEQUENCES: 8502
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
FORMATION FOR SEQ ID NO: 3947:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
-584-040-3947

Match 0.8%; Score 13.8; DB 1; Length 17;
Local Similarity 88.2%; Pred. No. 1.4e+02;
base 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

714 CTCACCGACAGACCA 730
17 CACACCGACAGACCA 1

173
-584-040-4119/c
ence 4119, Application US/08584040
nt No. 6346398
ERAL INFORMATION:
PLICANT: Pavco, Pamela
PLICANT: McSwigen, James
PLICANT: Stinchcomb, Dan T.
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064

TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
FORMATION FOR SEQ ID NO: 4119:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-4119

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1505 TTCATCTGGACATCA 1521
DB 17 TTCATCTGGATCATGA 1

RESULT 174
US-08-584-040-5545/c
Sequence 5545, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwigen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
FORMATION FOR SEQ ID NO: 5545:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-5545

Y Match 0.8%; Score 13.8; DB 1; Length 17;
Local Similarity 88.2%; Pred. No. 1.4e+02;
hes 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

714 CTCACCCAGAGACCA 730
|||||
17 CACACCCAGAGACCA 1

175
584-040-5694/C
ence 5694, Application US/08584040
nt No. 6346398
ERAL INFORMATION:
PPLICANT: Pavco, Pamela
PPLICANT: McSwigen, James
PPLICANT: Stinchcomb, Dan T.
PPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: GROWTH FACTOR
UMBER OF SEQUENCES: 8502
ORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
OMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
URRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
RIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
TTOREY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
ELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
RMATION FOR SEQ ID NO: 5694:
EQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
584-040-5694

Y Match 0.8%; Score 13.8; DB 1; Length 17;
Local Similarity 88.2%; Pred. No. 1.4e+02;
hes 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1505 TTCATCTGGAACCATCA 1521
|||||
17 TTCATCTGGAACCATCA 1

176
679-645-765/C
ence 765, Application US/08679645

; Patent No. 6350934
; GENERAL INFORMATION:
; APPLICANT: Zwick, Michael G.
; APPLICANT: Edington, Brent E.
; APPLICANT: McSwigen, James A.
; APPLICANT: Merlo, Patricia Ann Owens
; APPLICANT: Guo, Lining
; APPLICANT: Skokut, Thomas A.
; APPLICANT: Young, Scott A.
; APPLICANT: Folkerts, Otto
; APPLICANT: Merlo, Donald J.
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR
; TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
; TITLE OF INVENTION: IN PLANTS
; NUMBER OF SEQUENCES: 1263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/679,645
; FILING DATE: July 12, 1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/001,135
; FILING DATE: July 13, 1995
; APPLICATION NUMBER: 08/300,726
; FILING DATE: September 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 219/247
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 765:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-679-645-765

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 636 GTCAGCCAGAGCCACCA 652
|||||
DB 17 GTCAGCCAGAGCCACCA 1

RESULT 177
US-09-371-772B-1714/C
; Sequence 1714, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime

STRANDEDNESS: single
TOPOLOGY: linear
401-063-243

Y Match 0.8%; Score 13.8; DB 1; Length 17;
Local Similarity 88.2%; Pred. No. 1.4e+02;
hes 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1313 AGCAGAGGAGGAGGCCCC 1329
17 AGCAGAGGAGGAGGCCCC 1

181
866-108A-2756
ence 2756, Application US/09866108A
nt No. 6686188

RAL INFORMATION:
LICANT: GU, Yizhong
LICANT: JI, Yonggang
LICANT: PENN, Sharon G.
LICANT: HANZEL, David K.
LICANT: RANK, David R.
LICANT: CHEN, Wensheng
LICANT: SHANNON, Mark
LE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
E REFERENCE: AEOMICA-7
RENT APPLICATION NUMBER: US/09/866,108A
RENT FILING DATE: 2001-05-25
OR APPLICATION NUMBER: US 60/207,456
OR FILING DATE: 2000-05-26
OR APPLICATION NUMBER: GB 24263.6
OR FILING DATE: 2000-10-04
OR APPLICATION NUMBER: US 60/236,359
OR FILING DATE: 2000-09-27
OR APPLICATION NUMBER: PCT/US01/00666
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00667
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00664
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00669
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00665
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00668
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00663
OR FILING DATE: 2001-01-30
aining prior Application data removed - See File Wrapper or PALM.

BER OF SEQ ID NOS: 15755
TWARE: Aeomica Sequence Listing Engine
nt No. 6686188
ID NO 2756
NGTH: 17
PE: DNA
GANISM: Homo sapiens
866-108A-2756

Y Match 0.8%; Score 13.8; DB 1; Length 17;
Local Similarity 88.2%; Pred. No. 1.4e+02;
hes 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
1196 GCGACTATGAGGGGCTG 1212
1 GCGAGTATGAGGAGCTG 17

182
866-108A-7674/C
ence 7674, Application US/09866108A
nt No. 6686188
RAL INFORMATION:

APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aeomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 7674
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108A-7674

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1404 CTTAGCTTCTCTCCA 1420
DB 17 CTTGCTTCTCTCCA 1

RESULT 183
US-09-685-664B-1714/C
Sequence 1714, Application US/09685664B
Patent No. 6818447
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwigen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBH00-876-K (400/021)
CURRENT APPLICATION NUMBER: US/09/685,664B
CURRENT FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
PRIOR APPLICATION NUMBER: US 09/371,772
PRIOR FILING DATE: 1999-08-10
NUMBER OF SEQ ID NOS: 8231
SOFTWARE: PatentIn version 3.0

ID NO 1714
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
-685-664B-1714

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

714 CTCACCCAGAGACCA 730
|||||
17 CACACCCAGAGACCA 1

184
-685-664B-1886/C
ence 1886, Application US/09685664B
ent No. 6818447
RAL INFORMATION:
PLICANT: Ribozyme Pharmaceuticals, Inc.
PLICANT: Pavco, Pam
PLICANT: McSwiggen, Jim
PLICANT: Stinchcomb, Dan
PLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to the Regulation of Vascular Endothelial Growth Factor Receptor
REFERENCE: MBH00-876-K (400/021)
CURRENT APPLICATION NUMBER: US/09/685,664B
CURRENT FILING DATE: 2000-10-10
OR APPLICATION NUMBER: US 60/005,974
OR FILING DATE: 1995-10-26
OR APPLICATION NUMBER: US 08/584,040
OR FILING DATE: 1996-01-08
OR APPLICATION NUMBER: US 09/371,772
OR FILING DATE: 1999-08-10
NUMBER OF SEQ ID NOS: 8231
SOFTWARE: PatentIn version 3.0
ID NO 1886
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
-685-664B-1886

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1505 TTCATCTGAGACATCA 1521
|||||
17 TTCATCTGAGACATCA 1

185
-156-306B-6951/C
ence 6951, Application US/10156306B
ent No. 7022828
RAL INFORMATION:
PLICANT: Ribozyme Pharmaceuticals, Inc.
PLICANT: McSwiggen, James
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to the Regulation of Vascular Endothelial Growth Factor Receptor
REFERENCE: MBH01-664-A (400/050)
CURRENT APPLICATION NUMBER: US/10/156,306B
CURRENT FILING DATE: 2002-05-28
NUMBER OF SEQ ID NOS: 8014
SOFTWARE: PatentIn version 3.0
ID NO 6951
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
-156-306B-6951

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1402 AGCTTCAGCTTCCTC 1418
|||||
17 AGCTTCCTCTCTCTC 1

186
US-10-138-674B-1714/C
Sequence 1714, Application US/10138674B
Patent No. 7034009
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to the Regulation of Vascular Endothelial Growth Factor Receptor
REFERENCE: MBH00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/138,674B
CURRENT FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 20829
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1714
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-10-138-674B-1714

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

714 CTCACCCAGAGACCA 730
|||||
17 CACACCCAGAGACCA 1

187
US-10-138-674B-1886/C
Sequence 1886, Application US/10138674B
Patent No. 7034009
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to the Regulation of Vascular Endothelial Growth Factor Receptor
REFERENCE: MBH00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/138,674B
CURRENT FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 20829
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1886
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-10-138-674B-1886

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1505 TTCATCTGAGACATCA 1521
|||||
17 TTCATCTGAGACATCA 1

188
138-674B-6345/c
ence 6345, Application US/10138674B
nt No. 7034009
RAL INFORMATION:
LICANT: Sirna Therapeutics, Inc.
LICANT: MCVigen, Pam
LICANT: McSwigen, James
LICANT: Stinchcomb, Dan
LICANT: Escobedo, Jaime
LE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
E REFERENCE: MHB00-876-N (400/049)
RENT FILING DATE: 2002-05-03
BER OF SEQ ID NOS: 20829
TWARE: Patentin version 3.0
ID NO 6345
NGTH: 17
PR: RNA
3ANISW: Homo sapiens
138-674B-6345

Y Match 0.8%; Score 13.8; DB 1; Length 17;
Local Similarity 88.2%; Pred. No. 1.4e+02;
hes 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

713 ACTCAACGACGAGACC 729
17 ACACACGACGAGAGACC 1

189
513-974B-240/c
ence 240, Application US/08513974B
nt No. 6114139
ERAL INFORMATION:
PLICANT: Hinuma, Shuji
PLICANT: Hosoya, Masaki
PLICANT: Fujii, Ryo
PLICANT: Onhaki, Tetsuya
PLICANT: Fukusumi, Shoji
PLICANT: Ohgi, Kazuhiko
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
UMBER OF SEQUENCES: 380
ORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
OMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
URRANT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
RIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093389
FILING DATE: 19-AUG-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177

FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 240:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-513-974B-240

Query Match 0.8%; Score 13.6; DB 1; Length 23;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1307 AGGAGAGCCGACGAGCGC 1326
DB 23 AGGAGAGCCGACGAGCGC 4

RESULT 190
US-08-585-684B-2100
Sequence 2100, Application US/08585684B
Patent No. 5877021
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
APPLICANT: McSwigen, James
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/585,684B
FILING DATE: January 16, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/000,951
FILING DATE: July 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
FORMATION FOR SEQ ID NO: 2100:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
-585-684B-2100

Query Match
Local Similarity 60.0%; Score 13.4; DB 1; Length 15;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

1409 GCTTCTCTCCCAATG 1423
1 GCUCUCUCCCAUG 15

1191
-585-684B-2101
ence 2101, Application US/08585684B
GENERAL INFORMATION:
PATENT NO. 5877021
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
APPLICANT: McSwigen, James
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/585,684B
FILING DATE: January 16, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/000,951
FILING DATE: July 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
FORMATION FOR SEQ ID NO: 2101:
SEQUENCE CHARACTERISTICS:

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/ LENGTH: 15 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
US-08-585-684B-2101

Query Match
Best Local Similarity 53.3%; Score 13.4; DB 1; Length 15;
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1411 TTCTCTCCCAATG 1425
DB 1 UUCUCUCCCAUG 15

RESULT 192
US-09-038-073-2100
Sequence 2100, Application US/09038073
Patent No. 6194150
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
APPLICANT: McSwigen, James
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,073
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585,684
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
FORMATION FOR SEQ ID NO: 2100:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-038-073-2100

Query Match
Best Local Similarity 60.0%; Score 13.4; DB 1; Length 15;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1409 GCTTCTCTCCCAATG 1423
DB 1 GCUCUCUCCCAUG 15

RESULT 193

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038-073-2101
 ence 2101, Application US/09038073
 nt No. 6194150
 ERAL INFORMATION:
 PPLICANT: Stinchcomb, Daniel T.
 PPLICANT: Jarvis, Thale
 PPLICANT: McSwiggen, James
 TITLE OF INVENTION: METHOD AND REAGENT FOR THE
 TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
 TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
 UMBER OF SEQUENCES: 2751
 ORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Fast-Seq Version 1.5
 URENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/038,073
 FILING DATE:
 RIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/585,684
 FILING DATE:
 TTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard
 REGISTRATION NUMBER: 32,227
 REFERENCE/DOCKET NUMBER: 218/078
 ELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 ORAMTION FOR SEQ. ID NO: 2101:
 EQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 038-073-2101
 Y Match 0.8%; Score 13.4; DB 1; Length 15;
 Local Similarity 53.3%; Pred. No. 1.2e+02;
 hes 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
 1411 TTCTCCTCAATGTG 1425
 :||:||||||:|
 1 UUCUCUCCCAUGUG 15
 194
 502-185-16
 ence 16, Application US/08502185
 nt No. 5639736
 ERAL INFORMATION:
 PPLICANT: Robinson, Gregory S.
 TITLE OF INVENTION: Human VEGF-Specific
 TITLE OF INVENTION: Oligonucleotides
 UMBER OF SEQUENCES: 53
 ORRESPONDENCE ADDRESS:
 ADDRESSEE: Lappin & Kusmer
 STREET: 200 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE:
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/502,185
 FILING DATE:
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Kerner, Ann-Louise
 REGISTRATION NUMBER: 33,523
 REFERENCE/DOCKET NUMBER: HYZ-031CPDVI
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-330-1300
 TELEFAX: 617-330-1311
 INFORMATION FOR SEQ. ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-502-185-16
 Query Match 0.7%; Score 13; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1011 CTTCCTCTGCCC 1023
 Db 1 CTTCCTCTGCCC 13
 RESULT 195
 US-08-945-945-16
 Sequence 16, Application US/08398945
 Patent No. 5639872
 GENERAL INFORMATION:
 APPLICANT: Robinson, Gregory S.
 TITLE OF INVENTION: Human VEGF-Specific
 TITLE OF INVENTION: Oligonucleotides
 NUMBER OF SEQUENCES: 53
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lappin & Kusmer
 STREET: 200 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE:
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/398,945
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Kerner, Ann-Louise
 REGISTRATION NUMBER: 33,523
 REFERENCE/DOCKET NUMBER: HYZ-031CIP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-330-1300
 TELEFAX: 617-330-1311
 INFORMATION FOR SEQ. ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
-398-945-16

Query Match 0.7%; Score 13; DB 1; Length 15;
Local Similarity 100.0%; Pred. No. 1.4e+02;
Indels 0; Mismatches 0; Gaps 0;

1011 CTTCTCTCTGCC 1023

1 CTTCTCTCTGCC 13

196
-501-779-16
ence 16, Application US/08501779
nt No. 5661135
ERAL INFORMATION:
PPlicant: Robinson, Gregory S.
TITLE OF INVENTION: Human VEGF-Specific
TITLE OF INVENTION: Oligonucleotides
NUMBER OF SEQUENCES: 53
ORRESPONDENCE ADDRESS:
ADDRESSEE: Lappin & Kusmer
STREET: 200 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
OMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE:
URRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,779
ILING DATE:
CLASSIFICATION: 514
TTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-031CPDV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-330-1300
TELEFAX: 617-330-1311
FORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
-501-779-16

Query Match 0.7%; Score 13; DB 1; Length 15;
Local Similarity 100.0%; Pred. No. 1.4e+02;
Indels 0; Mismatches 0; Gaps 0;

1011 CTTCTCTCTGCC 1023

1 CTTCTCTCTGCC 13

197
-501-713-16
ence 16, Application US/08501713
nt No. 5710136
ERAL INFORMATION:
PPlicant: Robinson, Gregory S.
PPlicant: Smith, Lois E.H.

TITLE OF INVENTION: Inhibition of
TITLE OF INVENTION: Neovascularization Using
TITLE OF INVENTION: VEGF-Specific
TITLE OF INVENTION: Oligonucleotides
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lappin & Kusmer
STREET: 200 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,713
ILING DATE:
CLASSIFICATION: 435
TTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-031DV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-330-1300
TELEFAX: 617-330-1311
FORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-501-713-16

Query Match 0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1011 CTTCTCTCTGCC 1023

Db 1 CTTCTCTCTGCC 13

RESULT 198
US-08-378-860-16
Sequence 16, Application US/08378860
Patent No. 5731294
GENERAL INFORMATION:
APPLICANT: Robinson, Gregory S.
APPLICANT: Smith, Lois E.H.
TITLE OF INVENTION: Inhibition of
TITLE OF INVENTION: Neovascularization Using
TITLE OF INVENTION: VEGF-Specific
TITLE OF INVENTION: Oligonucleotides
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lappin & Kusmer
STREET: 200 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE:
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/378,860
FILING DATE: 514
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-031
ELECTRONIC INFORMATION:
TELEPHONE: 617-330-1300
TELEFAX: 617-330-1311
ORAMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
YPOTHEICAL: NO
NTI-SENSE: NO
378-860-16
Y Match 0.7%; Score 13; DB 1; Length 15;
Local Similarity 100.0%; Pred. No. 1.4e+02;
hes 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1011 CTTCCTCTGCCC 1023
1 CTTCCTCTGCCC 13
199
501-626-16
ence 16, Application US/08501626
nt No. 580156
ERAL INFORMATION:
PLICANT: Robinson, Gregory S.
TITLE OF INVENTION: Inhibition of
TITLE OF INVENTION: Neovascularization Using
TITLE OF INVENTION: VEGF-Specific
TITLE OF INVENTION: Oligonucleotides
UMBER OF SEQUENCES: 53
ORRESPONDENCE ADDRESS:
ADDRESSEE: Lappin & Kusmer
STREET: 200 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
OMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE:
URRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,626
FILING DATE:
CLASSIFICATION: 435
TTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-031DV4
ELECTRONIC INFORMATION:
TELEPHONE: 617-330-1300
TELEFAX: 617-330-1311
ORAMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
YPOTHEICAL: NO

ANTI-SENSE: NO
US-08-501-626-16
Query Match 0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1011 CTTCCTCTGCCC 1023
Db 1 CTTCCTCTGCCC 13
RESULT 200
US-08-501-356-16
Sequence 16, Application US/08501356
Patent No. 5814620
GENERAL INFORMATION:
APPLICANT: Robinson, Gregory S.
TITLE OF INVENTION: Inhibition of
TITLE OF INVENTION: Neovascularization Using
TITLE OF INVENTION: VEGF-Specific
TITLE OF INVENTION: Oligonucleotides
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lappin & Kusmer
STREET: 200 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,356
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-031DV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-330-1300
TELEFAX: 617-330-1311
ORAMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
YPOTHEICAL: NO
ANTI-SENSE: NO
US-08-501-356-16
Query Match 0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1011 CTTCCTCTGCCC 1023
Db 1 CTTCCTCTGCCC 13
RESULT 201
US-09-034-205-66/c
Sequence 66, Application US/09034205
Patent No. 6194149
GENERAL INFORMATION:
APPLICANT: Lyamichev, Victor I.

APPLICANT: Brow, Mary Ann D.
 APPLICANT: Fors, Lance P.
 TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING
 TITLE OF INVENTION: STRUCTURE-BRIDGING OLIGONUCLEOTIDES
 NUMBER OF SEQUENCES: 68
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MEDLEN & CARROLL, LLP
 STREET: 220 Montgomery Street, Suite 2200
 CITY: San Francisco
 STATE: CA
 COUNTRY: USA
 ZIP: 94104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/034,205
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: MacKnight, Kamrin T.
 REGISTRATION NUMBER: 38,230
 REFERENCE/DOCKET NUMBER: FORS-03268
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 705-8410
 TELEFAX: (415) 397-8338
 INFORMATION FOR SEQ ID NO: 66:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "DNA"
 -034-205-66
 Query Match 0.7%; Score 12.8; DB 1; Length 16;
 Local Similarity 87.5%; Pred. No. 1.7e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 1436 CCACAGGCGCTTGGC 1451
 |||||
 16 CCACAGGCGCTTGGC 1
 202
 -677-218B-66/C
 Sequence 66, Application US/09677218B
 int No. 635375
 GENERAL INFORMATION:
 APPLICANT: Lyamichev, Victor I.
 APPLICANT: Brow, Mary Ann D.
 APPLICANT: Fors, Lance P.
 TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING
 TITLE OF INVENTION: STRUCTURE-BRIDGING OLIGONUCLEOTIDES
 NUMBER OF SEQUENCES: 68
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MEDLEN & CARROLL, LLP
 STREET: 220 Montgomery Street, Suite 2200
 CITY: San Francisco
 STATE: CA
 COUNTRY: USA
 ZIP: 94104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/677,218B
 FILING DATE: 02-Oct-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/034,205
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: MacKnight, Kamrin T.
 REGISTRATION NUMBER: 38,230
 REFERENCE/DOCKET NUMBER: FORS-03268
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 705-8410
 TELEFAX: (415) 397-8338
 INFORMATION FOR SEQ ID NO: 66:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "DNA"
 SEQUENCE DESCRIPTION: SEQ ID NO: 66:
 US-09-677-218B-66
 Query Match 0.7%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 1.7e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 1436 CCACAGGCGCTTGGC 1451
 |||||
 16 CCACAGGCGCTTGGC 1
 RESULT 203
 US-09-677-192-66/C
 Sequence 66, Application US/09677192
 Patent No. 6358691
 GENERAL INFORMATION:
 APPLICANT: Lyamichev, Victor I.
 APPLICANT: Brow, Mary Ann D.
 APPLICANT: Fors, Lance P.
 TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING
 TITLE OF INVENTION: OLIGONUCLEOTIDES
 FILE REFERENCE: FORS-04708
 CURRENT APPLICATION NUMBER: US/09/677,192
 PRIOR FILING DATE: 2000-10-02
 CURRENT APPLICATION NUMBER: 09/034,205
 PRIOR FILING DATE: 1998-03-03
 NUMBER OF SEQ ID NOS: 68
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 66
 LENGTH: 16
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 US-09-677-192-66
 Query Match 0.7%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 1.7e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 1436 CCACAGGCGCTTGGC 1451
 |||||
 16 CCACAGGCGCTTGGC 1
 RESULT 204
 US-09-270-933-9/C
 Sequence 9, Application US/09270933
 Patent No. 6365375
 GENERAL INFORMATION:

LICANT: Dietmaier, Wolfgang
 LICANT: Ruschoff, Josef
 LE OF INVENTION: IMPROVED METHOD OF PRIMER-EXTENSION PREAMPLIFICATION
 LE OF INVENTION: PCR
 E REFERENCE: 4802
 RENT APPLICATION NUMBER: US/09/270,933
 RENT FILING DATE: 1999-03-16
 LER APPLICATION NUMBER: DE 198 13 317.0
 LER FILING DATE: 1998-03-26
 BER OF SEQ ID NOS: 17
 TWARE: Patentin Ver. 2.0
 ID NO 9
 NGTH: 16
 PE: DNA
 GANISM: Artificial Sequence
 ATURE:
 HER INFORMATION: Description of Artificial Sequence: Primer for
 HER INFORMATION: Human Genomic Sequence
 270-933-9

Y Match 0.7%; Score 12.8; DB 1; Length 16;
 Local Similarity 87.5%; Pred. No. 1.7e+02;
 hes 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1061 AGCAGGCTACCTGGC 1076
 16 ATCAGGCTACCTGTC 1

205
 060-299-412
 ence 412, Application US/09060299
 nt No. 6545137

ERAL INFORMATION:
 PPLICANT: Todd, John A
 PPLICANT: Hess, John W
 PPLICANT: Caskey, Charles T
 PPLICANT: Cox, Roger D
 PPLICANT: Gerhold, David
 PPLICANT: Hammond, Holly
 PPLICANT: Hey, Patricia
 PPLICANT: Kawaguchi, Yoshihiko
 PPLICANT: Merriman, Tony R
 PPLICANT: Metzker, Michael L
 TLE OF INVENTION: No. 6545137e1 Receptor
 UMBER OF SEQUENCES: 455

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Nixon and Vanderhye
 STREET: 1100 No. 6545137ch Glebe Road, Eighth Floor
 CITY: Arlington
 STATE: Virginia
 COUNTRY: US

OMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
 URRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/060,299
 FILING DATE: 15-APR-1998
 CLASSIFICATION: 435
 RIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/043,553
 FILING DATE: 15-APR-1997
 RIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/048,740
 FILING DATE: 05-JUN-1997
 TORNEY/AGENT INFORMATION:
 NAME: B.J. Sadoff
 REGISTRATION NUMBER: 36,663
 REFERENCE/DOCKET NUMBER: 620-35
 ELECOMMUNICATION INFORMATION:
 TELEPHONE: (703)816-4091

TELEFAX: (703)816-4100
 INFORMATION FOR SEQ ID NO: 412:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 US-09-060-299-412

Query Match 0.7%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 1.7e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 13 CCGCGGCGACGCGGCGC 28
 DB 1 CCGCGGCTACGTGCGC 16

RESULT 206
 US-09-402-923A-412
 Sequence 412, Application US/09402923A
 Patent No. 6555654
 GENERAL INFORMATION:
 APPLICANT: Todd, John A
 Hess, John W
 Caskey, Charles T
 Cox, Roger D
 Gerhold, David
 Hammond, Holly
 Hey, Patricia
 Kawaguchi, Yoshihiko
 Merriman, Tony R
 Metzker, Michael L
 TITLE OF INVENTION: No. 6555654e1 LDL-Receptor
 NUMBER OF SEQUENCES: 455
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Nixon and Vanderhye
 STREET: 1100 No. 6555654th Glebe Road, Eighth Floor
 CITY: Arlington
 STATE: Virginia
 COUNTRY: US
 ZIP: VA 22201-4714

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/402,923A
 FILING DATE: 14-Feb-2001

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/GB98/01102
 FILING DATE: 15-APR-1998
 APPLICATION NUMBER: US 60/043,553
 FILING DATE: 15-APR-1997
 APPLICATION NUMBER: US 60/048,740
 FILING DATE: 05-JUN-1997

ATTORNEY/AGENT INFORMATION:
 NAME: B.J. Sadoff
 REGISTRATION NUMBER: 36,663
 REFERENCE/DOCKET NUMBER: 620-81
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703)816-4091
 TELEFAX: (703)816-4100

INFORMATION FOR SEQ ID NO: 412:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 412:
 US-09-402-923A-412

Y Match 0.7%; Score 12.8; DB 1; Length 16;
Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

13 CCGCGGCGACGCGGCGC 28
|||||
1 CCGCGGCGTAGGTGGGC 16

207
-371-772B-5850/c
ence 5850, Application US/09371772B
ent No. 6566127
RAL INFORMATION:
PLICANT: Ribozyme Pharmaceuticals, Inc.
PLICANT: Pavco, Pam
PLICANT: MCSwigen, Jim
PLICANT: Stinchcomb, Dan
PLICANT: Escobedo, Jaime
FILE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
LE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
E REFERENCE: MBH00,876-J (237/198)
RENT FILING DATE: 1999-08-10
OR APPLICATION NUMBER: US 60/005,974
OR FILING DATE: 1995-10-26
OR APPLICATION NUMBER: US 08/584,040
OR FILING DATE: 1996-01-08
BER OF SEQ ID NOS: 14225
TWARE: PatentIn version 3.0
ID NO 5850
NGTH: 16
PE: RNA
GANISM: Homo sapiens
-371-772B-5850

Y Match 0.7%; Score 12.8; DB 1; Length 16;
Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1594 AAAATCTCAATCTTC 1609
|||||
16 AAAATCACAATCTTC 1

208
-371-772B-5863
ence 5863, Application US/09371772B
ent No. 6566127
RAL INFORMATION:
PLICANT: Ribozyme Pharmaceuticals, Inc.
PLICANT: Pavco, Pam
PLICANT: MCSwigen, Jim
PLICANT: Stinchcomb, Dan
PLICANT: Escobedo, Jaime
FILE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
LE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
E REFERENCE: MBH00,876-J (237/198)
RENT FILING DATE: 1999-08-10
OR APPLICATION NUMBER: US 60/005,974
OR FILING DATE: 1995-10-26
OR APPLICATION NUMBER: US 08/584,040
OR FILING DATE: 1996-01-08
BER OF SEQ ID NOS: 14225
TWARE: PatentIn version 3.0
ID NO 5863
NGTH: 16
PE: RNA
GANISM: Homo sapiens
-371-772B-5863

Y Match 0.7%; Score 12.8; DB 1; Length 16;

Best Local Similarity 81.2%; Pred. No. 1.7e+02;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 389 ACAAAGATGAGGAC 404
|||||
Db 1 ACAAUGAUGAGGAC 16

RESULT 209
US-09-479-005A-50/c
Sequence 50, Application US/09479005A
Patent No. 6656731
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
FILE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
E REFERENCE: MBH00-884-C
CURRENT APPLICATION NUMBER: US/09/479,005A
CURRENT FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 09/444,209
PRIOR FILING DATE: 1999-11-19
PRIOR APPLICATION NUMBER: US 09/159,274
PRIOR FILING DATE: 1998-09-22
PRIOR APPLICATION NUMBER: US 60/059,473
PRIOR FILING DATE: 1997-09-22
NUMBER OF SEQ ID NOS: 1208
SOFTWARE: PatentIn version 3.0
SEQ ID NO 50
LENGTH: 16
TYPE: RNA
GANISM: Homo sapiens
US-09-479-005A-50

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 527 AGTCCACAACTTCTT 542
|||||
Db 16 AATTCATTAATCTTCTT 1

RESULT 210
US-09-402-618B-66/c
Sequence 66, Application US/09402618B
Patent No. 6709815
GENERAL INFORMATION:
APPLICANT: Dong, Fang
APPLICANT: Lyamchev, Victor
APPLICANT: Prudent, James
APPLICANT: Fors, Lance
APPLICANT: Neri, Bruce
APPLICANT: Brow, Mary Ann
APPLICANT: Anderson, Todd
APPLICANT: Dahlberg, James
FILE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot
E REFERENCE: FORS-04012
CURRENT APPLICATION NUMBER: US/09/402,618B
CURRENT FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: PCT/US98/03194
PRIOR FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PatentIn version 3.0
SEQ ID NO 66
LENGTH: 16
TYPE: DNA
GANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-402-618B-66

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1436 CCACAGGCGCTTGGC 1451
|||||
16 CCACAGGCGCTTGGC 1

211
720-435A-410/c
ence 410, Application US/09720435A
nt No. 6803187
RAL INFORMATION:
LICANT: Stuyver, Lieven
LE OF INVENTION: Method for detection of drug-selected mutations in the protease
LE OF INVENTION: gene
E REFERENCE: 11362.0030, PCUS00 INNS:030
RENT APPLICATION NUMBER: US/09/720,435A
RENT FILING DATE: 2001-06-25
CR APPLICATION NUMBER: PCT/EP99/04317
CR FILING DATE: 1999-06-22
CR APPLICATION NUMBER: 98870143..9
CR FILING DATE: 1998-06-24
ERR OF SEQ ID NOS: 529
TWARE: PatentIn version 3.2
ID NO 410
NGTH: 16
PE: DNA
GANISM: Aids-associated retrovirus
720-435A-410

y Match 0.7%; Score 12.8; DB 1; Length 16;
Local Similarity 87.5%; Pred. No. 1.7e+02;
hes 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1586 TGAGTCACAAATCTC 1601
|||||
16 TGAGTCACAAATCTC 1

212
543-679A-1408/c
ence 1408, Application US/09543679A
nt No. 7034007
NERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICITION, LONG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:

TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1408:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1408:
US-09-543-679A-1408

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 636 GTCAGCCACAGCCAC 651
|||||
Db 16 GGCAGCCACAGCCAC 1

RESULT 213
US-09-543-679A-1453
Sequence 1453, Application US/09543679A
Patent No. 7034007
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICITION, LONG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1453:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1453:
US-09-543-679A-1453

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 537 CTTCTTCCCATCGCC 552

|||||
1 CTTCTTCCGCTCC 16

214
-543-679A-1454
ence 1454, Application US/09543679A
nt No. 7034007
GENERAL INFORMATION:
APPLICANT: NICE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICITION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111

CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ

COUNTRY: USA
ZIP: 08512

COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03

ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b

TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245

TELEX: <Unknown>
FORMATION FOR SEQ ID NO: 1454:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1454:
-543-679A-1454

Match 0.7%; Score 12.8; DB 1; Length 16;
Local Similarity 87.5%; Pred. No. 1.7e+02;
hes 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

537 CTTCTTCCGCTCC 552
1 CTTCTTCCGCTCC 16

215
-138-674B-5850/c
ence 5850, Application US/10138674B
nt No. 7034009
GENERAL INFORMATION:
APPLICANT: Sirta Therapeutics, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwigen, James
APPLICANT: Sclinchcomb, Dan
APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
LE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
E REFERENCE: MBH00-876-N (400/049)

CURRENT APPLICATION NUMBER: US/10/138,674B
CURRENT FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 20829
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 5850
LENGTH: 16
TYPE: RNA
ORGANISM: Homo sapiens
US-10-138-674B-5850

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1594 AAAATCTCATTTCTC 1609
Db 16 AAAATCACAATCTTC 1

RESULT 216
US-10-138-674B-5863
Sequence 5863, Application US/10138674B
Patent No. 7034009
GENERAL INFORMATION:
APPLICANT: Sirta Therapeutics, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwigen, James
APPLICANT: Sclinchcomb, Dan
APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
FILE REFERENCE: MBH00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/138,674B
CURRENT FILING DATE: 2002-05-03

NUMBER OF SEQ ID NOS: 20829
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 5863
LENGTH: 16
TYPE: RNA
ORGANISM: Homo sapiens
US-10-138-674B-5863

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 1.7e+02;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 389 ACAAAGATGAGGAC 404
Db 1 ACAAUGAUGAGGAC 16

RESULT 217
US-07-701-935-14
Sequence 14, Application US/07701935
Patent No. 5336595
GENERAL INFORMATION:
APPLICANT: Strader, C. D.
APPLICANT: Fong, T. M.
TITLE OF INVENTION: Method of Using Human Neurokinin-1
RECEPTOR SHORT FORM

NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: US

ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Releasee #1.0, Version #1.25

URGENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/701,935
 FILING DATE: 19910517
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Nicholson, William H.
 REGISTRATION NUMBER: 25,147
 REFERENCE/DOCKET NUMBER: 18409
 TELEPHONE: (908) 594-5315
 TELEFAX: (908) 594-4720
 ORAMATION FOR SEQ ID NO: 14:
 EQUENCE CHARACTERISTICS:
 LENGTH: 20 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 OLECULE TYPE:
 701-935-14

Y Match 0.7%; Score 12.6; DB 1; Length 20;
 Local Similarity 78.9%; Pred. No. 2.4e+02;
 hes 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

861 CGTAGTGGATCCACTA 879
 |||||
 1 CATAGTGTGATCCACTA 19

218
 117-965-14
 since 14, Application US/08117965
 nt No. 5484886
 ERAL INFORMATION:
 PPLICANT: Tung, Fong M.
 PPLICANT: Cathrine, Strader D.
 TITL OF INVENTION: Human Neurokinin-1 Receptor
 UMBER OF SEQUENCES: 27
 RRESPONDENCE ADDRESS:
 ADDRESSEE: Merck & Co., Inc.
 STREET: P.O. Box 2000
 CITY: Rahway
 STATE: New Jersey
 COUNTRY: US
 ZIP: 07065-0907
 OMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 OFTWARE: Patentn Release #1.0, Version #1.25
 URGENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/117,965
 FILING DATE:
 CLASSIFICATION: 514
 RIOR APPLICATION DATA:
 APPLICATION NUMBER: US 691,197
 FILING DATE: 25-APR-1991
 TTORNEY/AGENT INFORMATION:
 NAME: Nicholson, William H.
 REGISTRATION NUMBER: 25,147
 REFERENCE/DOCKET NUMBER: 18387
 ELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 594-5315
 TELEFAX: (908) 594-4720
 ORAMATION FOR SEQ ID NO: 14:
 EQUENCE CHARACTERISTICS:
 LENGTH: 20 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 OLECULE TYPE:
 117-965-14

Query Match 0.7%; Score 12.6; DB 1; Length 20;
 Best Local Similarity 78.9%; Pred. No. 2.4e+02;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 861 CGTAGTGGATCCACTA 879
 |||||
 Db 1 CATAGTGTGATCCACTA 19

RESULT 219
 US-08-785-750-2
 ; Sequence 2, Application US/08785750
 ; Patent No. 5846528
 ; GENERAL INFORMATION:
 ; APPLICANT: PODSAKOFF, GREGORY M.
 ; APPLICANT: KURTZMAN, GARY J.
 ; TITLE OF INVENTION: METHODS OF TREATING ANEMIA USING
 ; TITLE OF INVENTION: RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ROBINS & ASSOCIATES
 ; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
 ; CITY: MENLO PARK
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94025
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/785,750
 ; FILING DATE: 16-JAN-1997
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/588,355
 ; FILING DATE: 18-JAN-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MCCracken, THOMAS P.
 ; REGISTRATION NUMBER: 38,548
 ; REFERENCE/DOCKET NUMBER: 0800-0009.21
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 325-7812
 ; TELEFAX: (415) 325-7823
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 14 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-785-750-2

Query Match 0.7%; Score 12.4; DB 1; Length 14;
 Best Local Similarity 92.9%; Pred. No. 1.5e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 315 GGCAGCTGCCTACA 328
 |||||
 Db 1 GGCAGCTGCCTGCA 14

RESULT 220
 US-08-588-355-1
 ; Sequence 1, Application US/08588355
 ; Patent No. 5858351
 ; GENERAL INFORMATION:
 ; APPLICANT: PODSAKOFF, GREGORY M.
 ; APPLICANT: KESSLER, PAUL D.
 ; APPLICANT: BYRNE, BARRY J.
 ; APPLICANT: KURTZMAN, GARY J.
 ; TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE

TITLE OF INVENTION: CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VECTORS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/588,355
APPLICATION NUMBER: US/08/588,355
FILING DATE: 18-JAN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 0800-0009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 325-7812
TELEFAX: (650) 325-7823
FORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
589-355-1
Query Match 0.7%; Score 12.4; DB 1; Length 14;
Local Similarity 92.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
315 GGCAGCTGCTTACA 328
|||||||
1 GGCAGCTGCTTACA 14
116-780-5
ence 5, Application US/09116780
ent No. 5945335
RAL INFORMATION:
LICANT: Colosi, Peter
FILE OF INVENTION: Adenovirus Helper-Free Systems for Producing
FILE OF INVENTION: Recombinant AAV Virions Lacking Oncogenic Sequences
E REFERENCE: 2555.2.2
CURRENT APPLICATION NUMBER: US/09/116,780
CURRENT FILING DATE: 1998-07-16
LIER APPLICATION NUMBER: 08/745,957
LIER FILING DATE: 1996-11-07
LIER APPLICATION NUMBER: 60/006,402
LIER FILING DATE: 1995-11-09
BER OF SEQ ID NOS: 11
TMWARE: Patentin Ver. 2.0
ID NO 5
NGTH: 14
PE: DNA
GANISM: Artificial Sequence
ATURE:
HER INFORMATION: Description of Artificial Sequence: oligonucleotide
116-780-5
Query Match 0.7%; Score 12.4; DB 1; Length 14;
Local Similarity 92.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 315 GGCAGCTGCTTACA 328
|||||||
Db 1 GGCAGCTGCTTACA 14
RESULT 222
US-08-812-102-1
Sequence 1, Application US/08812102
Patent No. 5952221
GENERAL INFORMATION:
APPLICANT: KURTZMAN, GARY J.
APPLICANT: COLOSI, PETER C.
APPLICANT: YOSHIDA, JUN
APPLICANT: MIZUNO, MASAKI
APPLICANT: OKADA, HIDEO
TITLE OF INVENTION: GENE THERAPY FOR THE TREATMENT OF SOLID
TUMORS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VECTORS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,102
FILING DATE: 05-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,209
FILING DATE: 06-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 0800-0008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 325-7812
TELEFAX: (415) 325-7823
FORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-812-102-1
Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 315 GGCAGCTGCTTACA 328
|||||||
Db 1 GGCAGCTGCTTACA 14
RESULT 223
US-08-784-757-1
Sequence 1, Application US/08784757
Patent No. 5962313
GENERAL INFORMATION:
APPLICANT: PODSAKOFF, GREGORY M.
APPLICANT: KESSLER, PAUL D.
APPLICANT: BYRNE, BARRY J.
APPLICANT: KURTZMAN, GARY J.

TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE
TITLE OF INVENTION: CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS
NUMBER OF SEQUENCES: 9
ORRESPONDENCE ADDRESS:
ADDRESS: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,757
FILING DATE: 16-JAN-1997
CLASSIFICATION: 514
R10R APPLICATION DATA:
APPLICATION NUMBER: US 08/588,355
FILING DATE: 18-JAN-1996
TORNEY/AGENT INFORMATION:
NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 0800-0009.20
ELECTRONIC INFORMATION:
TELEPHONE: (415) 325-7812
TELEFAX: (415) 325-7823
ORINATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
784-757-1
Y Match 0.7%; Score 12.4; DB 1; Length 14;
Local Similarity 92.9%; Pred. No. 1.5e+02;
hes 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
315 GGCAGCTGCCTGCA 328
|||||
1 GGCAGCTGCCTGCA 14
224
745-957-1
ence 1, Application US/08745957
nt No. 6004797
ERAL INFORMATION:
PLICANT: COLOSI, PETER C.
TITLE OF INVENTION: ACCESSORY FUNCTIONS FOR USE IN
TITLE OF INVENTION: RECOMBINANT AAV VIRION PRODUCTION
NUMBER OF SEQUENCES: 17
ORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/745,957
FILING DATE: 07-NOV-1996
CLASSIFICATION: 530
R10R APPLICATION DATA:

APPLICATION NUMBER: US 60/006,402
FILING DATE: 09-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 0800-0007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3231
TELEFAX: (415) 327-3400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-745-957-1
Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 315 GGCAGCTGCCTGCA 328
|||||
Db 1 GGCAGCTGCCTGCA 14
RESULT 225
US-08-745-957-1
Sequence 124, Application US/08765340
Patent No. 6150092
GENERAL INFORMATION:
APPLICANT: UCHIDA, K.,
APPLICANT: UCHIDA, T.,
APPLICANT: TANAKA, Y.,
APPLICANT: MATSUDA, Y.,
APPLICANT: KONDO, S.,
TITLE OF INVENTION: AN ANTISENSE NUCLEIC ACID
TITLE OF INVENTION: COMPOUND
NUMBER OF SEQUENCES: 185
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
SOFTWARE: #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,340
FILING DATE: 23-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 145146/94
FILING DATE: 27-JUN-1994
APPLICATION NUMBER: JP 31130/94
FILING DATE: 21-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: SERUNIAN, LESLIE
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 1452-4005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 124:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
-765-340-124

Y Match 0.7%; Score 12.4; DB 1; Length 14;
: Local Similarity 92.9%; Pred. No. 1.5e+02;
:hes 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

468 AGTGTGAAGTTCA 481
|||||
14 AGTGTGAAGTTCA 1

: 226
: 309-042-1
:ence 1, Application US/09309042
:nt No. 621163
:ERAL INFORMATION:
:PPICANT: PODSAKOF, GREGORY M.
:PPICANT: KESSLER, PAUL D.
:PPICANT: BYRNE, BARRY J.
:PPICANT: KURTZMAN, GARY J.
:TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE
:TITLE OF INVENTION: CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VECTORS
:NUMBER OF SEQUENCES: 5
:ADDRESS/ADDRESS ADDRESS:
:ADDRESS/ADDRESS: ROBINS & ASSOCIATES
:STREET: 90 MIDDLEFIELD ROAD, SUITE 200
:CITY: MENLO PARK
:STATE: CA
:COUNTRY: USA
:ZIP: 94025

:COMPUTER READABLE FORM:
:MEDIUM TYPE: floppy disk
:COMPUTER: IBM PC compatible
:OPERATING SYSTEM: PC-DOS/MS-DOS
:SOFTWARE: Patentin Release #1.0, Version #1.30
:CURRENT APPLICATION DATA:
:APPLICATION NUMBER: US/09309,042
:FILING DATE:
:CLASSIFICATION:
:PRIOR APPLICATION DATA:
:APPLICATION NUMBER: 08/588,355
:FILING DATE:
:ATTORNEY/AGENT INFORMATION:
:NAME: MCCracken, THOMAS P.
:REGISTRATION NUMBER: 38,548
:REFERENCE/DOCKET NUMBER: 0800-0009
:TELECOMMUNICATION INFORMATION:
:TELEPHONE: (650) 325-7812
:TELEFAX: (650) 325-7823
:FORMATION FOR SEQ ID NO: 1:
:SEQUENCE CHARACTERISTICS:
:LENGTH: 14 base pairs
:TYPE: nucleic acid
:STRANDEDNESS: single
:TOPOLOGY: linear
:MOLECULE TYPE: DNA (genomic)
:309-042-1

Y Match 0.7%; Score 12.4; DB 1; Length 14;
: Local Similarity 92.9%; Pred. No. 1.5e+02;
:hes 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

315 GGCAGCTGCTTACA 328
|||||
1 GGCAGCTGCTTACA 14

: 227
: 063-667-17/c

Sequence 17, Application US/09063667C
Patent No. 6225291
GENERAL INFORMATION:
APPLICANT: LEWIN, ALFRED S.
APPLICANT: HAUSWIRTH, WILLIAM W.
APPLICANT: DRENER, KIMBERLY
TITLE OF INVENTION: MATERIALS AND METHODS FOR RIBOZYME TREATMENT OF
FILE REFERENCE: 4300, 011500
CURRENT APPLICATION NUMBER: US/09/063,667C
CURRENT FILING DATE: 1998-04-21
EARLIER APPLICATION NUMBER: 60/046,147
EARLIER FILING DATE: 1997-05-09
EARLIER APPLICATION NUMBER: 60/044,492
EARLIER FILING DATE: 1997-04-21
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
LENGTH: 14
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
OTHER INFORMATION: OLIGONUCLEOTIDE
US-09-063-667-17

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1375 CGAAGTACTCCAA 1388
|||||
Db 14 CGAAGTACTCCGA 1

RESULT 228
US-09-205-337-2
Sequence 2, Application US/09205337
Patent No. 6325998
GENERAL INFORMATION:
APPLICANT: PODSAKOF, GREGORY M.
APPLICANT: KURTZMAN, GARY J.
TITLE OF INVENTION: METHODS OF TREATING ANEMIA USING
RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESS/ADDRESS: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CA
COUNTRY: USA
ZIP: 94025

:COMPUTER READABLE FORM:
:MEDIUM TYPE: floppy disk
:COMPUTER: IBM PC compatible
:OPERATING SYSTEM: PC-DOS/MS-DOS
:SOFTWARE: Patentin Release #1.0, Version #1.30
:CURRENT APPLICATION DATA:
:APPLICATION NUMBER: US/09/205,337
:FILING DATE: 04-Dec-1998
:CLASSIFICATION: <Unknown>
:PRIOR APPLICATION DATA:
:APPLICATION NUMBER: 08/785,750
:FILING DATE: <Unknown>
:ATTORNEY/AGENT INFORMATION:
:NAME: MCCracken, THOMAS P.
:REGISTRATION NUMBER: 38,548
:REFERENCE/DOCKET NUMBER: 0800-0009.21
:TELECOMMUNICATION INFORMATION:
:TELEPHONE: (415) 325-7812
:TELEFAX: (415) 325-7823
:FORMATION FOR SEQ ID NO: 2:
:SEQUENCE CHARACTERISTICS:

LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
205-337-2

Y Match 0.7%; Score 12.4; DB 1; Length 14;
Local Similarity 92.9%; Pred. No. 1.5e+02;
hes 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

315 GGCAGCTGCTTACA 328
|||||
1 GGCAGCTGCTTACA 14

229
406-362-1
ence 1, Application US/09406362
nt No. 6335011
NERAL INFORMATION:
APPLICANT: PODSAKOFF, GREGORY M.
KESSLER, PAUL D.
BYRNE, BARRY J.
KURTZMAN, GARY J.
TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE
CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS

NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CA
COUNTRY: USA
ZIP: 94025

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/406,362
FILING DATE: 28-Sep-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/784,757
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 0800-0009.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 325-7812
TELEFAX: (415) 325-7823

FORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
406-362-1

Y Match 0.7%; Score 12.4; DB 1; Length 14;
Local Similarity 92.9%; Pred. No. 1.5e+02;
hes 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

315 GGCAGCTGCTTACA 328
|||||
1 GGCAGCTGCTTACA 14

RESULT 230
US-09-755-734-1
; Sequence 1, Application US/09755734
; Patent No. 6391858
; GENERAL INFORMATION:
; APPLICANT: PODSAKOFF, GREGORY M.
; KESSLER, PAUL D.
; BYRNE, BARRY J.
; KURTZMAN, GARY J.
; TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE
; CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VECTORS

NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CA
COUNTRY: USA
ZIP: 94025

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/755,734
FILING DATE: 04-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/588,355
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 0800-0009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 325-7812
TELEFAX: (650) 325-7823

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-755-734-1

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 315 GGCAGCTGCTTACA 328
|||||
Db 1 GGCAGCTGCTTACA 14

RESULT 231
US-09-406-363-1
; Sequence 1, Application US/09406363
; Patent No. 6482633
; GENERAL INFORMATION:
; APPLICANT: COLOSI, PETER C.
; TITLE OF INVENTION: ACCESSORY FUNCTIONS FOR USE IN
; RECOMBINANT AAV VIRION PRODUCTION

NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA

ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/406,363
FILING DATE: 28-Sep-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/745,957
FILING DATE: 11-Jul-1996
ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 0800-0007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
TELEFAX: (415)327-3231
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
-406-363-1
Y Match 0.7%; Score 12.4; DB 1; Length 14;
Local Similarity 92.9%; Pred. No. 1.5e+02;
hes 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
315 GGCAGCTGCTTACA 328
|||||
1 GGCAGCTGCTTACA 14
-232
-649-890-1
ence 1, Application US/09649890
nt No. 6531456
NERAL INFORMATION:
APPLICANT: KURTZMAN, GARY J.
COLOSI, PETER C.
YOSHIDA, JUN
MIZUNO, MASAAKI
OKADA, HIDEO
TITLE OF INVENTION: GENE THERAPY FOR THE TREATMENT OF SOLID
TUMORS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VECTORS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/649,890
FILING DATE: 28-Aug-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/812,102
FILING DATE: 05-MAR-1997
APPLICATION NUMBER: US 60/013,209
FILING DATE: 06-MAR-1996

ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 0800-0008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 325-7812
TELEFAX: (415) 325-7823
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-649-890-1
Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 315 GGCAGCTGCTTACA 328
|||||
Db 1 GGCAGCTGCTTACA 14
RESULT 233
US-09-969-204A-1
Sequence 1, Application US/09969204A
Patent No. 6610290
GENERAL INFORMATION:
APPLICANT: PODSAKOFF, GREGORY M.
KESSLER, PAUL D.
BYRNE, BARRY J.
KURTZMAN, GARY J.
TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE
CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS
VIRIONS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/969,204A
FILING DATE: 01-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/406,362
FILING DATE: 28-Sep-1999
APPLICATION NUMBER: 08/784,757
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 0800-0009, 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 325-7812
TELEFAX: (415)325-7823
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
969-204A-1

Y Match 0.7%; Score 12.4; DB 1; Length 14;
Local Similarity 92.9%; Pred. No. 1.5e+02;
hes 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

315 GGCACTGCTTACA 328
|||||
1 GGCACTGCTTACA 14

234
874-601-6
ence 6, Application US/09874601
nt No. 6632057
RAL INFORMATION:
LICANT: LEMIN, ALFRED S.
LICANT: SHAM, LYNN C.

LICANT: GRANT, MARIA B.
LE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD
E OF INVENTION: THE TREATMENT OF RETINAL DISEASES
E REFERENCE: 4300.014100
RENT APPLICATION NUMBER: US/09/874,601

OR APPLICATION NUMBER: 09/063,667
OR FILING DATE: 1998-04-21
OR APPLICATION NUMBER: 60/046,147
OR FILING DATE: 1997-05-09
OR APPLICATION NUMBER: 60/044,492
OR FILING DATE: 1997-04-21
BER OF SEQ ID NOS: 182
TWARE: Patentin version 3.0

ID NO 6
NGTH: 14
PE: RNA
GANISM: Artificial Sequence

ATURE:
ME/KEY: misc feature
CATION: (1..7)
HER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
874-601-6

Y Match 0.7%; Score 12.4; DB 1; Length 14;
Local Similarity 64.3%; Pred. No. 1.5e+02;
hes 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

689 TGCTGGCTTCCC 702
|||||
1 UGUGGUCUCCCC 14

235
177-871-1
ence 1, Application US/10177871
nt No. 6897063
NERAL INFORMATION:
APPLICANT: COLOSI, PETER C.
TITLE OF INVENTION: RECOMBINANT AAV VIRION PRODUCTION

NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/177,871
FILING DATE: 19-Jun-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/745,957
FILING DATE: 07-NOV-1996
APPLICATION NUMBER: US 60/006,402
FILING DATE: 09-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 0800-0007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
TELEFAX: (415)327-3231

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-177-871-1

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 315 GGCACTGCTTACA 328
|||||
Db 1 GGCACTGCTTACA 14

RESULT 236
US-09-341-700A-1573
; Sequence 1573, Application US/09341700A
; Patent No. 6972171
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Bysch, Wolfgang
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/P63763USO
; CURRENT APPLICATION NUMBER: US/09/341,700A
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: EP 97 101 531.8
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 1764
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1573
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: antisense oligonucleotide
US-09-341-700A-1573

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1145 TCCGCTGGGCTTC 1158
|||||
Db 1 TCCCTCTGGGCTTC 14

RESULT 237
US-09-543-679A-1511

ence 1511, Application US/09543679A
ent No. 7034007
GENERAL INFORMATION:
APPLICANT: Ntce, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE AMTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICTION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <Unknown>
FORMATION FOR SEQ ID NO: 1511:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1511:
-543-679A-1511
Match 0.7%; Score 12.4; DB 1; Length 14;
Local Similarity 92.9%; Pred. No. 1.5e+02;
hes 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
344 CCTCTGTGTGGGC 357
1 CCTCTGTGTGGGC 14
238
-363-240A-619/C
ence 619, Application US/08363240A
nt No. 5705388
GENERAL INFORMATION:
APPLICANT: Couture, Larry
APPLICANT: McSwigen, James
APPLICANT: Biesaler, Charles
APPLICANT: Pape, Michael
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: PREVENTION, INHIBITION OF
TITLE OF INVENTION: PROGRESSION AND REGRESSION
TITLE OF INVENTION: OF VASCULAR DISEASES
NUMBER OF SEQUENCES: 1243
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles

STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,240A
FILING DATE: December 23, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 210/096
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
FORMATION FOR SEQ ID NO: 619:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-363-240A-619
Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1253 TGTACAAAGTCAGC 1266
DB 14 TGGACAAAGTCAGC 1
RESULT 239
US-08-585-684B-797/C
Sequence 797, Application US/08585684B
Patent No. 5877021
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
APPLICANT: McSwigen, James
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/585,684B
FILING DATE: January 16, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/000,951
FILING DATE: July 7, 1995
ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 218/078
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEEX: 67-3510
 ORAMATION FOR SEQ ID NO: 797:
 EQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 585-684B-797

y Match 0.7%; Score 12.4; DB 1; Length 15;
 Local Similarity 92.9%; Pred. No. 1.7e+02;
 hes 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

296 CCTGGCAATTGTC 309
 |||||
 15 CCTGGCAATTGTC 2

240
 585-684B-798/c
 ence 798, Application US/08585684B
 nt No. 5877021
 ERAL INFORMATION:
 PPLICANT: Stinchcomb, Daniel T.
 PPLICANT: Jarvis, Thale
 TITLE OF INVENTION: METHOD AND REAGENT FOR THE
 TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
 TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
 UMBER OF SEQUENCES: 2751
 ORRESPONDENCE ADDRESS:
 ADDRESSER: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSeq Version 1.5
 URRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/585,684B
 FILING DATE: January 16, 1996
 RIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/000,951
 FILING DATE: July 7, 1995
 TORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 218/078
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEEX: 67-3510
 ORAMATION FOR SEQ ID NO: 798:
 EQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 585-684B-798
 y Match 0.7%; Score 12.4; DB 1; Length 15;

Best Local Similarity 92.9%; Pred. No. 1.7e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 296 CCTGGCAATTGTC 309
 |||||
 Db 14 CCTGGCAATTGTC 1

RESULT 241
 US-08-585-684B-2099
 ; Sequence 2099, Application US/08585684B
 ; Patent No. 5877021
 ; GENERAL INFORMATION:
 ; APPLICANT: Stinchcomb, Daniel T.
 ; APPLICANT: Jarvis, Thale
 ; APPLICANT: McSwiggen, James
 ; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
 ; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
 ; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
 ; NUMBER OF SEQUENCES: 2751
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSER: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/585,684B
 ; FILING DATE: January 16, 1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/000,951
 ; FILING DATE: July 7, 1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 218/078
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 2099:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 15 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-585-684B-2099
 Query Match 0.7%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 57.1%; Pred. No. 1.7e+02;
 Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 Qy 1409 GGTCTCTCCCAT 1422
 ||::||:|||||
 Db 2 GTUUCUUCUCCAU 15
 RESULT 242
 US-08-585-684B-2295
 ; Sequence 2295, Application US/08585684B
 ; Patent No. 5877021
 ; GENERAL INFORMATION:
 ; APPLICANT: Stinchcomb, Daniel T.
 ; APPLICANT: Jarvis, Thale
 ; APPLICANT: McSwiggen, James

TITLE OF INVENTION: METHOD AND REAGENT FOR THE
 TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
 TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
 NUMBER OF SEQUENCES: 2751
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FASTSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/585,684B
 FILING DATE: January 16, 1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/000,951
 FILING DATE: July 7, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 218/078
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 2295:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 -585-684B-2295
 Match 0.7%; Score 12.4; DB 1; Length 15;
 Local Similarity 57.1%; Pred. No. 1.7e+02;
 hes 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 1409 GCTTCTCCTCCCAAT 1422
 ||::||:|||||:
 2 GCUCUCUCUCAU 15
 243
 -585-684B-2296
 hence 2296, Application US/08585684B
 int No. 5877021
 GENERAL INFORMATION:
 APPLICANT: Stinchcomb, Daniel T.
 APPLICANT: Jarvis, Thale
 APPLICANT: McSwigen, James
 TITLE OF INVENTION: METHOD AND REAGENT FOR THE
 TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
 TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
 NUMBER OF SEQUENCES: 2751
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 OPERATING SYSTEM: IBM Compatible
 SOFTWARE: Wordperfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/550,120
 FILING DATE: October 30, 1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-269417
 FILING DATE: No. 598554ember 2, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren M. Cheek, Jr.
 REGISTRATION NUMBER: 33,367
 REFERENCE/DOCKET NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-8850
 TELEFAX:
 TELEX:
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 bases
 TYPE: nucleic acid
 STRANDEDNESS: single

OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FASTSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/585,684B
 FILING DATE: January 16, 1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/000,951
 FILING DATE: July 7, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 218/078
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 2296:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-585-684B-2296
 Query Match 0.7%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 57.1%; Pred. No. 1.7e+02;
 Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 QY 1409 GCTTCTCCTCCCAAT 1422
 ||::||:|||||:
 DB 1 GCUCUCUCUCAU 14
 RESULT 244
 US-08-550-120-13/C
 Sequence 13, Application US/08550120
 Patent No. 5985554
 GENERAL INFORMATION:
 APPLICANT: Hiroshi TANIMURA et al.
 TITLE OF INVENTION: METHOD FOR PROBING THE FUNCTION OF A PROTEIN
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Wenderoth, Lind & Ponack
 STREET: 805 Fifteenth Street, N.W., #700
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: Wordperfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/550,120
 FILING DATE: October 30, 1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-269417
 FILING DATE: No. 598554ember 2, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren M. Cheek, Jr.
 REGISTRATION NUMBER: 33,367
 REFERENCE/DOCKET NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-8850
 TELEFAX:
 TELEX:
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 bases
 TYPE: nucleic acid
 STRANDEDNESS: single

TOPOLOGY: linear
 OBJECT TYPE: other nucleic acid, synthetic DNA
 550-120-13

Y Match 0.7%; Score 12.4; DB 1; Length 15;
 Local Similarity 92.9%; Pred. No. 1.7e+02;
 hes 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

910 GACCGCTACACGCA 923
 |||||
 14 GACCGGTACACGCA 1

245
 269-519A-2/C
 ence 2, Application US/09269519A
 nt No. 6180347

AL INFORMATION:
 LICANT: Iida, Yukari
 LICANT: Koshimoto, Hiroyuki
 LICANT: Kondo, Satoshi
 LICANT: Tsuji, Akihiko
 LE OF INVENTION: Method for Monitoring Transcriptional Synthesis of RNA
 E REFERENCE: 200783
 RENT APPLICATION NUMBER: US/09/269,519A
 RENT FILING DATE: 1999-04-02
 OR APPLICATION NUMBER: PCT/JP98/00444
 OR FILING DATE: 1998-02-03
 OR APPLICATION NUMBER: JP 020632/1997
 BER OF SEQ ID NOS: 11
 TWARE: Patentin Ver. 2.1
 ID NO 2
 NGTH: 15
 PE: DNA
 CANISM: Artificial Sequence
 ATURE:
 HER INFORMATION: Description of Artificial Sequence: XELF-IF
 HER INFORMATION: acceptor probe
 269-519A-2

Y Match 0.7%; Score 12.4; DB 1; Length 15;
 Local Similarity 92.9%; Pred. No. 1.7e+02;
 hes 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1155 CTTCAAGCATGGCT 1168
 |||||
 14 CTTCAAGTATGGCT 1

246
 038-073-797/C
 ence 797, Application US/09038073
 nt No. 6194150

ERAL INFORMATION:
 PPICANT: Stinchcomb, Daniel T.
 PPICANT: Jarvis, Thale
 PPICANT: McSwigen, James
 TITLE OF INVENTION: METHOD AND REAGENT FOR THE
 TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
 TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
 UMBER OF SEQUENCES: 2751
 ORRESPONDENCE ADDRESS:
 ADDRESSER: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071

OMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FASTSO Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/038,073
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/585,684
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 218/078
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 797:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-038-073-797

Query Match 0.7%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 1.7e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 296 CTTGCAAAATTGTC 309
 |||||
 Db 15 CTTGGAATTTGTC 2

RESULT 247
 US-09-038-073-798/C
 Sequence 798, Application US/09038073
 Patent No. 6194150
 GENERAL INFORMATION:
 APPLICANT: Stinchcomb, Daniel T.
 APPLICANT: Jarvis, Thale
 APPLICANT: McSwigen, James
 TITLE OF INVENTION: METHOD AND REAGENT FOR THE
 TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
 TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
 NUMBER OF SEQUENCES: 2751
 CORRESPONDENCE ADDRESS:
 ADDRESSER: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FASTSO Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/038,073
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/585,684
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 218/078
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 798:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 -038-073-798

Local Similarity 92.9%; Score 12.4; DB 1; Length 15;
 Mismatches 0; Indels 0; Gaps 0;
 Conservative 13; Mismatches 1; Indels 0; Gaps 0;

296 CCTGCAATTGTC 309
 |||||
 14 CCTGGGAATTGTC 1

248
 -038-073-2099
 ence 2099, Application US/09038073
 ent No. 6194150
 ERAL INFORMATION:
 APPLICANT: Stinchcomb, Daniel T.
 APPLICANT: Jarvis, Thale
 TITLE OF INVENTION: METHOD AND REAGENT FOR THE
 TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
 TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
 NUMBER OF SEQUENCES: 2751
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FASTSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/038,073
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/585,684

FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 218/078
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440

TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 2099:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 -038-073-2099

Local Similarity 92.9%; Score 12.4; DB 1; Length 15;
 Mismatches 0; Indels 0; Gaps 0;
 Conservative 8; Mismatches 5; Indels 1; Gaps 0;

1409 GCTTCTCCTCCAT 1422
 |||||

Db 2 GCUUCUCCCAU 15

RESULT 249
 US-09-038-073-2295
 Sequence 2295, Application US/09038073
 Patent No. 6194150
 GENERAL INFORMATION:
 APPLICANT: Stinchcomb, Daniel T.
 APPLICANT: Jarvis, Thale
 TITLE OF INVENTION: METHOD AND REAGENT FOR THE
 TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
 TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
 NUMBER OF SEQUENCES: 2751
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FASTSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/038,073
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/585,684

FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 218/078
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440

TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 2295:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-038-073-2295

Query Match 0.7%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 57.1%; Pred. No. 1.7e+02;
 Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1409 GCTTCTCCTCCAT 1422
 |||||

Db 2 GCUUCUCCCAU 15

RESULT 250
 US-09-038-073-2296
 Sequence 2296, Application US/09038073
 Patent No. 6194150
 GENERAL INFORMATION:
 APPLICANT: Stinchcomb, Daniel T.
 APPLICANT: Jarvis, Thale
 TITLE OF INVENTION: METHOD AND REAGENT FOR THE
 TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
 TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
 NUMBER OF SEQUENCES: 2751
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,073

FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/585,684
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
ELECTRONIC COMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440

TELEX: 67-3510
ORAMATION FOR SEQ ID NO: 2296:
SEQUENCE CHARACTERISTICS:

LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
038-073-2296

Y Match 0.7%; Score 12.4; DB 1; Length 15;
Local Similarity 57.1%; Pred. No. 1.7e+02;
hes 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

1409 GCTTCCTCTCCAT 1422
||:|:|:|:|:|:
1 GCUUCUUCUCCAAU 14

251
081-646-167/c
ence 167, Application US/09081646
nt No. 6333152
RAL INFORMATION:
LICANT: Kinzler, Kenneth
LICANT: Vogelstein, Bert
LICANT: Zhang, Lin
LICANT: Zhou, Wei
LE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
E REFERENCE: 01107.74664
RENT APPLICATION NUMBER: US/09/081,646
RENT FILING DATE: 1998-05-20
LIER APPLICATION NUMBER: 60/047,352
LIER FILING DATE: 1997-05-21
BER OF SEQ ID NOS: 871
TWARE: FastSeq for Windows Version 3.0
ID NO 167
NGTH: 15
PE: DNA
GANISM: Homo sapiens
081-646-167

Y Match 0.7%; Score 12.4; DB 1; Length 15;
Local Similarity 92.9%; Pred. No. 1.7e+02;
hes 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
367 GTGATGTGATCAT 380

Db 15 GCGATGTGATCAT 2

RESULT 252
US-09-856-662-4
; Sequence 4, Application US/09856662
; Patent No. 6790616
; GENERAL INFORMATION:
; APPLICANT: MORIBE, Toyoki et al.
; TITLE OF INVENTION: Method for typing HLA class 1 genes
; FILE REFERENCE: 0032-0261P
; CURRENT APPLICATION NUMBER: US/09/856,662
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: JP P1998-335151
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 4
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:DNA probe A239A
US-09-856-662-4

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1307 AGGAGAGCCGAG 1320
|||||||
Db 2 AGGAGAGCCGAG 15

RESULT 253
US-09-341-700A-196/c
; Sequence 196, Application US/09341700A
; Patent No. 6972171
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Brysch, Wolfgang
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/P63763USO
; CURRENT APPLICATION NUMBER: US/09/341,700A
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: EP 97 101 531.8
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 1764
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 196
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: antisense oligonucleotide
US-09-341-700A-196

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 936 CAAGCGCAAGTGG 949
|||||||
Db 14 CAAGCGCAAGTGG 1

RESULT 254
US-10-156-306B-7875
; Sequence 7875, Application US/10156306B

Pat. No. 7022828
Patent Information:
Applicant: Ribozyme Pharmaceuticals, Inc.
Title of Invention: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Infection: Levels of IKK-Gamma and PKR
Reference: MBH01-664-A (400/050)
Current Application Number: US/10/156,306B
Filing Date: 2002-05-28
Number of SEQ ID NOS: 8014
Title: Patent in version 3.0
ID NO: 7875
Length: 15
Type: RNA
Organism: Homo sapiens
156-306B-7875

Match 0.7%; Score 12.4; DB 1; Length 15;
Local Similarity 57.1%; Pred. No. 1.7e+02;
Indels 0; Gaps 0;
Matches 8; Conservative 5; Mismatches 1;

105 CCCCTCCTCTGCT 118
|||:|:|:|:|:
1 CCCUCUCUCUCUCU 14

255
93-12600-15/c
ence 15, Application PC/TUS9312600
General Information:
Applicant: Denner, Larry A.
Applicant: Rege, Ajay A.
Applicant: Dixon, Richard A.F.
Title of Invention: ANTISENSE MOLECULES DIRECTED AGAINST A
NUMBER OF SEQUENCES: 29
Title of Invention: FIBROBLAST GROWTH FACTOR RECEPTOR GENE FAMILY
Correspondence Address:
Address: Dressler, Goldsmith, Shore &
Address: Milnamow, Ltd.
Street: 180 North Steetson, Suite 4700
City: Chicago
State: Illinois
Country: USA
ZIP: 60601

COMPUTER READABLE FORM:
Medium Type: Floppy disk
Operating System: IBM PC compatible
Software: Patent in Release #1.0, Version #1.25
Current Application Data:
Application Number: PCT/US93/12600
Filing Date: 28-DEC-1993

Classification:
Prior Application Data:
Application Number: US 07/999,706
Filing Date: December 31, 1992
Attorney/Agent Information:
Name: Katz, Martin L.
Registration Number: 25,011
Telecommunication Information:
Telephone: (312)616-5400
Telefax: (312)616-5460
Information for SEQ ID NO: 15:
Sequence Characteristics:
Length: 15 base pairs
Type: nucleic acid
Strandedness: single
Topology: linear
Molecule Type: DNA (genomic)
93-12600-15

Match 0.7%; Score 12.4; DB 1; Length 15;
Local Similarity 92.9%; Pred. No. 1.7e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1202 ATGAGGGGCTGGAA 1215
Db 15 ATGTGGGGCTGGAA 2

RESULT 256
US-08-513-974B-61
Sequence 61, Application US/08513974B
Patent No. 6114139
General Information:
Applicant: Hinuma, Shuji
Applicant: Hosoya, Masaki
Applicant: Fujii, Ryo
Applicant: Ohtaki, Tetsuya
Applicant: Fukusumi, Shoji
Applicant: Ohgi, Kazuhiko
Title of Invention: G PROTEIN COUPLED RECEPTOR PROTEIN,
Title of Invention: PRODUCTION, AND USE THEREOF
Number of Sequences: 380
Correspondence Address:
Address: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
Street: 130 Water Street
City: Boston
State: MA
Country: USA
ZIP: 02109

COMPUTER READABLE FORM:
Medium Type: Floppy disk
Operating System: IBM PC compatible
Software: Patent in Release #1.0, Version #1.30
Current Application Data:
Application Number: US/08/513,974B
Filing Date: 14-SEP-1995

Classification: 536
Prior Application Data:
Application Number: PCT/JP95/01599
Filing Date: 10-AUG-1995
Prior Application Data:
Application Number: JP 7-093989
Filing Date: 19-AUG-1995
Prior Application Data:
Application Number: JP 7-057186
Filing Date: 16-MAR-1995
Prior Application Data:
Application Number: JP 7-007177
Filing Date: 20-JAN-1995
Prior Application Data:
Application Number: JP 6-326611
Filing Date: 28-DEC-1994
Prior Application Data:
Application Number: JP 6-270017
Filing Date: 02-NOV-1994
Prior Application Data:
Application Number: JP 6-236357
Filing Date: 30-SEP-1994
Prior Application Data:
Application Number: JP 6-236356
Filing Date: 30-SEP-1994
Prior Application Data:
Application Number: JP 6-189274
Filing Date: 11-AUG-1994
Prior Application Data:
Application Number: JP 6-189273
Filing Date: 11-AUG-1994
Prior Application Data:
Application Number: JP 6-189272
Filing Date: 11-AUG-1994
Attorney/Agent Information:
Name: Resnick, David S.
Registration Number: 34,235

```

REFERENCE/DOCKET NUMBER: 45753
ELECTRONIC INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
ORAMTION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
OLECUE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA
FEATURE:
OTHER INFORMATION: N = inosine
513-974B-61

Y Match 0.7%; Score 12.4; DB 1; Length 29;
Local Similarity 65.0%; Pred.No.3.1e+02;
hes 13; Conservative 3; Mismatches 4; Indels 0, Gaps 0.

1046 TGAAGAAGTTATCCAGCAG 1065
:|:|:| | | | | |
2 KGWAGWAGGCGACGACGAG 21

257
776-971-32
ence 32, Application US/08776971B
nt No. 6228984
NERAL INFORMATION:
APPLICANT: Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
Fuji, Ryo
Fukusumi, Shoji
Kitada, Chieko
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
ELECTRONIC INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440

```

```

? INFORMATION FOR SEQ ID NO: 32:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 29 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: other nucleic acid
? DESCRIPTION: /desc = "synthetic DNA"
? SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-08-776-971-32

Query Match          0.7% Score 12.4; DB 1; Length 29;
Best Local Similarity 65.0%; Pred.No. 3,le+02;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0.

Oy      1046 TGAAGAAGTTATCCAGCAG 1065
       :|::||| | |||||
Db      2 KGMAGMAGGCAGCGCAGCAG 21

RESULT 258
US-09-461-436B-61
Sequence 61, Application US/09461436B
Patent No. 6538107
GENERAL INFORMATION:
APPLICANT: Shuji Hinuma
Yasunaki Ito
Ryo Fujii

TITLE OF INVENTION: G Protein Coupled Receptor Protein,
Production, And Use Thereof

NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edwards & Angell, LLP
STREET: 101 Federal Street
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02209

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/461,436B
FILING DATE: 14-Dec-1999
CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/513,974
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
APPLICATION NUMBER: 7-093989
FILING DATE: 19-APR-1995
APPLICATION NUMBER: 7-057186
FILING DATE: 16-MAR-1995
APPLICATION NUMBER: 7-007177
FILING DATE: 20-JAN-1995
APPLICATION NUMBER: 6-326611
FILING DATE: 28-DEC-1994
APPLICATION NUMBER: 6-270017
FILING DATE: 02-NOV-1994
APPLICATION NUMBER: 6-236357
FILING DATE: 30-SEP-1994
APPLICATION NUMBER: 6-236356
FILING DATE: 30-SEP-1994
APPLICATION NUMBER: 6-189274
FILING DATE: 11-AUG-1994
APPLICATION NUMBER: 6-189273
FILING DATE: 11-AUG-1994
APPLICATION NUMBER: 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:

```

NAME: CONLIN, DAVID G.
 REGISTRATION NUMBER: <Unknown>
 REFERENCE/DOCKET NUMBER: 45753 DIV2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-439-4444
 TELEFAX: 617-439-4170
 INFORMATION FOR SEQ ID NO: 61:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Other nucleic acid
 DESCRIPTION: /desc = "synthetic DNA"
 FEATURE:
 OTHER INFORMATION: /note= N is inosine, S is G or C, W is A or T;
 R is A or G, K is G or T, Y is C or T."
 SEQUENCE DESCRIPTION: SEQ ID NO: 61:
 -461-436B-61
 Y Match 0.7%; Score 12.4; DB 1; Length 29;
 Local Similarity 65.0%; Pred. No. 3.1e+02;
 hes 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 1046 TGAAGAGTTTATCCAGCAG 1065
 :||:|||||
 2 KGMAGMAGGCGCAGCCAGCAG 21
 -576-290-32
 Ince 32, Application US/09576290
 int No. 6794491
 ERAL INFORMATION:
 APPLICANT: Hinuma, Shuji
 APPLICANT: Habata, Yugo
 APPLICANT: Kawamata, Yuji
 APPLICANT: Hosoya, Masaki
 APPLICANT: Fujii, Ryo
 APPLICANT: Fukusumi, Shoji
 APPLICANT: Kitada, Chieko
 TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
 NUMBER OF SEQUENCES: 140
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/576,290
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/776,971
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7/343371
 FILING DATE: 28-DEC-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 8/59419
 FILING DATE: 15-MAR-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 8/211805
 FILING DATE: 12-AUG-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 8/246573

FILING DATE: 18-SEP-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 47176
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 32:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Other nucleic acid
 DESCRIPTION: /desc = "synthetic DNA"
 US-09-576-290-32
 Query Match 0.7%; Score 12.4; DB 1; Length 29;
 Best Local Similarity 65.0%; Pred. No. 3.1e+02;
 Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1046 TGAAGAGTTTATCCAGCAG 1065
 :||:|||||
 DB 2 KGMAGMAGGCGCAGCCAGCAG 21
 RESULT 260
 US-09-716-147-32
 Sequence 32, Application US/09716147
 Patent No. 6881545
 GENERAL INFORMATION:
 APPLICANT: Hinuma, Shuji
 APPLICANT: Habata, Yugo
 APPLICANT: Kawamata, Yuji
 APPLICANT: Hosoya, Masaki
 APPLICANT: Fujii, Ryo
 APPLICANT: Fukusumi, Shoji
 APPLICANT: Kitada, Chieko
 TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
 NUMBER OF SEQUENCES: 140
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/716,147
 FILING DATE: 17-NOV-1995
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/776,971B
 FILING DATE: 06-FEB-1997
 APPLICATION NUMBER: PCT/JP96/03821
 FILING DATE: 28-DEC-1996
 APPLICATION NUMBER: JP 7/343371
 FILING DATE: 28-DEC-1995
 APPLICATION NUMBER: JP 8/59419
 FILING DATE: 15-MAR-1996
 APPLICATION NUMBER: JP 8/211805
 FILING DATE: 12-AUG-1996
 APPLICATION NUMBER: JP 8/246573
 FILING DATE: 18-SEP-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,026

ATTORNEY/AGENT INFORMATION:

NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-5550
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
-608-584-8

Y Match 0.7%; Score 12; DB 1; Length 14;
Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

935 CCAAGCGCAAGG 946
|||||
14 CCAAGCGCAAGG 3

F 264
-720-435A-38/C
ence 38, Application US/09720435A
nt No. 6803187
RAL INFORMATION:

PLICANT: Stuyver, Lieven
LE OF INVENTION: Method for detection of drug-selected mutations in the protease
E REFERENCE: 11362.0030.PCUS00 INNS.030
RENT APPLICATION NUMBER: US/09/720,435A
RENT FILING DATE: 2001-06-25
OR APPLICATION NUMBER: PCT/EP99/04317
OR FILING DATE: 1999-06-22
OR APPLICATION NUMBER: 98870143.9
OR FILING DATE: 1998-06-24
BER OF SEQ ID NOS: 529
TMARE: Patent in version 3.2
ID NO 38
NGTH: 14
PE: DNA
GANISM: Aids-associated retrovirus
-720-435A-38

Y Match 0.7%; Score 12; DB 1; Length 14;
Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

663 CTGTGTCATCTG 674
|||||
13 CTGTGTCATCTG 2

F 265
-588-595-1
ence 1, Application US/08588595
nt No. 5958769
RAL INFORMATION:

PLICANT: Roberts, James M.
PLICANT: Coats, Steven R.
PLICANT: Fero, Matthew L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MEDIATING
TITLE OF INVENTION: CELL CYCLE PROGRESSION
NUMBER OF SEQUENCES: 13
ORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stuart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,595
FILING DATE: 18-JAN-1996

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14538A-19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleotide
US-08-588-595-1

Query Match 0.7%; Score 12; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 680 TGAGCTCTCCTGC 691
:||||:|
Db 1 UGCGUCUCCUGC 12

RESULT 266
US-09-180-437-143/C
Sequence 143, Application US/09180437
Patent No. 6251873
GENERAL INFORMATION:
APPLICANT: FUKUSAKO, Shioji
APPLICANT: MORISAWA, Yoshihumi
APPLICANT: KUSUYAMA, Takeshi
TITLE OF INVENTION: Antisense Compounds to CD14
FILE REFERENCE: 1110-209P
CURRENT APPLICATION NUMBER: US/09/180,437
CURRENT FILING DATE: 1998-11-06
EARLIER APPLICATION NUMBER: PCT/JP98/00953
EARLIER FILING DATE: 1998-03-09
EARLIER APPLICATION NUMBER: 09-053518 JAPAN
EARLIER FILING DATE: 1997-03-07
NUMBER OF SEQ ID NOS: 289
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 143
LENGTH: 15
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: other nucleic
US-09-180-437-143

Query Match 0.7%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 146 AGCCACAGACT 157
|||||
Db 12 AGCCACAGACT 1

RESULT 267
US-09-275-850-31/C
Sequence 31, Application US/09275850A
Patent No. 6261774
GENERAL INFORMATION:

```
LICANT: Pagratia, Nikos
LICANT: Gold, Larry
LICANT: Sheatland, Timur
LICANT: Javornik, Brenda
LE OF INVENTION: Truncation SELEX Method
E REFERENCE: NEX 79
RENT APPLICATION NUMBER: US/09/275, 850A
RENT FILING DATE: 1999-03-24
BER OF SEQ ID NOS: 351
TWARE: Patentin Ver. 2.0
ID NO 31
NGTH: 15
PE: RNA
GANISM: E. coli
275-850-31

Y Match      0.7%; Score 12; DB 1; Length 15;
Local Similarity 100.0%; Pred. No. 1.9e+02;
hes 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

832 CCCCTGCTGTG 843
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14 CCCCTGCTGTG 3

268
081-646-49/c
ence 49, Application US/09081646
nt No. 6333152
RAL INFORMATION:
LICANT: Kinzler, Kenneth
LICANT: Vogelstein, Bert
LICANT: Zhang, Lin
LICANT: Zhou, Wei
LE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
LE OF INVENTION: Cancer Cells
E REFERENCE: 01107.74664
RENT APPLICATION NUMBER: US/09/081, 646
RENT FILING DATE: 1998-05-20
LIER APPLICATION NUMBER: 60/047, 352
LIER FILING DATE: 1997-05-21
BER OF SEQ ID NOS: 871
TWARE: FastSeq for Windows Version 3.0
ID NO 49
NGTH: 15
PE: DNA
GANISM: Homo sapiens
081-646-49

Y Match      0.7%; Score 12; DB 1; Length 15;
Local Similarity 100.0%; Pred. No. 1.9e+02;
hes 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1522 GAAACACCCCTCA 1533
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14 GAAACACCCCTCA 3

269
081-646-560/c
ence 560, Application US/09081646
nt No. 6333152
RAL INFORMATION:
LICANT: Kinzler, Kenneth
LICANT: Vogelstein, Bert
LICANT: Zhang, Lin
LICANT: Zhou, Wei
LE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
LE OF INVENTION: Cancer Cells
E REFERENCE: 01107.74664
RENT APPLICATION NUMBER: US/09/081, 646
RENT FILING DATE: 1998-05-20
LIER APPLICATION NUMBER: 60/047, 352

; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 871
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 560
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-081-646-560

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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      12 CCTCCCTTCATG 1

RESULT 270
US-09-015-188-6/c
; Sequence 6, Application US/09015188C
; Patent No. 6399358
; GENERAL INFORMATION:
; APPLICANT: Williams, Kevin J
; APPLICANT: Tabas, Ira
; TITLE OF INVENTION: A Human Gene Encoding Human Chondroitin
; FILE REFERENCE: JEPF-0231
; CURRENT APPLICATION NUMBER: US/09/015, 188C
; CURRENT FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-015-188-6

Query Match      0.7%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      641 CCACAGCCACCA 652
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Db      12 CCACAGCCACCA 1

RESULT 271
US-09-720-435A-39/c
; Sequence 39, Application US/09720435A
; Patent No. 6803187
; GENERAL INFORMATION:
; APPLICANT: Stuyver, Lieven
; TITLE OF INVENTION: Method for detection of drug-selected mutations in the protease
; FILE REFERENCE: 11362.0030.PCUS00 INNS:030
; CURRENT APPLICATION NUMBER: US/09/720, 435A
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: PCT/EP99/04317
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 98870143.9
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: Patentin Version 3.2
; SEQ ID NO 39
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Aids-associated retrovirus
US-09-720-435A-39

Query Match      0.7%; Score 12; DB 1; Length 15;
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: Local Similarity 100.0%; Pred. No. 1.9e+02;
:hes 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

663 CTGTCTCATCTG 674

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12 CTGTCTCATCTG 1

: 272

:907-111-31/C
ence 31, Application US/09907111

ant No. 6855496

RAL INFORMATION:

PLICANT: Pagratia, Nikos

PLICANT: Gold, Larry

PLICANT: Sheatland, Timur

PLICANT: Javornik, Brenda

LE OF INVENTION: Truncation SELEX Method

REFERENCE: NEX 79

URRENT APPLICATION NUMBER: US/09/907,111

OR FILING DATE: 2001-07-17

OR APPLICATION NUMBER: 09/275,850

OR FILING DATE: 1999-03-24

BER OF SEQ ID NOS: 351

TMARE: PatentIn Ver. 2.0

ID NO 31

NGTH: 15

PE: RNA

GANISM: E. coli

:907-111-31

:Y Match 0.7%; Score 12; DB 1; Length 15;
: Local Similarity 100.0%; Pred. No. 1.9e+02;
:hes 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

832 CCCCTGCTGTG 843

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14 CCCCTGCTGTG 3

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Time: 6 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2006, 06:21:45 ; Search time 30 Seconds
(without alignments)
3.467 Million cell updates/sec

Title: US-09-930-503A-6

Perfect score: 1766

Sequence: 1 aatcagagccacgcgcgggc.....cgagtgcattcagagatg 1766

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 0.5

Searched: 1462 seqs, 29446 residues

Total number of hits satisfying chosen parameters: 2924

Minimum DB seq length: 8

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1464 summaries

Database : us-09-930-503a-6.sl.rnpbm4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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142	25	1.4	25	1	US-11-060-756-301167	Sequence 301167,	215	21.8	1.2	27	1	US-11-060-756-270235	Sequence 270235,
143	25	1.4	25	1	US-11-121-849-111033	Sequence 111033,	216	21.8	1.2	27	1	US-08-796-570A-8	Sequence 8, Appl1
144	25	1.4	25	1	US-11-121-849-111034	Sequence 111034,	217	21.8	1.2	27	1	US-09-929-752-6	Sequence 6, Appl1
145	25	1.4	25	1	US-11-121-849-111035	Sequence 111035,	218	21.8	1.2	27	1	US-10-064-497-21	Sequence 21, Appl1
146	25	1.4	25	1	US-11-121-849-111036	Sequence 111036,	219	21.8	1.2	27	1	US-10-067-477-8	Sequence 8, Appl1
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153	25	1.4	25	1	US-11-121-849-111043	Sequence 111043,	226	21	1.2	21	1	US-09-930-503-26	Sequence 26, Appl1
154	25	1.4	25	1	US-11-121-849-192687	Sequence 192687,	227	21	1.2	21	1	US-09-930-503-28	Sequence 28, Appl1
155	25	1.4	25	1	US-11-121-849-192688	Sequence 192688,	228	21	1.2	21	1	US-09-930-503-31	Sequence 31, Appl1
156	25	1.4	25	1	US-11-121-849-192689	Sequence 192689,	229	21	1.2	21	1	US-09-930-503-33	Sequence 33, Appl1
157	25	1.4	25	1	US-11-121-849-192690	Sequence 192690,	230	21	1.2	21	1	US-09-930-503-38	Sequence 38, Appl1
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159	25	1.4	25	1	US-11-121-849-192692	Sequence 192692,	232	21	1.2	21	1	US-09-930-503-42	Sequence 42, Appl1
160	25	1.4	25	1	US-11-121-849-192693	Sequence 192693,	233	21	1.2	21	1	US-09-930-503-45	Sequence 45, Appl1
161	25	1.4	25	1	US-11-121-849-192694	Sequence 192694,	234	21	1.2	21	1	US-09-930-503-47	Sequence 47, Appl1
162	25	1.4	25	1	US-11-121-849-192695	Sequence 192695,	235	21	1.2	21	1	US-09-930-503-50	Sequence 50, Appl1
163	25	1.4	25	1	US-11-121-849-192696	Sequence 192696,	236	21	1.2	21	1	US-09-930-503-52	Sequence 52, Appl1
164	25	1.4	25	1	US-11-121-849-192697	Sequence 192697,	237	21	1.2	21	1	US-09-930-503-53	Sequence 53, Appl1
165	25	1.4	25	1	US-10-005-956-1306	Sequence 1306, Ap	238	21	1.2	21	1	US-09-930-503-57	Sequence 57, Appl1
166	25	1.4	25	1	US-11-036-317-481475	Sequence 481475,	239	21	1.2	21	1	US-09-930-503-59	Sequence 59, Appl1
167	24	1.4	27	1	US-10-005-956-1304	Sequence 1304, Ap	240	21	1.2	21	1	US-10-005-956-347	Sequence 347, App
168	24	1.4	29	1	US-10-044-592-23	Sequence 23, Appl	241	21	1.2	21	1	US-10-005-956-404	Sequence 404, App
169	24	1.4	29	1	US-10-278-087A-61	Sequence 61, Appl	242	21	1.2	21	1	US-10-005-956-407	Sequence 407, App
170	24	1.4	29	1	US-11-054-211-32	Sequence 32, Appl	243	21	1.2	21	1	US-10-005-956-408	Sequence 408, App
171	23.6	1.3	24	1	US-10-005-956-1215	Sequence 1215, Ap	244	21	1.2	21	1	US-10-005-956-409	Sequence 409, App
172	23.4	1.3	25	1	US-10-719-900-67260	Sequence 67260, A	245	21	1.2	21	1	US-10-005-956-467	Sequence 467, App
173	23.4	1.3	25	1	US-10-719-900-237659	Sequence 237659,	246	21	1.2	21	1	US-10-005-956-473	Sequence 473, App
174	23.4	1.3	25	1	US-10-719-900-247410	Sequence 247410,	247	21	1.2	21	1	US-10-005-956-534	Sequence 534, App
175	23.4	1.3	25	1	US-10-719-900-253859	Sequence 253859,	248	21	1.2	21	1	US-10-005-956-534	Sequence 534, App
176	23.4	1.3	25	1	US-10-719-900-890393	Sequence 890393,	249	21	1.2	21	1	US-10-005-956-534	Sequence 534, App
177	23.4	1.3	25	1	US-10-809-189-67914	Sequence 67914, A	250	21	1.2	21	1	US-10-005-956-534	Sequence 534, App
178	23.4	1.3	25	1	US-10-809-189-67926	Sequence 67926, A	251	21	1.2	21	1	US-10-005-956-534	Sequence 534, App
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C 255	21	1.2	21	1	US-10-310-914A-386281	Sequence 386281, App	328	21	1.2	21	1	US-11-127-877-503	Sequence 503, App	
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283	21	1.2	21	1	US-11-127-877-455	Sequence 455, App	356	21	1.2	21	1	US-11-127-877-531	Sequence 531, App	
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289	21	1.2	21	1	US-11-127-877-461	Sequence 461, App	362	20.8	1.2	25	1	US-10-809-189-67919	Sequence 67919, A	
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292	21	1.2	21	1	US-11-127-877-464	Sequence 464, App	365	20.8	1.2	25	1	US-11-060-756-36930	Sequence 36930, A	
293	21	1.2	21	1	US-11-127-877-465	Sequence 465, App	366	20.8	1.2	25	1	US-11-060-756-36934	Sequence 36934, A	
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295	21	1.2	21	1	US-11-127-877-467	Sequence 467, App	368	20.8	1.2	25	1	US-11-060-756-36935	Sequence 36935, A	
296	21	1.2	21	1	US-11-127-877-468	Sequence 468, App	369	20.8	1.2	25	1	US-11-060-756-233624	Sequence 233624, App	
297	21	1.2	21	1	US-11-127-877-469	Sequence 469, App	370	20.8	1.2	25	1	US-11-060-756-233625	Sequence 233625, App	
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304	21	1.2	21	1	US-11-127-877-477	Sequence 477, App	377	20.2	1.1	25	1	US-10-719-900-152541	Sequence 152541, A	
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325	21	1.2	21	1	US-11-127-877-500	Sequence 500, App	398	20.2	1.1	25	1	US-11-060-756-123000	Sequence 123000, A	

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404	20	1.1	20	1	US-09-930-503-25	Sequence 25, Appl	477	19	1.1	19	1	US-11-083-784-491162	Sequence 491162,
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412	20	1.1	20	1	US-09-930-503-49	Sequence 49, Appl	485	19	1.1	19	1	US-11-083-784-491170	Sequence 491170,
413	20	1.1	20	1	US-10-146-354A-34	Sequence 34, Appl	486	19	1.1	19	1	US-11-083-784-491171	Sequence 491171,
414	20	1.1	20	1	US-10-146-354A-46	Sequence 46, Appl	487	19	1.1	19	1	US-11-083-784-491172	Sequence 491172,
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416	20	1.1	20	1	US-10-146-354A-48	Sequence 48, Appl	489	19	1.1	19	1	US-11-083-784-491174	Sequence 491174,
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425	19.2	1.1	24	1	US-09-931-700-13	Sequence 35, Appl	498	19	1.1	19	1	US-11-083-784-491184	Sequence 491184,
426	19.2	1.1	19	1	US-09-930-503-35	Sequence 35, Appl	499	19	1.1	19	1	US-11-083-784-491185	Sequence 49

545	19	1.1	19	1	US-11-083-784-491234	Sequence 491234,	618	19	1.1	19	1	US-11-101-244-491155	Sequence 491155,	690	19	1.1	19	1	US-11-101-244-491232	Sequence 491232,	667	19	1.1	19	1	US-11-101-244-491127	Sequence 491127,	645	19	1.1	19	1	US-11-101-244-491188	Sequence 491188,	646	19	1.1	19	1	US-11-101-244-491177	Sequence 491177,	633	19	1.1	19	1	US-11-101-244-491166	Sequence 491166,	622	19	1.1	19	1	US-11-101-244-491155	Sequence 491155,	610	19	1.1	19	1	US-11-101-244-491137	Sequence 491137,	589	19	1.1	19	1	US-11-101-244-491126	Sequence 491126,	578	19	1.1	19	1	US-11-083-784-491287	Sequence 491287,	577	19	1.1	19	1	US-11-083-784-491285	Sequence 491285,	576	19	1.1	19	1	US-11-083-784-491284	Sequence 491284,	575	19	1.1	19	1	US-11-083-784-491283	Sequence 491283,	574	19	1.1	19	1	US-11-083-784-491282	Sequence 491282,	573	19	1.1	19	1	US-11-083-784-491281	Sequence 491281,	572	19	1.1	19	1	US-11-083-784-491280	Sequence 491280,	571	19	1.1	19	1	US-11-083-784-491279	Sequence 491279,	570	19	1.1	19	1	US-11-083-784-491278	Sequence 491278,	569	19	1.1	19	1	US-11-083-784-491276	Sequence 491276,	568	19	1.1	19	1	US-11-083-784-491275	Sequence 491275,	567	19	1.1	19	1	US-11-083-784-491269	Sequence 491269,	566	19	1.1	19	1	US-11-083-784-491268	Sequence 491268,	565	19	1.1	19	1	US-11-083-784-491265	Sequence 491265,	559	19	1.1	19	1	US-11-083-784-491264	Sequence 491264,	558	19	1.1	19	1	US-11-083-784-491263	Sequence 491263,	558	19	1.1	19	1	US-11-083-784-491251	Sequence 491251,	554	19	1.1	19	1	US-11-083-784-491252	Sequence 491252,	555	19	1.1	19	1	US-11-083-784-491255	Sequence 491255,	556	19	1.1	19	1	US-11-083-784-491269	Sequence 491269,	552	19	1.1	19	1	US-11-083-784-491270	Sequence 491270,	553	19	1.1	19	1	US-11-083-784-491271	Sequence 491271,	554	19	1.1	19	1	US-11-083-784-491272	Sequence 491272,	555	19	1.1	19	1	US-11-083-784-491273	Sequence 491273,	556	19	1.1	19	1	US-11-083-784-491274	Sequence 491274,	557	19	1.1	19	1	US-11-083-784-491275	Sequence 491275,	558	19	1.1	19	1	US-11-083-784-491276	Sequence 491276,	559	19	1.1	19	1	US-11-083-784-491278	Sequence 491278,	570	19	1.1	19	1	US-11-083-784-491279	Sequence 491279,	571	19	1.1	19	1	US-11-083-784-491280	Sequence 491280,	572	19	1.1	19	1	US-11-083-784-491281	Sequence 491281,	573	19	1.1	19	1	US-11-083-784-491282	Sequence 491282,	574	19	1.1	19	1	US-11-083-784-491283	Sequence 491283,	575	19	1.1	19	1	US-11-083-784-491284	Sequence 491284,	576	19	1.1	19	1	US-11-083-784-491285	Sequence 491285,	577	19	1.1	19	1	US-11-083-784-491286	Sequence 491286,	578	19	1.1	19	1	US-11-083-784-491287	Sequence 491287,	579	19	1.1	19	1	US-11-083-784-491288	Sequence 491288,	580	19	1.1	19	1	US-11-083-784-491291	Sequence 491291,	581	19	1.1	19	1	US-11-083-784-491292	Sequence 491292,	582	19	1.1	19	1	US-11-083-784-491294	Sequence 491294,	583	19	1.1	19	1	US-11-083-784-491296	Sequence 491296,	584	19	1.1	19	1	US-11-083-784-491297	Sequence 491297,	585	19	1.1	19	1	US-11-083-784-491298	Sequence 491298,	586	19	1.1	19	1	US-11-101-244-491124	Sequence 491124,	587	19	1.1	19	1	US-11-101-244-491125	Sequence 491125,	588	19	1.1	19	1	US-11-101-244-491126	Sequence 491126,	589	19	1.1	19	1	US-11-101-244-491127	Sequence 491127,	590	19	1.1	19	1	US-11-101-244-491128	Sequence 491128,	591	19	1.1	19	1	US-11-101-244-491129	Sequence 491129,	592	19	1.1	19	1	US-11-101-244-491130	Sequence 491130,	593	19	1.1	19	1	US-11-101-244-491131	Sequence 491131,	594	19	1.1	19	1	US-11-101-244-491132	Sequence 491132,	595	19	1.1	19	1	US-11-101-244-491133	Sequence 491133,	596	19	1.1	19	1	US-11-101-244-491134	Sequence 491134,	597	19	1.1	19	1	US-11-101-244-491135	Sequence 491135,	598	19	1.1	19	1	US-11-101-244-491136	Sequence 491136,	599	19	1.1	19	1	US-11-101-244-491137	Sequence 491137,	600	19	1.1	19	1	US-11-101-244-491138	Sequence 491138,	601	19	1.1	19	1	US-11-101-244-491139	Sequence 491139,	602	19	1.1	19	1	US-11-101-244-491140	Sequence 491140,	603	19	1.1	19	1	US-11-101-244-491141	Sequence 491141,	604	19	1.1	19	1	US-11-101-244-491142	Sequence 491142,	605	19	1.1	19	1	US-11-101-244-491143	Sequence 491143,	606	19	1.1	19	1	US-11-101-244-491144	Sequence 491144,	607	19	1.1	19	1	US-11-101-244-491145	Sequence 491145,	608	19	1.1	19	1	US-11-101-244-491146	Sequence 491146,	609	19	1.1	19	1	US-11-101-244-491147	Sequence 491147,	610	19	1.1	19	1	US-11-101-244-491148	Sequence 491148,	611	19	1.1	19	1	US-11-101-244-491149	Sequence 491149,	612	19	1.1	19	1	US-11-101-244-491150	Sequence 491150,	613	19	1.1	19	1	US-11-101-244-491151	Sequence 491151,	614	19	1.1	19	1	US-11-101-244-491152	Sequence 491152,	615	19	1.1	19	1	US-11-101-244-491153	Sequence 491153,	616	19	1.1	19	1	US-11-101-244-491154	Sequence 491154,	617	19	1.1	19	1	US-11-101-244-491155	Sequence 491155,
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C 837	16.4	0.9	18	1	US-10-951-303-2971	Sequence 2971, App	C 910	16	0.9	20	1	US-10-370-860A-10	Sequence 10, App1
C 838	16.4	0.9	18	1	US-10-310-914A-336642	Sequence 336642, App	C 911	16	0.9	20	1	US-10-370-860A-12	Sequence 12, App1
839	16.4	0.9	18	1	US-10-310-914A-999588	Sequence 999588, App	912	16	0.9	20	1	US-10-310-914A-157270	Sequence 157270, App
840	16.4	0.9	18	1	US-10-310-914A-1071407	Sequence 1071407, App	913	16	0.9	20	1	US-10-310-914A-454995	Sequence 454995, App
841	16.4	0.9	18	1	US-10-310-914A-1378476	Sequence 1378476, App	C 914	15.8	0.9	19	1	US-10-206-693-14	Sequence 14, App1
842	16.4	0.9	19	1	US-10-310-914A-687663	Sequence 687663, App	915	15.8	0.9	19	1	US-10-206-693-240	Sequence 240, App
843	16.4	0.9	19	1	US-10-310-914A-1378477	Sequence 1378477, App	916	15.8	0.9	19	1	US-10-310-914A-151357	Sequence 151357, App
C 844	16.4	0.9	19	1	US-10-310-914A-1384285	Sequence 1384285, App	C 917	15.8	0.9	19	1	US-10-310-914A-235218	Sequence 235218, App
C 845	16.4	0.9	19	1	US-11-083-784-49684	Sequence 49684, A	918	15.8	0.9	19	1	US-10-310-914A-360899	Sequence 360899, App
C 846	16.4	0.9	19	1	US-11-083-784-209546	Sequence 209546, App	919	15.8	0.9	19	1	US-10-310-914A-432064	Sequence 432064, App
C 847	16.4	0.9	19	1	US-11-083-784-405179	Sequence 405179, App	920	15.8	0.9	19	1	US-10-310-914A-542218	Sequence 542218, App
848	16.4	0.9	19	1	US-11-083-784-427206	Sequence 427206, App	C 921	15.8	0.9	19	1	US-10-310-914A-854052	Sequence 854052, App
849	16.4	0.9	19	1	US-11-083-784-491396	Sequence 491396, App	922	15.8	0.9	19	1	US-10-310-914A-885297	Sequence 885297, App
850	16.4	0.9	19	1	US-11-083-784-521114	Sequence 521114, App	C 923	15.8	0.9	19	1	US-10-310-914A-1016265	Sequence 1016265, App
851	16.4	0.9	19	1	US-11-083-784-531574	Sequence 531574, App	924	15.8	0.9	19	1	US-10-310-914A-1023203	Sequence 1023203, App
852	16.4	0.9	19	1	US-11-083-784-531575	Sequence 531575, App	925	15.8	0.9	19	1	US-10-310-914A-1026538	Sequence 1026538, App
853	16.4	0.9	19	1	US-11-083-784-531674	Sequence 531674, App	C 926	15.8	0.9	19	1	US-10-310-914A-1078351	Sequence 1078351, App
854	16.4	0.9	19	1	US-11-083-784-531675	Sequence 531675, App	C 927	15.8	0.9	19	1	US-10-310-914A-1105562	Sequence 1105562, App
855	16.4	0.9	19	1	US-11-083-784-531774	Sequence 531774, App	C 928	15.8	0.9	19	1	US-10-310-914A-1138736	Sequence 1138736, App
856	16.4	0.9	19	1	US-11-083-784-531775	Sequence 531775, App	929	15.8	0.9	19	1	US-10-310-914A-1153367	Sequence 1153367, App
857	16.4	0.9	19	1	US-11-083-784-531872	Sequence 531872, App	C 930	15.8	0.9	19	1	US-11-014-373-235	Sequence 235, App
858	16.4	0.9	19	1	US-11-083-784-531873	Sequence 531873, App	931	15.8	0.9	19	1	US-11-014-373-512	Sequence 512, App
859	16.4	0.9	19	1	US-11-083-784-531972	Sequence 531972, App	932	15.8	0.9	19	1	US-11-083-784-2836	Sequence 2836, App
860	16.4	0.9	19	1	US-11-083-784-531973	Sequence 531973, App	933	15.8	0.9	19	1	US-11-083-784-496532	Sequence 496532, A
861	16.4	0.9	19	1	US-11-083-784-532071	Sequence 532071, App	934	15.8	0.9	19	1	US-11-083-784-496527	Sequence 496527, A
862	16.4	0.9	19	1	US-11-083-784-532072	Sequence 532072, App	935	15.8	0.9	19	1	US-11-083-784-96612	Sequence 96612, A
C 863	16.4	0.9	19	1	US-11-083-784-578805	Sequence 578805, App	C 936	15.8	0.9	19	1	US-11-083-784-104234	Sequence 104234, App
864	16.4	0.9	19	1	US-11-083-784-723652	Sequence 723652, App	937	15.8	0.9	19	1	US-11-083-784-1169311	Sequence 1169311, App
865	16.4	0.9	19	1	US-11-083-784-723752	Sequence 723752, App	938	15.8	0.9	19	1	US-11-083-784-1169848	Sequence 1169848, App
866	16.4	0.9	19	1	US-11-083-784-911949	Sequence 911949, App	939	15.8	0.9	19	1	US-11-083-784-117020	Sequence 117020, App
C 867	16.4	0.9	19	1	US-11-083-784-928479	Sequence 928479, App	940	15.8	0.9	19	1	US-11-083-784-117049	Sequence 117049, App
868	16.4	0.9	19	1	US-11-083-784-1141172	Sequence 1141172, App	941	15.8	0.9	19	1	US-11-083-784-117107	Sequence 117107, App
C 869	16.4	0.9	19	1	US-11-083-784-1259943	Sequence 1259943, App	942	15.8	0.9	19	1	US-11-083-784-117181	Sequence 117181, App
C 870	16.4	0.9	19	1	US-11-083-784-1473036	Sequence 1473036, App	943	15.8	0.9	19	1	US-11-083-784-117219	Sequence 117219, App
871	16.4	0.9	19	1	US-11-083-784-1484938	Sequence 1484938, App	944	15.8	0.9	19	1	US-11-083-784-117250	Sequence 117250, App
872	16.4	0.9	19	1	US-11-101-244-49684	Sequence 49684, A	945	15.8	0.9	19	1	US-11-083-784-155785	Sequence 155785, App
C 873	16.4	0.9	19	1	US-11-101-244-209546	Sequence 209546, App	946	15.8	0.9	19	1	US-11-083-784-190805	Sequence 190805, App
C 874	16.4	0.9	19	1	US-11-101-244-405179	Sequence 405179, App	947	15.8	0.9	19	1	US-11-083-784-190884	Sequence 190884, App
875	16.4	0.9	19	1	US-11-101-244-427206	Sequence 427206, App	948	15.8	0.9	19	1	US-11-083-784-198455	Sequence 198455, App
876	16.4	0.9	19	1	US-11-101-244-491396	Sequence 491396, App	949	15.8	0.9	19	1	US-11-083-784-198486	Sequence 198486, App
877	16.4	0.9	19	1	US-11-101-244-521114	Sequence 521114, App	950	15.8	0.9	19	1	US-11-083-784-198511	Sequence 198511, App
878	16.4	0.9	19	1	US-11-101-244-531574	Sequence 531574, App	951	15.8	0.9	19	1	US-11-083-784-198533	Sequence 198533, App
879	16.4	0.9	19	1	US-11-101-244-531575	Sequence 531575, App	952	15.8	0.9	19	1	US-11-083-784-198551	Sequence 198551, App
880	16.4	0.9	19	1	US-11-101-244-531674	Sequence 531674, App	953	15.8	0.9	19	1	US-11-083-784-198589	Sequence 198589, App
881	16.4	0.9	19	1	US-11-101-244-531675	Sequence 531675, App	954	15.8	0.9	19	1	US-11-083-784-198623	Sequence 198623, App
882	16.4	0.9	19	1	US-11-101-244-531774	Sequence 531774, App	955	15.8	0.9	19	1	US-11-083-784-198673	Sequence 198673, App
883	16.4	0.9	19	1	US-11-101-244-531775	Sequence 531775, App	956	15.8	0.9	19	1	US-11-083-784-198715	Sequence 198715, App
884	16.4	0.9	19	1	US-11-101-244-531872	Sequence 531872, App	957	15.8	0.9	19	1	US-11-083-784-207465	Sequence 207465, App
885	16.4	0.9	19	1	US-11-101-244-531873	Sequence 531873, App	958	15.8	0.9	19	1	US-11-083-784-222312	Sequence 222312, App
886	16.4	0.9	19	1	US-11-101-244-531972	Sequence 531972, App	959	15.8	0.9	19	1	US-11-083-784-225150	Sequence 225150, App
887	16.4	0.9	19	1	US-11-101-244-531973	Sequence 531973, App	C 960	15.8	0.9	19	1	US-11-083-784-256569	Sequence 256569, App
888	16.4	0.9	19	1	US-11-101-244-532071	Sequence 532071, App	C 961	15.8	0.9	19	1	US-11-083-784-256617	Sequence 256617, App
C 889	16.4	0.9	19	1	US-11-101-244-532072	Sequence 532072, App	C 962	15.8	0.9	19	1	US-11-083-784-259212	Sequence 259212, App
C 890	16.4	0.9	19	1	US-11-101-244-578805	Sequence 578805, App	C 963	15.8	0.9	19	1	US-11-083-784-275438	Sequence 275438, App
891	16.4	0.9	19	1	US-11-101-244-723652	Sequence 723652, App	964	15.8	0.9	19	1	US-11-083-784-398635	Sequence 398635, App
892	16.4	0.9	19	1	US-11-101-244-723752	Sequence 723752, App	C 965	15.8	0.9	19	1	US-11-083-784-411303	Sequence 411303, App
893	16.4	0.9	19	1	US-11-101-244-911949	Sequence 911949, App	C 966	15.8	0.9	19	1	US-11-083-784-425415	Sequence 425415, App
C 894	16.4	0.9	19	1	US-11-101-244-928479	Sequence 928479, App	967	15.8	0.9	19	1	US-11-083-784-482138	Sequence 482138, App
C 895	16.4	0.9	19	1	US-11-101-244-1141172	Sequence 1141172, App	968	15.8	0.9	19	1	US-11-083-784-482438	Sequence 482438, App
C 896	16.4	0.9	19	1	US-11-101-244-1259943	Sequence 1259943, App	969	15.8	0.9	19	1	US-11-083-784-490736	Sequence 490736, App
C 897	16.4	0.9	19	1	US-11-101-244-1473036	Sequence 1473036, App	970	15.8	0.9	19	1	US-11-083-784-490744	Sequence 490744, App
C 898	16.4	0.9	19	1	US-11-101-244-1484938	Sequence 1484938, App	971	15.8	0.9	19	1	US-11-083-784-490754	Sequence 490754, App
C 899	16.4	0.9	20	1	US-09-967-669-87	Sequence 87, App1	972	15.8	0.9	19	1	US-11-083-784-491303	Sequence 491303, App
900	16.4	0.9	20	1	US-10-996-951-3	Sequence 3, App1	973	15.8	0.9	19	1	US-11-083-784-491346	Sequence 491346, App
901	16.4	0.9	20	1	US-10-310-914A-157159	Sequence 157159, App	974	15.8	0.9	19	1	US-11-083-784-491367	Sequence 491367, App
902	16.4	0.9	20	1	US-10-310-914A-428826	Sequence 428826, App	975	15.8	0.9	19	1	US-11-083-784-491377	Sequence 491377, App
903	16.4	0.9	20	1	US-10-310-914A-677516	Sequence 677516, App	976	15.8	0.9	19	1	US-11-083-784-504820	Sequence 504820, App
C 904	16.4	0.9	20	1	US-10-310-914A-1236794	Sequence 1236794, App	C 977	15.8	0.9	19	1	US-11-083-784-520347	Sequence 520347, App
C 905	16	0.9	17	1	US-09-780-164-770	Sequence 770, App	978	15.8	0.9	19	1	US-11-083-784-521051	Sequence 521051, App
C 906	16	0.9	19	1	US-11-083-784-523603	Sequence 523603, App	C 979	15.8	0.9	19	1	US-11-083-784-537233	Sequence 537233, App
C 907	16	0.9	19	1	US-11-083-784-1146200	Sequence 1146200, App	980	15.8	0.9	19	1	US-11-083-784-548577	Sequence 548577, App
C 908	16	0.9	19	1	US-11-101-244-523603	Sequence 523603, App	981	15.8	0.9	19	1	US-11-083-784-647566	Sequence 647566, App
C 909	16	0.9	19	1	US-11-101-244-1146200	Sequence 1146200, App	982	15.8	0.9	19	1	US-11-083-784-647654	Sequence 647654, App

c 983	15.8	0.9	19	1	US-11-083-784-651197	Sequence 651197,	c1056	15.8	0.9	19	1	US-11-101-244-520347	Sequence 520347,
c 984	15.8	0.9	19	1	US-11-083-784-692671	Sequence 692671,	1057	15.8	0.9	19	1	US-11-101-244-521051	Sequence 521051,
c 985	15.8	0.9	19	1	US-11-083-784-809922	Sequence 809922,	c1058	15.8	0.9	19	1	US-11-101-244-531233	Sequence 531233,
c 986	15.8	0.9	19	1	US-11-083-784-835805	Sequence 835805,	1059	15.8	0.9	19	1	US-11-101-244-548572	Sequence 548572,
c 987	15.8	0.9	19	1	US-11-083-784-895312	Sequence 895312,	1060	15.8	0.9	19	1	US-11-101-244-647566	Sequence 647566,
c 988	15.8	0.9	19	1	US-11-083-784-946407	Sequence 946407,	1061	15.8	0.9	19	1	US-11-101-244-647654	Sequence 647654,
c 989	15.8	0.9	19	1	US-11-083-784-951796	Sequence 951796,	c1062	15.8	0.9	19	1	US-11-101-244-651197	Sequence 651197,
c 990	15.8	0.9	19	1	US-11-083-784-973051	Sequence 973051,	c1063	15.8	0.9	19	1	US-11-101-244-659671	Sequence 659671,
c 991	15.8	0.9	19	1	US-11-083-784-978358	Sequence 978358,	c1064	15.8	0.9	19	1	US-11-101-244-809922	Sequence 809922,
c 992	15.8	0.9	19	1	US-11-083-784-1073668	Sequence 1073668,	c1065	15.8	0.9	19	1	US-11-101-244-835805	Sequence 835805,
c 993	15.8	0.9	19	1	US-11-083-784-1077487	Sequence 1077487,	c1066	15.8	0.9	19	1	US-11-101-244-895312	Sequence 895312,
c 994	15.8	0.9	19	1	US-11-083-784-1112807	Sequence 1112807,	c1067	15.8	0.9	19	1	US-11-101-244-946407	Sequence 946407,
c 995	15.8	0.9	19	1	US-11-083-784-1112871	Sequence 1112871,	c1068	15.8	0.9	19	1	US-11-101-244-951796	Sequence 951796,
c 996	15.8	0.9	19	1	US-11-083-784-1115683	Sequence 1115683,	c1070	15.8	0.9	19	1	US-11-101-244-978358	Sequence 978358,
c 997	15.8	0.9	19	1	US-11-083-784-1115733	Sequence 1115733,	c1071	15.8	0.9	19	1	US-11-101-244-1073668	Sequence 1073668,
c 998	15.8	0.9	19	1	US-11-083-784-1141062	Sequence 1141062,	c1072	15.8	0.9	19	1	US-11-101-244-1077487	Sequence 1077487,
c 999	15.8	0.9	19	1	US-11-083-784-1145497	Sequence 1145497,	c1073	15.8	0.9	19	1	US-11-101-244-1112807	Sequence 1112807,
c 1000	15.8	0.9	19	1	US-11-083-784-1159730	Sequence 1159730,	c1074	15.8	0.9	19	1	US-11-101-244-1115683	Sequence 1115683,
c1001	15.8	0.9	19	1	US-11-083-784-1257590	Sequence 1257590,	c1075	15.8	0.9	19	1	US-11-101-244-1115733	Sequence 1115733,
c1002	15.8	0.9	19	1	US-11-083-784-1323231	Sequence 1323231,	c1076	15.8	0.9	19	1	US-11-101-244-111062	Sequence 111062,
c1003	15.8	0.9	19	1	US-11-083-784-1350821	Sequence 1350821,	c1077	15.8	0.9	19	1	US-11-101-244-1145497	Sequence 1145497,
c1004	15.8	0.9	19	1	US-11-083-784-1351424	Sequence 1351424,	c1078	15.8	0.9	19	1	US-11-101-244-1159730	Sequence 1159730,
c1005	15.8	0.9	19	1	US-11-083-784-1370891	Sequence 1370891,	c1079	15.8	0.9	19	1	US-11-101-244-1257590	Sequence 1257590,
c1006	15.8	0.9	19	1	US-11-083-784-1388942	Sequence 1388942,	c1080	15.8	0.9	19	1	US-11-101-244-1350821	Sequence 1350821,
c1007	15.8	0.9	19	1	US-11-083-784-1513262	Sequence 1513262,	c1081	15.8	0.9	19	1	US-11-101-244-1351424	Sequence 1351424,
c1008	15.8	0.9	19	1	US-11-083-784-1513264	Sequence 1513264,	c1082	15.8	0.9	19	1	US-11-101-244-1370891	Sequence 1370891,
c1009	15.8	0.9	19	1	US-11-083-784-1564341	Sequence 1564341,	c1083	15.8	0.9	19	1	US-11-101-244-1388942	Sequence 1388942,
c1010	15.8	0.9	19	1	US-11-083-784-1564359	Sequence 1564359	c1084	15.8	0.9	19	1	US-11-101-244-1513262	Sequence 1513262,
c1011	15.8	0.9	19	1	US-11-101-244-2836	Sequence 2836, Ap	c1085	15.8	0.9	19	1	US-11-101-244-1513264	Sequence 1513264,
c1012	15.8	0.9	19	1	US-11-101-244-49632	Sequence 49632, A	c1086	15.8	0.9	19	1	US-11-101-244-1513266	Sequence 1513266,
c1013	15.8	0.9	19	1	US-11-101-244-49652	Sequence 49652, A	c1087	15.8	0.9	19	1	US-11-101-244-1564341	Sequence 1564341,
c1014	15.8	0.9	19	1	US-11-101-244-49612	Sequence 49612, A	c1088	15.8	0.9	19	1	US-11-101-244-1582659	Sequence 1582659,
c1015	15.8	0.9	19	1	US-11-101-244-104234	Sequence 104234,	c1089	15.8	0.9	19	1	US-11-069-611-235	Sequence 235, App
c1016	15.8	0.9	19	1	US-11-101-244-116911	Sequence 116911,	c1090	15.8	0.9	19	1	US-09-780-533A-1841	Sequence 1841, Ap
c1017	15.8	0.9	19	1	US-11-101-244-116984	Sequence 116984,	c1091	15.4	0.9	17	1	US-09-848-754A-3109	Sequence 3109, Ap
c1018	15.8	0.9	19	1	US-11-101-244-117020	Sequence 117020,	c1092	15.4	0.9	17	1	US-10-138-674A-2435	Sequence 2435, Ap
c1019	15.8	0.9	19	1	US-11-101-244-117049	Sequence 117049,	c1093	15.4	0.9	17	1	US-10-287-949A-2435	Sequence 2435, Ap
c1020	15.8	0.9	19	1	US-11-101-244-117107	Sequence 117107,	c1094	15.4	0.9	17	1	US-10-712-672-1375	Sequence 1375, Ap
c1021	15.8	0.9	19	1	US-11-101-244-117181	Sequence 117181,	c1095	15.4	0.9	17	1	US-10-951-303-2435	Sequence 2435, Ap
c1022	15.8	0.9	19	1	US-11-101-244-117219	Sequence 117219,	c1096	15.4	0.9	18	1	US-09-850-948-19	Sequence 19, App1
c1023	15.8	0.9	19	1	US-11-101-244-117250	Sequence 117250,	c1097	15.4	0.9	18	1	US-10-273-575-19	Sequence 19, App1
c1024	15.8	0.9	19	1	US-11-101-244-115785	Sequence 115785,	c1098	15.4	0.9	18	1	US-10-680-402-70	Sequence 70, App1
c1025	15.8	0.9	19	1	US-11-101-244-190805	Sequence 190805,	c1100	15.4	0.9	18	1	US-10-310-914A-677466	Sequence 677466,
c1026	15.8	0.9	19	1	US-11-101-244-190884	Sequence 190884,	c1101	15.4	0.9	18	1	US-10-310-914A-677474	Sequence 677474,
c1027	15.8	0.9	19	1	US-11-101-244-198455	Sequence 198455,	c1102	15.4	0.9	18	1	US-10-310-914A-800869	Sequence 800869,
c1028	15.8	0.9	19	1	US-11-101-244-198486	Sequence 198486,	c1103	15.4	0.9	18	1	US-10-310-914A-888641	Sequence 888641,
c1029	15.8	0.9	19	1	US-11-101-244-198511	Sequence 198511,	c1104	15.4	0.9	18	1	US-10-310-914A-892826	Sequence 892826,
c1030	15.8	0.9	19	1	US-11-101-244-198553	Sequence 198553,	c1105	15.4	0.9	18	1	US-10-310-914A-1042518	Sequence 1042518,
c1031	15.8	0.9	19	1	US-11-101-244-198551	Sequence 198551,	c1106	15.4	0.9	18	1	US-10-310-914A-1145229	Sequence 1145229,
c1032	15.8	0.9	19	1	US-11-101-244-198589	Sequence 198589,	c1107	15.4	0.9	18	1	US-10-310-914A-1360814	Sequence 1360814,
c1033	15.8	0.9	19	1	US-11-101-244-198623	Sequence 198623,	c1108	15.4	0.9	19	1	US-10-665-951-1515	Sequence 1515, Ap
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c1036	15.8	0.9	19	1	US-11-101-244-207465	Sequence 207465,	c1111	15.4	0.9	19	1	US-10-758-155-1762	Sequence 1762, Ap
c1037	15.8	0.9	19	1	US-11-101-244-223212	Sequence 223212,	c1112	15.4	0.9	19	1	US-10-831-620-1515	Sequence 1515, Ap
c1038	15.8	0.9	19	1	US-11-101-244-225150	Sequence 225150,	c1113	15.4	0.9	19	1	US-10-831-620-1515	Sequence 1515, Ap
c1039	15.8	0.9	19	1	US-11-101-244-225659	Sequence 225659,	c1114	15.4	0.9	19	1	US-10-923-330-2166	Sequence 216, App
c1040	15.8	0.9	19	1	US-11-101-244-256617	Sequence 256617,	c1115	15.4	0.9	19	1	US-10-923-330-2166	Sequence 216, App
c1041	15.8	0.9	19	1	US-11-101-244-259212	Sequence 259212,	c1116	15.4	0.9	19	1	US-10-844-076-1515	Sequence 1515, Ap
c1042	15.8	0.9	19	1	US-11-101-244-275438	Sequence 275438,	c1117	15.4	0.9	19	1	US-10-844-076-1515	Sequence 1515, Ap
c1043	15.8	0.9	19	1	US-11-101-244-398635	Sequence 398635,	c1118	15.4	0.9	19	1	US-10-844-076-1762	Sequence 1762, Ap
c1044	15.8	0.9	19	1	US-11-101-244-411203	Sequence 411203,	c1119	15.4	0.9	19	1	US-10-923-182-62	Sequence 62, App1
c1045	15.8	0.9	19	1	US-11-101-244-425415	Sequence 425415,	c1120	15.4	0.9	19	1	US-10-923-182-149	Sequence 149, App
c1046	15.8	0.9	19	1	US-11-101-244-482386	Sequence 482386,	c1121	15.4	0.9	19	1	US-10-962-888-1515	Sequence 1515, Ap
c1047	15.8	0.9	19	1	US-11-101-244-482386	Sequence 482386,	c1122	15.4	0.9	19	1	US-10-962-888-1762	Sequence 1762, Ap
c1048	15.8	0.9	19	1	US-11-101-244-482386	Sequence 482386,	c1123	15.4	0.9	19	1	US-10-944-611-1515	Sequence 1515, Ap
c1049	15.8	0.9	19	1	US-11-101-244-490744	Sequence 490744,	c1124	15.4	0.9	19	1	US-10-944-611-1762	Sequence 1762, Ap
c1050	15.8	0.9	19	1	US-11-101-244-490754	Sequence 490754,	c1125	15.4	0.9	19	1	US-10-206-693-35	Sequence 35, App1
c1051	15.8	0.9	19	1	US-11-101-244-491301	Sequence 491301,	c1126	15.4	0.9	19	1	US-10-206-693-35	Sequence 35, App1
c1052	15.8	0.9	19	1	US-11-101-244-491346	Sequence 491346,	c1127	15.4	0.9	19	1	US-10-310-914A-288078	Sequence 288078,
c1053	15.8	0.9	19	1	US-11-101-244-491367	Sequence 491367,	c1128	15.4	0.9	19	1	US-10-310-914A-394088	Sequence 394088,
c1054	15.8	0.9	19	1	US-11-101-244-491377	Sequence 491377,							
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1130	15.4	0.9	19	1	US-10-310-914A-477720	Sequence 477720,
1131	15.4	0.9	19	1	US-10-310-914A-523254	Sequence 523254,
1132	15.4	0.9	19	1	US-10-310-914A-522262	Sequence 522262,
c1133	15.4	0.9	19	1	US-10-310-914A-629950	Sequence 629950,
1134	15.4	0.9	19	1	US-10-310-914A-742052	Sequence 742052,
c1135	15.4	0.9	19	1	US-10-310-914A-860138	Sequence 860138,
1136	15.4	0.9	19	1	US-10-310-914A-181389	Sequence 181389,
c1137	15.4	0.9	19	1	US-10-310-914A-1280868	Sequence 1280868,
1138	15.4	0.9	19	1	US-10-310-914A-1309499	Sequence 1309499,
1139	15.4	0.9	19	1	US-10-310-914A-1319661	Sequence 1319661,
c1140	15.4	0.9	19	1	US-10-310-914A-1375299	Sequence 1375299,
1141	15.4	0.9	19	1	US-11-083-784-2195	Sequence 2195, Ap
c1142	15.4	0.9	19	1	US-11-083-784-19634	Sequence 19634, A
1143	15.4	0.9	19	1	US-11-083-784-51038	Sequence 51038, A
c1144	15.4	0.9	19	1	US-11-083-784-61485	Sequence 61485, A
c1145	15.4	0.9	19	1	US-11-083-784-66269	Sequence 66269, A
c1146	15.4	0.9	19	1	US-11-083-784-66270, A	Sequence 66270, A
c1147	15.4	0.9	19	1	US-11-083-784-132395	Sequence 132395,
c1148	15.4	0.9	19	1	US-11-083-784-143402	Sequence 143402,
c1149	15.4	0.9	19	1	US-11-083-784-202084	Sequence 202084,
1150	15.4	0.9	19	1	US-11-083-784-202116	Sequence 202116,
1151	15.4	0.9	19	1	US-11-083-784-202174	Sequence 202174,
1152	15.4	0.9	19	1	US-11-083-784-202197	Sequence 202197,
c1154	15.4	0.9	19	1	US-11-083-784-232135	Sequence 232135,
c1155	15.4	0.9	19	1	US-11-083-784-232235	Sequence 232235,
c1156	15.4	0.9	19	1	US-11-083-784-237477	Sequence 237477,
1157	15.4	0.9	19	1	US-11-083-784-262644	Sequence 262644,
1158	15.4	0.9	19	1	US-11-083-784-304519	Sequence 304519,
1159	15.4	0.9	19	1	US-11-083-784-360639	Sequence 360639,
c1160	15.4	0.9	19	1	US-11-083-784-368528	Sequence 368528,
c1162	15.4	0.9	19	1	US-11-083-784-371445	Sequence 371445,
1163	15.4	0.9	19	1	US-11-083-784-421451	Sequence 421451,
c1164	15.4	0.9	19	1	US-11-083-784-460346	Sequence 460346,
c1165	15.4	0.9	19	1	US-11-083-784-460400	Sequence 460400,
1166	15.4	0.9	19	1	US-11-083-784-501423	Sequence 501423,
c1167	15.4	0.9	19	1	US-11-083-784-578794	Sequence 578794,
c1168	15.4	0.9	19	1	US-11-083-784-671090	Sequence 671090,
1169	15.4	0.9	19	1	US-11-083-784-674587	Sequence 674587,
c1170	15.4	0.9	19	1	US-11-083-784-688433	Sequence 688433,
1171	15.4	0.9	19	1	US-11-083-784-704511	Sequence 704511,
c1172	15.4	0.9	19	1	US-11-083-784-704520	Sequence 704520,
c1173	15.4	0.9	19	1	US-11-083-784-751946	Sequence 751946,
c1174	15.4	0.9	19	1	US-11-083-784-820807	Sequence 820807,
c1175	15.4	0.9	19	1	US-11-083-784-896406	Sequence 896406,
1176	15.4	0.9	19	1	US-11-083-784-917716	Sequence 917716,
c1177	15.4	0.9	19	1	US-11-083-784-917915	Sequence 917915,
c1178	15.4	0.9	19	1	US-11-083-784-926899	Sequence 926899,
c1179	15.4	0.9	19	1	US-11-083-784-976398	Sequence 976398,
c1180	15.4	0.9	19	1	US-11-083-784-1028300	Sequence 1028300,
c1181	15.4	0.9	19	1	US-11-083-784-1077507	Sequence 1077507,
1182	15.4	0.9	19	1	US-11-083-784-1098844	Sequence 1098844,
c1183	15.4	0.9	19	1	US-11-083-784-1245691	Sequence 1245691,
c1184	15.4	0.9	19	1	US-11-083-784-1277052	Sequence 1277052,
c1185	15.4	0.9	19	1	US-11-083-784-1277082	Sequence 1277082,
1186	15.4	0.9	19	1	US-11-083-784-1299074	Sequence 1299074,
1187	15.4	0.9	19	1	US-11-083-784-1302380	Sequence 1302380,
c1188	15.4	0.9	19	1	US-11-083-784-1335689	Sequence 1335689,
1189	15.4	0.9	19	1	US-11-083-784-1362687	Sequence 1362687,
c1190	15.4	0.9	19	1	US-11-083-784-1374698	Sequence 1374698,
c1191	15.4	0.9	19	1	US-11-083-784-1410088	Sequence 1410088,
1192	15.4	0.9	19	1	US-11-083-784-1450085	Sequence 1450085,
c1193	15.4	0.9	19	1	US-11-083-784-1464506	Sequence 1464506,
c1194	15.4	0.9	19	1	US-11-083-784-1474304	Sequence 1474304,
c1195	15.4	0.9	19	1	US-11-083-784-1485805	Sequence 1485805,
1196	15.4	0.9	19	1	US-11-083-784-1498825	Sequence 1498825,
c1197	15.4	0.9	19	1	US-11-083-784-1498858	Sequence 1498858,
c1198	15.4	0.9	19	1	US-11-083-784-1515826	Sequence 1515826,
c1199	15.4	0.9	19	1	US-11-083-784-1515845	Sequence 1515845,
1200	15.4	0.9	19	1	US-11-101-244-2195	Sequence 2195, Ap
c1201	15.4	0.9	19	1	US-11-101-244-19634	Sequence 19634, A
c1202	15.4	0.9	19	1	US-11-101-244-51038	Sequence 51038, A
c1203	15.4	0.9	19	1	US-11-101-244-61485	Sequence 61485, A
c1204	15.4	0.9	19	1	US-11-101-244-66269	Sequence 66269, A
c1205	15.4	0.9	19	1	US-11-101-244-66270	Sequence 66270, A
c1206	15.4	0.9	19	1	US-11-101-244-119668	Sequence 119668,
c1207	15.4	0.9	19	1	US-11-101-244-132395	Sequence 132395,
c1208	15.4	0.9	19	1	US-11-101-244-140302	Sequence 140302,
1209	15.4	0.9	19	1	US-11-101-244-202084	Sequence 202084,
1210	15.4	0.9	19	1	US-11-101-244-202116	Sequence 202116,
1211	15.4	0.9	19	1	US-11-101-244-202174	Sequence 202174,
1212	15.4	0.9	19	1	US-11-101-244-202197	Sequence 202197,
c1213	15.4	0.9	19	1	US-11-101-244-232135	Sequence 232135,
c1214	15.4	0.9	19	1	US-11-101-244-232335	Sequence 232335,
c1215	15.4	0.9	19	1	US-11-101-244-371445	Sequence 371445,
1216	15.4	0.9	19	1	US-11-101-244-426244	Sequence 426244,
1217	15.4	0.9	19	1	US-11-101-244-426245	Sequence 426245,
1218	15.4	0.9	19	1	US-11-101-244-304519	Sequence 304519,
1219	15.4	0.9	19	1	US-11-101-244-368528	Sequence 368528,
c1220	15.4	0.9	19	1	US-11-101-244-371445	Sequence 371445,
c1221	15.4	0.9	19	1	US-11-101-244-421451	Sequence 421451,
1222	15.4	0.9	19	1	US-11-101-244-425085	Sequence 425085,
c1223	15.4	0.9	19	1	US-11-101-244-460346	Sequence 460346,
c1224	15.4	0.9	19	1	US-11-101-244-460400	Sequence 460400,
c1225	15.4	0.9	19	1	US-11-101-244-501423	Sequence 501423,
c1226	15.4	0.9	19	1	US-11-101-244-578794	Sequence 578794,
c1227	15.4	0.9	19	1	US-11-101-244-671090	Sequence 671090,
1228	15.4	0.9	19	1	US-11-101-244-674587	Sequence 674587,
c1229	15.4	0.9	19	1	US-11-101-244-688433	Sequence 688433,
1230	15.4	0.9	19	1	US-11-101-244-704511	Sequence 704511,
1231	15.4	0.9	19	1	US-11-101-244-704520	Sequence 704520,
c1232	15.4	0.9	19	1	US-11-101-244-751946	Sequence 751946,
c1233	15.4	0.9	19	1	US-11-101-244-820807	Sequence 820807,
c1234	15.4	0.9	19	1	US-11-101-244-896406	Sequence 896406,
1235	15.4	0.9	19	1	US-11-101-244-911965	Sequence 911965,
c1236	15.4	0.9	19	1	US-11-101-244-917716	Sequence 917716,
c1237	15.4	0.9	19	1	US-11-101-244-926899	Sequence 926899,
c1238	15.4	0.9	19	1	US-11-101-244-976398	Sequence 976398,
c1239	15.4	0.9	19	1	US-11-101-244-1028300	Sequence 1028300,
c1240	15.4	0.9	19	1	US-11-101-244-1077507	Sequence 1077507,
1241	15.4	0.9	19	1	US-11-101-244-1098844	Sequence 1098844,
c1242	15.4	0.9	19	1	US-11-101-244-1245691	Sequence 1245691,
c1243	15.4	0.9	19	1	US-11-101-244-1277052	Sequence 1277052,
1244	15.4	0.9	19	1	US-11-101-244-1277082	Sequence 1277082,
c1245	15.4	0.9	19	1	US-11-101-244-1299074	Sequence 1299074,
1246	15.4	0.9	19	1	US-11-101-244-1302380	Sequence 1302380,
c1247	15.4	0.9	19	1	US-11-101-244-1362687	Sequence 1362687,
1248	15.4	0.9	19	1	US-11-101-244-1374698	Sequence 1374698,
c1249	15.4	0.9	19	1	US-11-101-244-1410088	Sequence 1410088,
c1250	15.4	0.9	19	1	US-11-101-244-1450085	Sequence 1450085,
c1252	15.4	0.9	19	1	US-11-101-244-1464506	Sequence 1464506,
c1253	15.4	0.9	19	1	US-11-101-244-1474304	Sequence 1474304,
c1254	15.4	0.9	19	1	US-11-101-244-1485805	Sequence 1485805,
1255	15.4	0.9	19	1	US-11-101-244-1498825	Sequence 1498825,
c1256	15.4	0.9	19	1	US-11-101-244-1498858	Sequence 1498858,
c1257	15.4	0.9	19	1	US-11-101-244-1515826	Sequence 1515826,
c1258	15.4	0.9	19	1	US-11-101-244-1515845	Sequence 1515845,
1259	15.4	0.9	19	1	US-11-058-582-229	Sequence 229, App
c1260	15.4	0.9	19	1	US-09-866-108-6966	Sequence 6966, Ap
1261	15	0.8	17	1	US-09-866-108-6967	Sequence 6967, Ap
c1262	15.4	0.9	19	1	US-11-058-582-492	Sequence 492, App
1263	15	0.8	17	1	US-09-866-108-6967	Sequence 6967, Ap
1264	15	0.8	17	1	US-09-866-108-6968	Sequence 6968, Ap
1265	15	0.8	17	1	US-10-723-361-6966	Sequence 6966, App
1266	15	0.8	17	1	US-10-723-361-6967	Sequence 6967, Ap
1267	15	0.8	17	1	US-10-723-361-6968	Sequence 6968, Ap
1268	15	0.8	18	1	US-10-241-313-5	Sequence 5, Appl1
c1269	15	0.8	18	1	US-10-854-018-13	Sequence 13, Appl1
1270	15	0.8	18	1	US-10-510-914A-449129	Sequence 449129,
c1271	15	0.8	18	1	US-10-510-914A-460346	Sequence 460346,
c1272	15	0.8	18	1	US-10-510-914A-47846	Sequence 47846,
c1273	15	0.8	18	1	US-10-510-914A-1113869	Sequence 1113869,
c1274	15	0.8	18	1	US-10-510-914A-1357464	Sequence 1357464,

c1275	15	0.8	18	1	US-11-044-498-3	Sequence 3, Appl1	1348	14.4	0.8	18	1	US-10-349-143-10970	Sequence 10970, A
c1276	14.8	0.8	18	1	US-09-067-638B-50	Sequence 50, Appl	c1349	14.4	0.8	18	1	US-10-138-674-3013	Sequence 3013, Ap
c1277	14.8	0.8	18	1	US-10-116-325-50	Sequence 50, Appl	c1350	14.4	0.8	18	1	US-10-1287-949A-3013	Sequence 3013, Ap
c1278	14.8	0.8	18	1	US-10-388-263-50	Sequence 50, Appl	c1351	14.4	0.8	18	1	US-10-702-817-9	Sequence 9, Appl1
c1279	14.8	0.8	18	1	US-10-016-248-66	Sequence 66, Appl	c1352	14.4	0.8	18	1	US-10-509-009-22	Sequence 22, Appl
c1280	14.8	0.8	18	1	US-10-698-689-50	Sequence 50, Appl	c1353	14.4	0.8	18	1	US-10-951-303-3013	Sequence 3013, Ap
c1281	14.8	0.8	18	1	US-10-698-689-214	Sequence 214, App	c1354	14.4	0.8	18	1	US-10-750-185-14622	Sequence 14622, A
c1282	14.8	0.8	18	1	US-10-830-475-50	Sequence 50, Appl	c1355	14.4	0.8	18	1	US-10-623-14622	Sequence 14622, A
c1283	14.8	0.8	18	1	US-10-649-467-50	Sequence 89, Appl	c1356	14.4	0.8	18	1	US-10-110-914A-183276	Sequence 183276, A
c1284	14.8	0.8	18	1	US-10-934-798-89	Sequence 208, App	c1357	14.4	0.8	18	1	US-10-310-914A-189415	Sequence 189415, A
c1285	14.8	0.8	18	1	US-10-934-798-208	Sequence 77047, A	c1358	14.4	0.8	18	1	US-10-10-914A-249340	Sequence 249340, A
c1286	14.8	0.8	18	1	US-10-310-914A-77047	Sequence 83639, A	c1359	14.4	0.8	18	1	US-10-310-914A-417734	Sequence 417734, A
c1287	14.8	0.8	18	1	US-10-310-914A-83639	Sequence 101443, A	c1360	14.4	0.8	18	1	US-10-310-914A-436231	Sequence 436231, A
c1288	14.8	0.8	18	1	US-10-310-914A-101443	Sequence 213729, A	c1361	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 441528, A
c1289	14.8	0.8	18	1	US-10-310-914A-213729	Sequence 309009, A	c1362	14.4	0.8	18	1	US-10-310-914A-448431	Sequence 448431, A
c1290	14.8	0.8	18	1	US-10-310-914A-309009	Sequence 336351, A	c1363	14.4	0.8	18	1	US-10-310-914A-452242	Sequence 452242, A
c1291	14.8	0.8	18	1	US-10-310-914A-336351	Sequence 427752, A	c1364	14.4	0.8	18	1	US-10-310-914A-462065	Sequence 462065, A
c1292	14.8	0.8	18	1	US-10-310-914A-427752	Sequence 465296, A	c1365	14.4	0.8	18	1	US-10-310-914A-463056	Sequence 463056, A
c1293	14.8	0.8	18	1	US-10-310-914A-465296	Sequence 472856, A	c1366	14.4	0.8	18	1	US-10-310-914A-463056	Sequence 463056, A
c1294	14.8	0.8	18	1	US-10-310-914A-472856	Sequence 519019, A	c1367	14.4	0.8	18	1	US-10-310-914A-463056	Sequence 463056, A
c1295	14.8	0.8	18	1	US-10-310-914A-519019	Sequence 519948, A	c1368	14.4	0.8	18	1	US-10-310-914A-463056	Sequence 463056, A
c1296	14.8	0.8	18	1	US-10-310-914A-519948	Sequence 519969, A	c1369	14.4	0.8	18	1	US-10-310-914A-463056	Sequence 463056, A
c1297	14.8	0.8	18	1	US-10-310-914A-519969	Sequence 585840, A	c1370	14.4	0.8	18	1	US-10-310-914A-463056	Sequence 463056, A
c1298	14.8	0.8	18	1	US-10-310-914A-585840	Sequence 601989, A	c1371	14.4	0.8	18	1	US-10-310-914A-463056	Sequence 463056, A
c1299	14.8	0.8	18	1	US-10-310-914A-601989	Sequence 645930, A	c1372	14.4	0.8	18	1	US-10-310-914A-463056	Sequence 463056, A
c1300	14.8	0.8	18	1	US-10-310-914A-645930	Sequence 666092, A	c1373	14.4	0.8	18	1	US-10-310-914A-463056	Sequence 463056, A
c1301	14.8	0.8	18	1	US-10-310-914A-696092	Sequence 707873, A	c1374	14.4	0.8	18	1	US-10-310-914A-463056	Sequence 463056, A
c1302	14.8	0.8	18	1	US-10-310-914A-707873	Sequence 768979, A	c1375	14.4	0.8	18	1	US-10-310-914A-463056	Sequence 463056, A
c1303	14.8	0.8	18	1	US-10-310-914A-768979	Sequence 795204, A	c1376	14.4	0.8	18	1	US-10-310-914A-463056	Sequence 463056, A
c1304	14.8	0.8	18	1	US-10-310-914A-795204	Sequence 809520, A	c1377	14.4	0.8	18	1	US-10-310-914A-463056	Sequence 463056, A
c1305	14.8	0.8	18	1	US-10-310-914A-809520	Sequence 847106, A	c1378	14.4	0.8	18	1	US-10-310-914A-463056	Sequence 463056, A
c1306	14.8	0.8	18	1	US-10-310-914A-847106	Sequence 874025, A	c1379	14.4	0.8	18	1	US-10-310-914A-463056	Sequence 463056, A
c1307	14.8	0.8	18	1	US-10-310-914A-874025	Sequence 885132, A	c1380	14.4	0.8	18	1	US-10-310-914A-463056	Sequence 463056, A
c1308	14.8	0.8	18	1	US-10-310-914A-885132	Sequence 923895, A	c1381	14.4	0.8	18	1	US-10-310-914A-463056	Sequence 463056, A
c1309	14.8	0.8	18	1	US-10-310-914A-923895	Sequence 937032, A	c1382	14.4	0.8	18	1	US-10-310-914A-463056	Sequence 463056, A
c1310	14.8	0.8	18	1	US-10-310-914A-937032	Sequence 965107, A	c1383	14.4	0.8	18	1	US-10-310-914A-463056	Sequence 463056, A
c1311	14.8	0.8	18	1	US-10-310-914A-946378	Sequence 965107, A	c1384	14.4	0.8	18	1	US-10-310-914A-463056	Sequence 463056, A
c1312	14.8	0.8	18	1	US-10-310-914A-965107	Sequence 965107, A	c1385	14.4	0.8	18	1	US-10-310-914A-463056	Sequence 463056, A
c1313	14.8	0.8	18	1	US-10-310-914A-971333	Sequence 961336, A	c1386	14.4	0.8	18	1	US-10-310-914A-463056	Sequence 463056, A
c1314	14.8	0.8	18	1	US-10-310-914A-981336	Sequence 984119, A	c1387	14.4	0.8	18	1	US-10-310-914A-463056	Sequence 463056, A
c1315	14.8	0.8	18	1	US-10-310-914A-984119	Sequence 999023, A	c1388	14.4	0.8	18	1	US-10-310-914A-463056	Sequence 463056, A
c1316	14.8	0.8	18	1	US-10-310-914A-990023	Sequence 999023, A	c1389	14.4	0.8	18	1	US-10-310-914A-463056	Sequence 463056, A
c1317	14.8	0.8	18	1	US-10-310-914A-999624	Sequence 1004988, A	c1390	14.4	0.8	18	1	US-10-310-914A-463056	Sequence 463056, A
c1318	14.8	0.8	18	1	US-10-310-914A-1004988	Sequence 1093982, A	c1391	14.4	0.8	18	1	US-10-310-914A-463056	Sequence 463056, A
c1319	14.8	0.8	18	1	US-10-310-914A-1093982	Sequence 1169386, A	c1392	14.4	0.8	18	1	US-10-310-914A-463056	Sequence 463056, A
c1320	14.8	0.8	18	1	US-10-310-914A-1169386	Sequence 1219917, A	c1393	14.4	0.8	18	1	US-10-310-914A-463056	Sequence 463056, A
c1321	14.8	0.8	18	1	US-10-310-914A-1219917	Sequence 1234776, A	c1394	14.4	0.8	18	1	US-10-310-914A-463056	Sequence 463056, A
c1322	14.8	0.8	18	1	US-10-310-914A-1234776	Sequence 1249080, A	c1395	14.4	0.8	18	1	US-10-310-914A-463056	Sequence 463056, A
c1323	14.8	0.8	18	1	US-10-310-914A-1249080	Sequence 1255023, A	c1396	14.4	0.8	18	1	US-10-310-914A-463056	Sequence 463056, A
c1324	14.8	0.8	18	1	US-10-310-914A-1255023	Sequence 129744, A	c1397	14.4	0.8	18	1	US-10-310-914A-463056	Sequence 463056, A
c1325	14.8	0.8	18	1	US-10-310-914A-1329744	Sequence 1337516, A	c1398	14.4	0.8	18	1	US-10-310-914A-463056	Sequence 463056, A
c1326	14.8	0.8	18	1	US-10-310-914A-1337516	Sequence 1366802, A	c1399	14.4	0.8	18	1	US-10-310-914A-463056	Sequence 463056, A
c1327	14.8	0.8	18	1	US-10-310-914A-1366802	Sequence 1368827, A	c1400	14.4	0.8	18	1	US-10-310-914A-463056	Sequence 463056, A
c1328	14.8	0.8	18	1	US-10-310-914A-1368827	Sequence 3801, App	c1401	14.4	0.8	18	1	US-10-310-914A-463056	Sequence 463056, A
c1329	14.8	0.8	18	1	US-11-069-908-3801	Sequence 50, Appl	c1402	14.4	0.8	18	1	US-10-712-672-343	Sequence 343, App
c1330	14.8	0.8	18	1	US-11-226-882A-501	Sequence 467163, A	c1403	14.4	0.8	18	1	US-10-723-361-6965	Sequence 6965, App
c1331	14.6	0.8	22	1	US-10-310-914A-467163	Sequence 14, Appl	c1404	14.4	0.8	18	1	US-10-723-361-6965	Sequence 6965, App
c1332	14.6	0.8	22	1	US-10-310-914A-467164	Sequence 14, Appl	c1405	14.4	0.8	18	1	US-10-723-361-6965	Sequence 6965, App
c1333	14.6	0.8	22	1	US-09-930-503-14	Sequence 14, Appl	c1406	14.4	0.8	18	1	US-10-723-361-6965	Sequence 6965, App
c1334	14.4	0.8	16	1	US-10-712-672-1732	Sequence 1566, App	c1407	14.4	0.8	18	1	US-10-723-361-6965	Sequence 6965, App
c1335	14.4	0.8	17	1	US-09-864-785-1566	Sequence 1302, App	c1408	14.4	0.8	18	1	US-10-723-361-6965	Sequence 6965, App
c1336	14.4	0.8	17	1	US-09-930-503-13	Sequence 1302, App	c1409	14.4	0.8	18	1	US-10-723-361-6965	Sequence 6965, App
c1337	14.4	0.8	17	1	US-09-780-533A-920	Sequence 3108, App	c1410	14.4	0.8	18	1	US-10-723-361-6965	Sequence 6965, App
c1338	14.4	0.8	17	1	US-09-848-754A-3108	Sequence 1361, App	c1411	14.4	0.8	18	1	US-10-723-361-6965	Sequence 6965, App
c1339	14.4	0.8	17	1	US-09-930-423-1361	Sequence 769, App	c1412	14.4	0.8	18	1	US-10-723-361-6965	Sequence 6965, App
c1340	14.4	0.8	17	1	US-09-780-164-769	Sequence 1361, App	c1413	14.4	0.8	18	1	US-10-723-361-6965	Sequence 6965, App
c1341	14.4	0.8	17	1	US-09-745-237A-1361	Sequence 1302, App	c1414	14.4	0.8	18	1	US-10-723-361-6965	Sequence 6965, App
c1342	14.4	0.8	17	1	US-10-238-700-1302	Sequence 342, App	c1415	14.4	0.8	18	1	US-10-723-361-6965	Sequence 6965, App
c1343	14.4	0.8	17	1	US-10-712-672-342	Sequence 1302, App	c1416	14.4	0.8	18	1	US-10-723-361-6965	Sequence 6965, App
c1344	14.4	0.8	17	1	US-10-724-270-1302	Sequence 12, Appl	c1417	14.4	0.8	18	1	US-10-723-361-6965	Sequence 6965, App
c1345	14.4	0.8	18	1	US-09-930-503-12	Sequence 11, Appl	c1418	14.4	0.8	18	1	US-10-723-361-6965	Sequence 6965, App
c1346	14.4	0.8	18	1	US-09-774-381-11	Sequence 42, Appl	c1419	14.4	0.8	18	1	US-10-723-361-6965	Sequence 6965, App
c1347	14.4	0.8	18	1	US-10-133-779-42	Sequence 42, Appl	c1420	14.4	0.8	18	1	US-10-723-361-6965	Sequence 6965, App

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c1421 13.8 0.8 17 1 US-09-848-754A-891 Sequence 891, App
c1422 13.8 0.8 17 1 US-09-848-754A-990 Sequence 990, App
c1423 13.8 0.8 17 1 US-09-848-754A-1483 Sequence 1483, App
c1424 13.8 0.8 17 1 US-09-848-754A-1525 Sequence 1525, App
c1425 13.8 0.8 17 1 US-09-776-474-250 Sequence 250, App
c1426 13.8 0.8 17 1 US-09-930-423-839 Sequence 839, App
c1427 13.8 0.8 17 1 US-09-827-395A-381 Sequence 381, App
c1428 13.8 0.8 17 1 US-09-740-332-964 Sequence 964, App
c1429 13.8 0.8 17 1 US-09-745-237A-839 Sequence 839, App
c1430 13.8 0.8 17 1 US-09-817-879A-964 Sequence 964, App
c1431 13.8 0.8 17 1 US-10-060-756A-4268 Sequence 4268, App
c1432 13.8 0.8 17 1 US-10-156-201-6951 Sequence 6951, App
c1433 13.8 0.8 17 1 US-10-061-201-1453 Sequence 1453, App
c1434 13.8 0.8 17 1 US-10-430-882-381 Sequence 381, App
c1435 13.8 0.8 17 1 US-10-297-068-1039 Sequence 1039, App
c1436 13.8 0.8 17 1 US-10-342-902-2345 Sequence 2345, App
c1437 13.8 0.8 17 1 US-10-342-902-2346 Sequence 2346, App
c1438 13.8 0.8 17 1 US-10-138-674-1714 Sequence 1714, App
c1439 13.8 0.8 17 1 US-10-138-674-1886 Sequence 1886, App
c1440 13.8 0.8 17 1 US-10-138-674-6345 Sequence 6345, App
c1441 13.8 0.8 17 1 US-10-287-949A-1714 Sequence 1714, App
c1442 13.8 0.8 17 1 US-10-287-949A-1886 Sequence 1886, App
c1443 13.8 0.8 17 1 US-10-287-949A-6345 Sequence 6345, App
c1444 13.8 0.8 17 1 US-10-712-672-345 Sequence 345, App
c1445 13.8 0.8 17 1 US-10-712-672-506 Sequence 506, App
c1446 13.8 0.8 17 1 US-10-712-672-763 Sequence 763, App
c1447 13.8 0.8 17 1 US-10-712-672-764 Sequence 764, App
c1448 13.8 0.8 17 1 US-10-712-672-765 Sequence 765, App
c1449 13.8 0.8 17 1 US-10-712-672-766 Sequence 766, App
c1450 13.8 0.8 17 1 US-10-669-841-2148 Sequence 2148, App
c1451 13.8 0.8 17 1 US-10-669-841-3557 Sequence 3557, App
c1452 13.8 0.8 17 1 US-10-669-841-3557 Sequence 3557, App
c1453 13.8 0.8 17 1 US-10-723-361-2756 Sequence 2756, App
c1454 13.8 0.8 17 1 US-10-723-361-2756 Sequence 2756, App
c1455 13.8 0.8 17 1 US-10-498-462-376 Sequence 376, App
c1456 13.8 0.8 17 1 US-10-498-462-1855 Sequence 1855, App
c1457 13.8 0.8 17 1 US-10-498-462-2044 Sequence 2044, App
c1458 13.8 0.8 17 1 US-10-890-776A-4268 Sequence 4268, App
c1459 13.8 0.8 17 1 US-10-951-303-1114 Sequence 1114, App
c1460 13.8 0.8 17 1 US-10-951-303-1886 Sequence 1886, App
c1461 13.8 0.8 17 1 US-10-492-570-396 Sequence 396, App
c1462 13.8 0.8 17 1 US-10-492-570-397 Sequence 397, App
c1463 13.8 0.8 17 1 US-10-492-570-1002 Sequence 1002, App
c1464 13.8 0.8 17 1 US-11-189-546-9 Sequence 9, App11
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ALIGNMENTS

```

RESULT 1
US-10-310-914A-386265/c
; Sequence 386265, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Biointformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 386265
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-386265
Query Match 1.6%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 152 AGACTCTGCTGCAGAGGGGGTTGTGT 179
DB 28 AGACTCTGCTGCAGAGGGGGTTGTGT 1
RESULT 2
US-10-310-914A-386266/c
; Sequence 386266, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Biointformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 386266
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-386266
Query Match 1.6%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 152 AGACTCTGCTGCAGAGGGGGTTGTGT 179
DB 28 AGACTCTGCTGCAGAGGGGGTTGTGT 1
RESULT 3
US-10-005-956-1216
; Sequence 1216, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1216
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-005-956-1216
Query Match 1.5%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1590 TCAAAAATTCATTTTTCCTTCT 1616
DB 1 TCAAAAATTCATTTTTCCTTCT 27
RESULT 4
US-10-310-914A-386278/c
; Sequence 386278, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
```

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; APPLICANT: Shuler, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 386278
; LENGTH: 26
; TYPE: RNA
; ORGANISM: Human
; US-10-310-914A-386278

Query Match          1.5%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1538 GGGACTTGCAAAAAGGTCAGTATGG 1563
Db 26 GGGACTTGCAAAAAGGTCAGTATGG 1

RESULT 5
US-10-005-956-1305/C
; Sequence 1305, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1305
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: wherein "n" equals a C3 phosphoramidite linker.
US-10-005-956-1305

Query Match 1.5%; Score 26; DB 1; Length 27;
Best Local Similarity 96.3%; Pred. No. 1.9e+02;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1539 GGACTTGCAAAAAGGTCAGTATGGGT 1565
Db 27 GGACTTGCAAAAAGGTCAGTATGGGT 1

RESULT 6
US-09-747-429-12/C
; Sequence 12, Application US/09747429
; Patent No. US20020146810A1
; GENERAL INFORMATION:
; APPLICANT: Rameshwar, Pranela
; APPLICANT: Gascon, Pedro
; TITLE OF INVENTION: A Human Preprothachykinin Gene Promoter
; FILE REFERENCE: UMDNJ NIMS 97-16
; CURRENT APPLICATION NUMBER: US/09/747,429
; CURRENT FILING DATE: 2000-12-23
; PRIOR APPLICATION NUMBER: US 60/171,970
; PRIOR FILING DATE: 1999-12-23

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; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic sequence
; US-09-747-429-12

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1041 CTACCTGAGAGAGTTTATCCAGCAG 1065
Db 25 CTACCTGAGAGAGTTTATCCAGCAG 1

RESULT 7
US-09-747-429-13
; Sequence 13, Application US/09747429
; Patent No. US20020146810A1
; GENERAL INFORMATION:
; APPLICANT: Rameshwar, Pranela
; APPLICANT: Gascon, Pedro
; TITLE OF INVENTION: A Human Preprothachykinin Gene Promoter
; FILE REFERENCE: UMDNJ NIMS 97-16
; CURRENT APPLICATION NUMBER: US/09/747,429
; CURRENT FILING DATE: 2000-12-23
; PRIOR APPLICATION NUMBER: US 60/171,970
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic sequence
US-09-747-429-13

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 400 AGGACAGTGAGGAGCTATTTCTGG 424
Db 1 AGGACAGTGAGGAGCTATTTCTGG 25

RESULT 8
US-10-005-956-1125/C
; Sequence 1125, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1125
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-005-956-1125

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 707 GCTACTACTCAACACAGACCAT 731
Db 25 GCTACTACTCAACACAGACCAT 1

RESULT 9

US-10-005-956-1300/c
; Sequence 1300, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1300
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-005-956-1300

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 544 CCCATCGCCGCTGCTTCGCCAGTA 568
Db 25 CCCATCGCCGCTGCTTCGCCAGTA 1

RESULT 10
US-10-628-066-12/c
; Sequence 12, Application US/10628066
; Publication No. US20040086919A1
; GENERAL INFORMATION:
; APPLICANT: Rameshwar, Prianela
; APPLICANT: Gascon, Pedro
; TITLE OF INVENTION: A Human Preprotachykinin Gene Promoter
; FILE REFERENCE: UMDNJ NJS 97-16
; CURRENT APPLICATION NUMBER: US/10/628,066
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/747,429
; PRIOR FILING DATE: 2000-12-23
; PRIOR APPLICATION NUMBER: US 60/171,970
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic sequence
US-10-628-066-12

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1041 CTACCTGAAGAGTTTATCCAGCAG 1065
Db 25 CTACCTGAAGAGTTTATCCAGCAG 1

RESULT 11

US-10-628-066-13
; Sequence 13, Application US/10628066
; Publication No. US20040086919A1
; GENERAL INFORMATION:
; APPLICANT: Rameshwar, Prianela
; APPLICANT: Gascon, Pedro
; TITLE OF INVENTION: A Human Preprotachykinin Gene Promoter
; FILE REFERENCE: UMDNJ NJS 97-16
; CURRENT APPLICATION NUMBER: US/10/628,066
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/747,429
; PRIOR FILING DATE: 2000-12-23
; PRIOR APPLICATION NUMBER: US 60/171,970
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic sequence
US-10-628-066-13

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 400 AGGACAGTGACGAACATATTTCTCG 424
Db 1 AGGACAGTGACGAACATATTTCTCG 25

RESULT 12
US-10-719-900-67259
; Sequence 67259, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 67259
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-67259

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 926 AAGTCTCTGCCAAGCGCAAGTGCT 950
Db 1 AAGTCTCTGCCAAGCGCAAGTGCT 25

RESULT 13
US-10-719-900-247409
; Sequence 247409, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:

```
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 247409
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-247409

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1120 ATCTACTGCTGCTCAATGACAGGT 1144
Db      1 ATCTACTGCTGCTCAATGACAGGT 25

RESULT 14
US-10-719-900-253860
; Sequence 253860, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 253860
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-253860

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1136 ATGACAGTTCGCTCGGGCTTCAA 1160
Db      1 ATGACAGTTCGCTCGGGCTTCAA 25

RESULT 15
US-10-809-189-67915
; Sequence 67915, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affimetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67915
```

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; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-67915

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1261 GTCAGCCGCTTGAGACCACTATCT 1285
Db      1 GTCAGCCGCTTGAGACCACTATCT 25

RESULT 16
US-10-809-189-67925
; Sequence 67925, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affimetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67925
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-67925

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1123 TACTGCTGCTCAATGACAGTTCC 1147
Db      1 TACTGCTGCTCAATGACAGTTCC 25

RESULT 17
US-11-060-756-34833
; Sequence 34833, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.1.2
; SEQ ID NO 34833
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34833

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      394 AGAATGAGACAGTGCAGACTATT 418
```

Db 1 AGAATGAGCAGTGACGACTATT 25

RESULT 18
US-11-060-756-34834
; Sequence 34834, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34834
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34834

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 393 AAGAATGAGCAGTGACGACTATT 417
Db 1 AAGAATGAGCAGTGACGACTATT 25

RESULT 19
US-11-060-756-34835
; Sequence 34835, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34835
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34835

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 801 CATCTGTGTGACTGTGCTGATCTAC 825
Db 1 CATCTGTGTGACTGTGCTGATCTAC 25

RESULT 20
US-11-060-756-34836
; Sequence 34836, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756

CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34836
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34836

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 771 TCCGACACAGATTATGAGAAAGTG 795
Db 1 TCCGACACAGATTATGAGAAAGTG 25

RESULT 21
US-11-060-756-34837
; Sequence 34837, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34837
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34837

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 802 ATCTGTGTGACTGTGCTGATCTACT 826
Db 1 ATCTGTGTGACTGTGCTGATCTACT 25

RESULT 22
US-11-060-756-34838
; Sequence 34838, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34838
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34838

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 768 GCATCCGACACAGATTATGAGAAA 792
|||||

Db 1 GCATCCGAACAGATTATGAGAA 25

RESULT 23

US-11-060-756-34839
; Sequence 34839, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34839
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34839

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 767 AGCATCCGAACAGATTATGAGAA 791

Db 1 AGCATCCGAACAGATTATGAGAA 25

RESULT 24

US-11-060-756-34840
; Sequence 34840, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34840
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34840

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 765 AGAGCATCCGAACAGATTATGAG 789

Db 1 AGAGCATCCGAACAGATTATGAG 25

RESULT 25

US-11-060-756-34841
; Sequence 34841, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18

; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34841
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34841

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 766 GAGCATCCGAACAGATTATGAGA 790

Db 1 GAGCATCCGAACAGATTATGAGA 25

RESULT 26

US-11-060-756-34842
; Sequence 34842, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34842
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34842

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1047 GAAGAAGTTATCCAGCAGGCTTAC 1071

Db 1 GAAGAAGTTATCCAGCAGGCTTAC 25

RESULT 27

US-11-060-756-34843
; Sequence 34843, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34843
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34843

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1637 GAGCTGAACCAATCATGAACTTT 1661

Db 1 GAGCTGAACCAATCATGAACTTT 25


```
RESULT 28
US-11-060-756-34844
; Sequence 34844, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34844
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34844

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 708 CTACTACTCAACACAGAGACCATG 732
Db 1 CTACTACTCAACACAGAGACCATG 25

RESULT 29
US-11-060-756-34845
; Sequence 34845, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34845
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34845

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 764 CAGGCAATCCGAACAGATTATATGA 788
Db 1 CAGGCAATCCGAACAGATTATATGA 25

RESULT 30
US-11-060-756-34846
; Sequence 34846, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
```

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SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34846
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34846

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 ATCTCAATCTTCCCTATCTTGCC 1621
Db 1 ATCTCAATCTTCCCTATCTTGCC 25

RESULT 31
US-11-060-756-34847
; Sequence 34847, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34847
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34847

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1046 TGAAGAATTATCCAGCAGGTCTA 1070
Db 1 TGAAGAATTATCCAGCAGGTCTA 25

RESULT 32
US-11-060-756-34848
; Sequence 34848, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34848
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34848

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 770 ATCCGAACAAGATTATGAGAAAGT 794
Db 1 ATCCGAACAAGATTATGAGAAAGT 25
```

```
RESULT 33
US-11-060-756-34849
; Sequence 34849, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34849
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34849

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1596 AATCTCAATCTTCCTATCTTTC 1620
Db      1 AATCTCAATCTTCCTATCTTTC 25
|||||

RESULT 34
US-11-060-756-34850
; Sequence 34850, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34850
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34850

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      395 GAATGAGACAGTGAAGCACTATTT 419
Db      1 GAATGAGACAGTGAAGCACTATTT 25
|||||

RESULT 35
US-11-060-756-34851
; Sequence 34851, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 34851
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34851

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1636 TGACTCAAAACCAATCAGTGAAGTT 1660
Db      1 TGACTCAAAACCAATCAGTGAAGTT 25
|||||

RESULT 36
US-11-060-756-34852
; Sequence 34852, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34852
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34852

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1037 ATCTCTACCTGAAGAGTTATCCA 1061
Db      1 ATCTCTACCTGAAGAGTTATCCA 25
|||||

RESULT 37
US-11-060-756-34853
; Sequence 34853, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34853
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34853

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      772 CCGAACAGATTATGAGAAAGTGT 796
Db      1 CCGAACAGATTATGAGAAAGTGT 25
|||||
```

```
RESULT 38
US-11-060-756-34854
; Sequence 34854, Application US/11060756
; Publication No. US20050221354A1
; ORGANISM: probe
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34854
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34854

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 769 CATCGAACAAGATTATGAGAAG 793
Db 1 CATCGAACAAGATTATGAGAAG 25
|||||

RESULT 39
US-11-060-756-34855
; Sequence 34855, Application US/11060756
; Publication No. US20050221354A1
; ORGANISM: probe
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34855
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34855

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 804 CTGTGTGACTGTGCTGATCTACTTC 828
Db 1 CTGTGTGACTGTGCTGATCTACTTC 25
|||||

RESULT 40
US-11-060-756-34856
; Sequence 34856, Application US/11060756
; Publication No. US20050221354A1
; ORGANISM: probe
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34856

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 800 ACATCTGTGACTGTGCTGATCTA 824
Db 1 ACATCTGTGACTGTGCTGATCTA 25
|||||

RESULT 41
US-11-060-756-34857
; Sequence 34857, Application US/11060756
; Publication No. US20050221354A1
; ORGANISM: probe
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34857
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34857

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1599 CTCATATCTTCCCTATCTTTGCCAC 1623
Db 1 CTCATATCTTCCCTATCTTTGCCAC 25
|||||

RESULT 42
US-11-060-756-34858
; Sequence 34858, Application US/11060756
; Publication No. US20050221354A1
; ORGANISM: probe
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34858
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34858

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1039 CTCCTGGAAGAAGTTATCCAGC 1063
Db 1 CTCCTGGAAGAAGTTATCCAGC 25
|||||

RESULT 43
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```
US-11-060-756-34859
; Sequence 34859, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34859
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34859

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1038 TCTCTACCTGAAGAAGTTATCCAG 1062
Db      1 TCTCTACCTGAAGAAGTTATCCAG 25

RESULT 44
US-11-060-756-34860
; Sequence 34860, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34860
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34860

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      763 CCAGAGCATCCGACAGATTATG 787
Db      1 CCAGAGCATCCGACAGATTATG 25

RESULT 45
US-11-060-756-34861
; Sequence 34861, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34861
; LENGTH: 25

; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34861

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1598 TCTCAATCTTCCCTATCTTTGCCA 1622
Db      1 TCTCAATCTTCCCTATCTTTGCCA 25

RESULT 46
US-11-060-756-34862
; Sequence 34862, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34862
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34862

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1041 CTACCTGAGAAGTTATCCAGCAG 1065
Db      1 CTACCTGAGAAGTTATCCAGCAG 25

RESULT 47
US-11-060-756-34863
; Sequence 34863, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34863
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34863

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      392 AAAGATGAGGACAGTGCAGACTA 416
Db      1 AAAGATGAGGACAGTGCAGACTA 25

RESULT 48
US-11-060-756-34864
```

```
; Sequence 34864, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34864
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34864

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1040 TCTACTGAAGAAGTTATCCAGCA 1064
Db      1 TCTACTGAAGAAGTTATCCAGCA 25

RESULT 49
US-11-060-756-34865
; Sequence 34865, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34865
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34865

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      803 TCTGTGACTGTGCTGATCTACTT 827
Db      1 TCTGTGACTGTGCTGATCTACTT 25

RESULT 50
US-11-060-756-34866
; Sequence 34866, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34866
; LENGTH: 25
; TYPE: DNA

; ORGANISM: probe
US-11-060-756-34867

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1048 AAGAAGTTATCCAGCAGCTTACC 1072
Db      1 AAGAAGTTATCCAGCAGCTTACC 25

RESULT 51
US-11-060-756-34867
; Sequence 34867, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34867
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34867

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      783 TTATGAGAAGCTGATCCACATCTGT 807
Db      1 TTATGAGAAGCTGATCCACATCTGT 25

RESULT 52
US-11-060-756-34868
; Sequence 34868, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34868
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34868

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1036 GATCTTACTGAAGAAGTTATCC 1060
Db      1 GATCTTACTGAAGAAGTTATCC 25

RESULT 53
US-11-060-756-34869
; Sequence 34869, Application US/11060756
```

```
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34869
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34869

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      707 GCTACTACTCAACGACGAGCCAT 731
Db      1 GCTACTACTCAACGACGAGACAT 25

RESULT 54
US-11-060-756-34870
; Sequence 34870, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34870
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34870

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      474 GAACCTTACCTATGCTGTCACAC 498
Db      1 GAACCTTACCTATGCTGTCACAC 25

RESULT 55
US-11-060-756-34871
; Sequence 34871, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34871
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe

US-11-060-756-34871
Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      782 TTTATGAGAAAGTGTACCAATCTG 806
Db      1 TTTATGAGAAAGTGTACCAATCTG 25

RESULT 56
US-11-060-756-34872
; Sequence 34872, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34872
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34872

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      457 GCATTCAATACAGTGTGAACCTCA 481
Db      1 GCATTCAATACAGTGTGAACCTCA 25

RESULT 57
US-11-060-756-34873
; Sequence 34873, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34873
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34873

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1410 CTTTCCTCAATGCTGCTCTCTAG 1434
Db      1 CTTTCCTCAATGCTGCTCTCTAG 25

RESULT 58
US-11-060-756-34874
; Sequence 34874, Application US/11060756
; Publication No. US20050221354A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 34874
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34874

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 807 TGTGACTGTGCTGATCTACTCTTC 831
Db 1 TGTGACTGTGCTGATCTACTCTTC 25

RESULT 59
US-11-060-756-34875
; Sequence 34875, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 34875
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34875

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 554 CTGCTTCGGCAGATCTACTCCAT 578
Db 1 CTGCTTCGGCAGATCTACTCCAT 25

RESULT 60
US-11-060-756-34876
; Sequence 34876, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 34876
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34876

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 776 ACAAGATTATGAGAAAGTGACCA 800
Db 1 ACAAGATTATGAGAAAGTGACCA 25

RESULT 61
US-11-060-756-117862
; Sequence 117862, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 117862
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-117862

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1715 ATTCCATTCTCGAAGTGAAGCTTGG 1739
Db 1 ATTCCATTCTCGAAGTGAAGCTTGG 25

RESULT 62
US-11-060-756-121089
; Sequence 121089, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 121089
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-121089

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1508 ATCTGAACCATCAGAAACACCCCTC 1532
Db 1 ATCTGAACCATCAGAAACACCCCTC 25

RESULT 63
US-11-060-756-124386
; Sequence 124386, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 124386
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-124386

Query Match
Best Local Similarity 100.0%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1628 ATGCTGTGACTCAACCAATCA 1652
1 ATGCTGTGACTCAACCAATCA 25

RESULT 64
US-11-060-756-124823
; Sequence 124823, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 124823
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-124823

Query Match
Best Local Similarity 100.0%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1711 ATGCATTCATTCTCGAAGTACT 1735
1 ATGCATTCATTCTCGAAGTACT 25

RESULT 65
US-11-060-756-127403
; Sequence 127403, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 127403
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-127403
```

```

Query Match
Best Local Similarity 100.0%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1493 ATGGAATTCCTTCATCTGGAACC 1517
1 ATGGAATTCCTTCATCTGGAACC 25

RESULT 66
US-11-060-756-130804
; Sequence 130804, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 130804
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-130804

Query Match
Best Local Similarity 100.0%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1378 AGTGACTCGAAGCATGACAGAGA 1402
1 AGTGACTCGAAGCATGACAGAGA 25

RESULT 67
US-11-060-756-138470
; Sequence 138470, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 138470
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-138470

Query Match
Best Local Similarity 100.0%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1644 ACCAATCATGTAAGTTTGCTGAGC 1668
1 ACCAATCATGTAAGTTTGCTGAGC 25

RESULT 68
US-11-060-756-139174
; Sequence 139174, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
```



```
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 139174
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-139174
```

```
Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1279 ACCATCTCACAGTGTGGGGGCC 1303
Db 1 ACCATCTCACAGTGTGGGGGCC 25

RESULT 69
US-11-060-756-140183
; Sequence 140183, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 140183
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-140183
```

```
Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1240 ACCCAGGCGAGTGTGTACAAAGTCA 1264
Db 1 ACCCAGGCGAGTGTGTACAAAGTCA 25

RESULT 70
US-11-060-756-147282
; Sequence 147282, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 147282
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-147282
```

```
Query Match 1.4%; Score 25; DB 1; Length 25;
```

```
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1214 AAATGAATCCACCCGGATCTCCA 1238
Db 1 AAATGAATCCACCCGGATCTCCA 25

RESULT 71
US-11-060-756-149065
; Sequence 149065, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 149065
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-149065
```

```
Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1572 AAACATTCATCCTTGAGTCAAAA 1596
Db 1 AAACATTCATCCTTGAGTCAAAA 25
```

```
RESULT 72
US-11-060-756-149921
; Sequence 149921, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 149921
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-149921
```

```
Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1592 AAAAATCTCAATCTTCCCTATCT 1616
Db 1 AAAAATCTCAATCTTCCCTATCT 25
```

```
RESULT 73
US-11-060-756-149974
; Sequence 149974, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
```

```
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 149974
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-149974

Query Match      1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1593 AAAAATCTCAATTTCTTCCCTTCTT 1617
Db      1 AAAAATCTCAATTTCTTCCCTTCTT 25

RESULT 74
US-11-060-756-151784
; Sequence 151784, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 151784
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-151784

Query Match      1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1363 AACTGCTCTTCACGAGTACTCCA 1387
Db      1 AACTGCTCTTCACGAGTACTCCA 25

RESULT 75
US-11-060-756-152840
; Sequence 152840, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 152840
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-152840

Query Match      1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1643 AACCAATCATCTGAACCTTGCTGAG 1667
Db      1 AACCAATCATCTGAACCTTGCTGAG 25

RESULT 76
US-11-060-756-154707
; Sequence 154707, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 154707
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-154707

Query Match      1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1702 AAGAGCCCAATGCATTCATTCTG 1726
Db      1 AAGAGCCCAATGCATTCATTCTG 25

RESULT 77
US-11-060-756-160866
; Sequence 160866, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 160866
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-160866

Query Match      1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1701 CAAGAGCCCAATGCATTCATTCT 1725
Db      1 CAAGAGCCCAATGCATTCATTCT 25

RESULT 78
US-11-060-756-162417
; Sequence 162417, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
```

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; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 162417
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-162417

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1646 CAAATCACTGAACCTTGCTGAGCCT 1670
Db 1 CAAATCACTGAACCTTGCTGAGCCT 25

RESULT 79
US-11-060-756-163702
; Sequence 163702, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 163702
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-163702

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1651 CACTGAACCTTGCTGAGCCTGTAA 1675
Db 1 CACTGAACCTTGCTGAGCCTGTAA 25

RESULT 80
US-11-060-756-164016
; Sequence 164016, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 164016
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-164016

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1373 CACGAAGTACTCCAGACCATGAC 1397
Db 1 CACGAAGTACTCCAGACCATGAC 25

RESULT 81
US-11-060-756-167974
; Sequence 167974, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 167974
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-167974

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1248 CAGTGTACAAAGTACGCCCTG 1272
Db 1 CAGTGTACAAAGTACGCCCTG 25

RESULT 82
US-11-060-756-169980
; Sequence 169980, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 169980
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-169980

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1185 CATCAGCCCGCGCATATGAGGG 1209
Db 1 CATCAGCCCGCGCATATGAGGG 25

RESULT 83
US-11-060-756-170236
; Sequence 170236, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 170236
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-170236

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 170236
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-170236

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1627 CATGCTGTGACTCACCAACCAATC 1651
Db      1 CATGCTGTGACTCACCAACCAATC 25

RESULT 84
US-11-060-756-170323
; Sequence 170323, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 170323
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-170323

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1488 CATGCATGGAATTCCTTCATCTG 1512
Db      1 CATGCATGGAATTCCTTCATCTG 25

RESULT 85
US-11-060-756-170981
; Sequence 170981, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 170981
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-170981

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1715 CATTCATCTTGACTCAAAAATC 1599
Db      1 CATTCATCTTGACTCAAAAATC 25

RESULT 86
US-11-060-756-171771
; Sequence 171771, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 171771
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-171771

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1714 CATTCATTTCTGGAAGTGACTTG 1738
Db      1 CATTCATTTCTGGAAGTGACTTG 25

RESULT 87
US-11-060-756-171898
; Sequence 171898, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 171898
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-171898

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1719 CATTTCTGGAAGTGACTTTGGCTGC 1743
Db      1 CATTTCTGGAAGTGACTTTGGCTGC 25

RESULT 88
US-11-060-756-173421
; Sequence 173421, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 173421
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-173421

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

;;
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 173421
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-173421

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1370 CTCACGAGTGTGCTCAAGCCAT 1394
Db 1 CTCACGAGTGTGCTCAAGCCAT 25

RESULT 89
US-11-060-756-174120
; Sequence 174120, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 174120
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-174120

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1693 CTTTCTCAAGAGCCCATTCATT 1717
Db 1 CTTTCTCAAGAGCCCATTCATT 25

RESULT 90
US-11-060-756-176669
; Sequence 176669, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 176669
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-176669

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1699 CTCAGAGCCCATGATTCATT 1723

Db 1 CTCAGAGCCCATGATTCATT 25

RESULT 91
US-11-060-756-177313
; Sequence 177313, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 177313
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-177313

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1625 CTCATGCTGTGTGCTCAACCAAA 1649
Db 1 CTCATGCTGTGTGCTCAACCAAA 25

RESULT 92
US-11-060-756-177851
; Sequence 177851, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 177851
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-177851

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 CTCCTTCATGATGGAATTCCT 1505
Db 1 CTCCTTCATGATGGAATTCCT 25

RESULT 93
US-11-060-756-178612
; Sequence 178612, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756

```
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 178612
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-178612
```

```
Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1359 CTCCAGTCGCTCTTCACGAAGTGAC 1383
Db      1 CTCCAGTCGCTCTTCACGAAGTGAC 25
```

RESULT 94

```
US-11-060-756-178926
; Sequence 178926, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 178926
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-178926
```

```
Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1284 CTCACAGTCGTGGGGCCCCACAG 1308
Db      1 CTCACAGTCGTGGGGCCCCACAG 25
```

RESULT 95

```
US-11-060-756-179517
; Sequence 179517, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 179517
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-179517
```

```
Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1740 CTGCATGCGAGTGTCTATTTCAGGA 1764
      |||||||||||||||||||||||||
```

```
Db      1 CTGCATGCGAGTGTCTATTTCAGGA 25
```

```
RESULT 96
US-11-060-756-179873
; Sequence 179873, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 179873
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-179873
```

```
Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1365 CTGCTCTTCACGAAGTGATCCGAAG 1389
Db      1 CTGCTCTTCACGAAGTGATCCGAAG 25
```

RESULT 97

```
US-11-060-756-182148
; Sequence 182148, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 182148
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-182148
```

```
Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1631 CTGTGTGACTCAACCAATCACTG 1655
Db      1 CTGTGTGACTCAACCAATCACTG 25
```

```
RESULT 98
US-11-060-756-182797
; Sequence 182797, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT FILING DATE: 2005-02-18
```

NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 182797
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-11-060-756-182797

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1510 CTGAACCATGAGAAACACCTCTCAC 1534
Db 1 CTGAACCATGAGAAACACCTCTCAC 25

RESULT 99
US-11-060-756-185584
Sequence 185584, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REFERENCE: AM101083 (031896-042000)
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 185584
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-11-060-756-185584

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1375 CGAAGTGACTCCAGACCATGACAG 1399
Db 1 CGAAGTGACTCCAGACCATGACAG 25

RESULT 100
US-11-060-756-187465
Sequence 187465, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REFERENCE: AM101083 (031896-042000)
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 187465
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-11-060-756-187465

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1483 CCTTCATGATGAGAAATTCCTTC 1507
Db 1 CCTTCATGATGAGAAATTCCTTC 25

RESULT 101
US-11-060-756-192020
Sequence 192020, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REFERENCE: AM101083 (031896-042000)
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 192020
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-11-060-756-192020

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1131 CCTCAATGACAGGTTCCGCTGAGGC 1155
Db 1 CCTCAATGACAGGTTCCGCTGAGGC 25

RESULT 102
US-11-060-756-192401
Sequence 192401, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REFERENCE: AM101083 (031896-042000)
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 192401
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-11-060-756-192401

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1624 CCTCATGCTGTGTGATCTCAACCA 1648
Db 1 CCTCATGCTGTGTGATCTCAACCA 25

RESULT 103
US-11-060-756-193467
Sequence 193467, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REFERENCE: AM101083 (031896-042000)
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1483 CCTTCATGATGAGAAATTCCTTC 1507
Db 1 CCTTCATGATGAGAAATTCCTTC 25

```
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 193467
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-193467
```

```
Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1280 CCATCTCCACAGTGTGTGGGGCCCA 1304
          |||||
DB       1 CCATCTCCACAGTGTGTGGGGCCCA 25
```

```
RESULT 104
US-11-060-756-193692
; Sequence 193692, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 193692
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-193692
```

```
Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1718 CCATTCTGGAAGTGACTTTGGCTG 1742
          |||||
DB       1 CCATTCTGGAAGTGACTTTGGCTG 25
```

```
RESULT 105
US-11-060-756-195758
; Sequence 195758, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 195758
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-195758
```

```
Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1361 CCAACTGCTCTTCAACAAGTGAATC 1385
          |||||
DB       1 CCAACTGCTCTTCAACAAGTGAATC 25
```

```
RESULT 106
US-11-060-756-195777
; Sequence 195777, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 195777
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-195777
```

```
Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1286 CCACAGTGTGTGGGGCCCAAGAGA 1310
          |||||
DB       1 CCACAGTGTGTGGGGCCCAAGAGA 25
```

```
RESULT 107
US-11-060-756-196323
; Sequence 196323, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 196323
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-196323
```

```
Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1645 CCAATCACTGAAGTGTGCTGAGCC 1669
          |||||
DB       1 CCAATCACTGAAGTGTGCTGAGCC 25
```

```
RESULT 108
US-11-060-756-197870
; Sequence 197870, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
```


SEQ ID NO 197870
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-197870

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1479 GCCTCCCTTCATGCATGGAATTC 1503
Db 1 GCCTCCCTTCATGCATGGAATTC 25

RESULT 109
US-11-060-756-198758
; Sequence 198758, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 198758
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-198758

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1130 GCCTCAATGACAGGTCGCTGGG 1154
Db 1 GCCTCAATGACAGGTCGCTGGG 25

RESULT 110
US-11-060-756-202952
; Sequence 202952, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 202952
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-202952

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1630 GCTGTGACTCAACCAATCACT 1654
Db 1 GCTGTGACTCAACCAATCACT 25

RESULT 111
US-11-060-756-204546
; Sequence 204546, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 204546
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-204546

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1367 GCCTTCACGAGTCAAGCTCCAGAC 1391
Db 1 GCCTTCACGAGTCAAGCTCCAGAC 25

RESULT 112
US-11-060-756-205830
; Sequence 205830, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 205830
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-205830

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1692 GCTTTCTCAAGGCCCAATGCAT 1716
Db 1 GCTTTCTCAAGGCCCAATGCAT 25

RESULT 113
US-11-060-756-206207
; Sequence 206207, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 206207

```

; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-206207

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1713 GCATTCATTCTCGAAGTACCTT 1737
Db 1 GCATTCATTCTCGAAGTACCTT 25

RESULT 114
US-11-060-756-207277
; Sequence 207277, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 207277
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-207277

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1247 GCAGTGTGTACAAAGTCAGCCGCT 1271
Db 1 GCAGTGTGTACAAAGTCAGCCGCT 25

RESULT 115
US-11-060-756-207312
; Sequence 207312, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 207312
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-207312

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1742 GCATCGAGTGTCTATTTCAGATG 1766
Db 1 GCATCGAGTGTCTATTTCAGATG 25

RESULT 116
US-11-060-756-213399
; Sequence 213399, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 213399
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-213399

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1376 GAAAGTACTCCAAAGACCATGACAGA 1400
Db 1 GAAAGTACTCCAAAGACCATGACAGA 25

RESULT 117
US-11-060-756-220646
; Sequence 220646, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 220646
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-220646

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1381 GACTCCAAAGACCATGACAGAGCT 1405
Db 1 GACTCCAAAGACCATGACAGAGCT 25

RESULT 118
US-11-060-756-227033
; Sequence 227033, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 227033
; LENGTH: 25
```

;; TYPE: DNA
;; ORGANISM: probe
US-11-060-756-227033

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1204 GAGGGCTGGAATGAATCCACC 1228
Db 1 GAGGGCTGGAATGAATCCACC 25

RESULT 119
US-11-060-756-238277
; Sequence 238277, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 238277
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-238277

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1589 GTCAAAAATCTCAATTTCTCCCTA 1613
Db 1 GTCAAAAATCTCAATTTCTCCCTA 25

RESULT 120
US-11-060-756-242329
; Sequence 242329, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 242329
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-242329

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1670 TGTAAATATAAGTCGACCCAGCT 1694
Db 1 TGTAAATATAAGTCGACCCAGCT 25

RESULT 121
US-11-060-756-246182

; Sequence 246182, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 246182
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-246182

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1207 GGCGTGAATGAATCCACCCGCT 1231
Db 1 GGCGTGAATGAATCCACCCGCT 25

RESULT 122
US-11-060-756-247883
; Sequence 247883, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 247883
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-247883

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1538 GGAAGTTGCAAAAAGGTCAGTATG 1562
Db 1 GGAAGTTGCAAAAAGGTCAGTATG 25

RESULT 123
US-11-060-756-251001
; Sequence 251001, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 251001
; LENGTH: 25
; TYPE: DNA

```
; ORGANISM: probe
US-11-060-756-251001

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1553 GGTCAATGAGTGGTAAACAT 1577
Db 1 GGTCAATGAGTGGTAAACAT 25

RESULT 124
US-11-060-756-256929
; Sequence 256929, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 256929
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-256929

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1212 GGAATGAAATCCACCGGTATCTC 1236
Db 1 GGAATGAAATCCACCGGTATCTC 25

RESULT 125
US-11-060-756-264993
; Sequence 264993, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 264993
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-264993

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1561 TGGGTAGGAAACATTCATCCT 1585
Db 1 TGGGTAGGAAACATTCATCCT 25

RESULT 126
US-11-060-756-266512
; Sequence 266512, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 266512
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-266512

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1632 TGTGTGACTCAACCAATCATCTGA 1656
Db 1 TGTGTGACTCAACCAATCATCTGA 25

RESULT 127
US-11-060-756-267837
; Sequence 267837, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 267837
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-267837

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1253 TGTCAAAAGTCAGCGCCTGGAGAC 1277
Db 1 TGTCAAAAGTCAGCGCCTGGAGAC 25

RESULT 128
US-11-060-756-271421
; Sequence 271421, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 271421
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
```

US-11-060-756-271421

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1394 TGACAGAGAGCTTCAGCTTCCTC 1418

Db 1 TGACAGAGAGCTTCAGCTTCCTC 25

RESULT 129

US-11-060-756-271732
Sequence 271732, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:

APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REFERENCE: AM101083 (031896-042000)
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 271732
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-11-060-756-271732

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1712 TGATTCATTTCTGGAAGTACTT 1736

Db 1 TGATTCATTTCTGGAAGTACTT 25

RESULT 130

US-11-060-756-273114
Sequence 273114, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:

APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REFERENCE: AM101083 (031896-042000)
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 273114
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-11-060-756-273114

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1741 TGCATGCGAGTCTCATTTGAGAT 1765

Db 1 TGCATGCGAGTCTCATTTGAGAT 25

RESULT 131

US-11-060-756-273130
Sequence 273130, Application US/11060756
Publication No. US20050221354A1

GENERAL INFORMATION:

APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REFERENCE: AM101083 (031896-042000)
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 273130
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-11-060-756-273130

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1490 TGCATGGAATTCCTTCATCTGGA 1514

Db 1 TGCATGGAATTCCTTCATCTGGA 25

RESULT 132

US-11-060-756-274140
Sequence 274140, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:

APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REFERENCE: AM101083 (031896-042000)
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 274140
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-11-060-756-274140

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1629 TGCTGTGACTCAACCAATCAGC 1653

Db 1 TGCTGTGACTCAACCAATCAGC 25

RESULT 133

US-11-060-756-274779
Sequence 274779, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:

APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REFERENCE: AM101083 (031896-042000)
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 274779
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-11-060-756-274779

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1478 TGCCTCCCTTCATGATGAAATTC 1502
DB 1 TGCTCCCTTCATGATGAAATTC 25

RESULT 134
US-11-060-756-275674
Sequence 275674, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REFERENCE: AM101083 (031896-042000)
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 275674
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-11-060-756-275674

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1717 TCATTTCTGGAAGTGACTTTGGCT 1741
DB 1 TCATTTCTGGAAGTGACTTTGGCT 25

RESULT 135
US-11-060-756-276554
Sequence 276554, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REFERENCE: AM101083 (031896-042000)
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 276554
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-11-060-756-276554

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1697 TCCTCAAGAGCCCATGCAATTCAT 1721
DB 1 TCCTCAAGAGCCCATGCAATTCAT 25

RESULT 136
US-11-060-756-281504
Sequence 281504, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:

APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REFERENCE: AM101083 (031896-042000)
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 281504
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-11-060-756-281504

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1650 TCACTGAACCTTGTGAGCCTGTA 1674
DB 1 TCACTGAACCTTGTGAGCCTGTA 25

RESULT 137
US-11-060-756-283191
Sequence 283191, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REFERENCE: AM101083 (031896-042000)
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 283191
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-11-060-756-283191

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1626 TCATGCTGTGTGACTCAACCAAT 1650
DB 1 TCATGCTGTGTGACTCAACCAAT 25

RESULT 138
US-11-060-756-285749
Sequence 285749, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REFERENCE: AM101083 (031896-042000)
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 285749
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-11-060-756-285749

```
Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1700 TCAAGAGCCCAATGCATTCATTTTC 1724
Db          1 TCAAGAGCCCAATGCATTCATTTTC 25

RESULT 139
US-11-060-756-285791
; Sequence 285791, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 285791
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-285791

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1133 TCAATGACAGGTTCCGTCGTGGCCTT 1157
Db          1 TCAATGACAGGTTCCGTCGTGGCCTT 25

RESULT 140
US-11-060-756-295627
; Sequence 295627, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 295627
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-295627

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1694 TTTTCTCAAGAGCCCAATGCATTC 1718
Db          1 TTTTCTCAAGAGCCCAATGCATTC 25

RESULT 141
US-11-060-756-300784
; Sequence 300784, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
```

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; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 300784
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-300784

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1696 TTCTCAAGAGCCCAATGCATTTCCA 1720
Db          1 TTCTCAAGAGCCCAATGCATTTCCA 25

RESULT 142
US-11-060-756-301167
; Sequence 301167, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 301167
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-301167

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1716 TTCCATTTCTGGAAGTACTTTGGC 1740
Db          1 TTCCATTTCTGGAAGTACTTTGGC 25

RESULT 143
US-11-121-849-111033
; Sequence 111033, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S.
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 111033
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-111033
```

```
Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1363 AACTGCTCTTCACGAGAGTACTCCA 1387
DB 1 AACTGCTCTTCACGAGAGTACTCCA 25

RESULT 144
US-11-121-849-111034
; Sequence 111034, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 111034
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-111034

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1376 GAAGTACTCCAGACCATGACAGA 1400
DB 1 GAAGTACTCCAGACCATGACAGA 25

RESULT 145
US-11-121-849-111035
; Sequence 111035, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 111035
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-111035

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1382 ACTCCAAGACCATGACAGAGCTT 1406
DB 1 ACTCCAAGACCATGACAGAGCTT 25

RESULT 146
US-11-121-849-111036
; Sequence 111036, Application US/11121849
; Publication No. US20050272080A1
```

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; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 111036
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-111036

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1420 AATGTGCTCTCTAGGCCACAGGCC 1444
DB 1 AATGTGCTCTCTAGGCCACAGGCC 25

RESULT 147
US-11-121-849-111037
; Sequence 111037, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 111037
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-111037

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1478 TGCCCTCCCTCATGATGGAATTC 1502
DB 1 TGCCCTCCCTCATGATGGAATTC 25

RESULT 148
US-11-121-849-111038
; Sequence 111038, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 111038
; LENGTH: 25
```


TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-111038

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1495 GGAATTCCTTCATCTGGAACCAT 1519
DB 1 GGAATTCCTTCATCTGGAACCAT 25

RESULT 149
US-11-121-849-111039
Sequence 111039, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma

TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 111039
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-111039

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1499 ATTCCCTTCATCTGGAACCATGAGA 1523
DB 1 ATTCCCTTCATCTGGAACCATGAGA 25

RESULT 150
US-11-121-849-111040
Sequence 111040, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 111040
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-111040

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1511 TGGAACTTCAGAAACACCTTCACA 1535
DB 1 TGGAACTTCAGAAACACCTTCACA 25

RESULT 151
US-11-121-849-111041
Sequence 111041, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma

TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 111041
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-111041

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1537 TGGGACTTCGAAAGGCTCAGTAT 1561
DB 1 TGGGACTTCGAAAGGCTCAGTAT 25

RESULT 152
US-11-121-849-111042
Sequence 111042, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 111042
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-111042

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1561 TGGGTTAGGAAACATTCATCCT 1585
DB 1 TGGGTTAGGAAACATTCATCCT 25

RESULT 153
US-11-121-849-111043
Sequence 111043, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03

```
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 111043
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-111043
```

```
Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1570 GAAACATTCATCCTTGAGTCGAA 1594
Db 1 GAAACATTCATCCTTGAGTCGAA 25
```

```
RESULT 154
US-11-121-849-192687
; Sequence 192687, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
```

```
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 192687
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-192687
```

```
Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1117 ATCATCTACTGCTGCTCAATGACA 1141
Db 1 ATCATCTACTGCTGCTCAATGACA 25
```

```
RESULT 155
US-11-121-849-192688
; Sequence 192688, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
```

```
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 192688
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-192688
```

```
Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1118 TCATCTACTGCTGCTCAATGACAG 1142
```

```
Db 1 TCATCTACTGCTGCTCAATGACAG 25
```

```
RESULT 156
US-11-121-849-192689
; Sequence 192689, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 192689
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-192689
```

```
Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1120 ATCTACTGCTGCTCAATGACAGT 1144
Db 1 ATCTACTGCTGCTCAATGACAGT 25
```

```
RESULT 157
US-11-121-849-192690
; Sequence 192690, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 192690
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-192690
```

```
Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1027 ATCAACCCAGATCTCTACTGAGAA 1051
Db 1 ATCAACCCAGATCTCTACTGAGAA 25
```

```
RESULT 158
US-11-121-849-192691
; Sequence 192691, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
```

```

; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 192691
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-192691

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1028 TCAACCCAGATCTCTACTGGAAGAA 1052
Db      1 TCAACCCAGATCTCTACTGGAAGAA 25

RESULT 159
US-11-121-849-192692
; Sequence 192692, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 192692
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-192692

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1033 CCAGATCTCTACTGGAAGATTTA 1057
Db      1 CCAGATCTCTACTGGAAGATTTA 25

RESULT 160
US-11-121-849-192693
; Sequence 192693, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 192693
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-192693

Query Match          1.4%; Score 25; DB 1; Length 25;

Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1034 CAGATCTCTACTGGAAGATTAT 1058
Db      1 CAGATCTCTACTGGAAGATTAT 25

RESULT 161
US-11-121-849-192694
; Sequence 192694, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 192694
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-192694

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1036 GATCTCTACTGGAAGATTATCC 1060
Db      1 GATCTCTACTGGAAGATTATCC 25

RESULT 162
US-11-121-849-192695
; Sequence 192695, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 192695
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-192695

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1039 CTCTACTGGAAGATTATCCAGC 1063
Db      1 CTCTACTGGAAGATTATCCAGC 25

RESULT 163
US-11-121-849-192696
; Sequence 192696, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
```

```
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 192696
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-192696

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1065 GGTCTACCTGGCCATCATGTGGCTG 1089
Db      1 GGTCTACCTGGCCATCATGTGGCTG 25

RESULT 164
US-11-121-849-192697
; Sequence 192697, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 192697
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-192697

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1066 GTTACCTGGCCATCATGTGGCTG 1090
Db      1 GTTACCTGGCCATCATGTGGCTG 25

RESULT 165
US-10-005-956-1306/c
; Sequence 1306, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
```

```
; SEQ ID NO 1306
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: wherein "n" equals a C3 phosphoramidite linker.
; NAME/KEY: misc feature
; LOCATION: (21)..(21)
; OTHER INFORMATION: wherein "n" equals a C3 phosphoramidite linker.
US-10-005-956-1306

Query Match          1.4%; Score 25; DB 1; Length 27;
Best Local Similarity 92.6%; Pred. No. 2.3e+02;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1345 TCCTGGACCTGACCTCCACTGCTCT 1371
Db      27 TCCTGNACCTGACCTCNACTGCTCT 1

RESULT 166
US-11-036-317-481475
; Sequence 481475, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; PRIOR FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 481475
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-481475

Query Match          1.4%; Score 24; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      922 GAGCAAGTCTTGCACGCGCAG 945
Db      2 GAGCAAGTCTTGCACGCGCAG 25

RESULT 167
US-10-005-956-1304
; Sequence 1304, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1304
; LENGTH: 27
; TYPE: DNA
```

```
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: wherein "n" equals a C3 phosphoramidite linker.
; NAME/KEY: misc_feature
; LOCATION: (17)..(17)
; OTHER INFORMATION: wherein "n" equals a C3 phosphoramidite linker.
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: wherein "n" equals a C3 phosphoramidite linker.
US-10-005-956-1304

Query Match 1.4%; Score 24; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1608 TCCCTATCTTGCCACCCCTCATGCTGT 1634
Db 1 TCCCTATCTTGCCACCCCTCATGCTGT 27

RESULT 168
US-10-044-592-23/c
; Sequence 23. Application US/10044592
; Publication No. US20020143152A1
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; TITLE OF INVENTION: Polypeptides, their Production and Use
; FILE REFERENCE: 2463US2P
; CURRENT APPLICATION NUMBER: US/10/044,592
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 09/403639
; PRIOR FILING DATE: 1999-25-10
; PRIOR APPLICATION NUMBER: PCT/JP98/01923
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: JP 9-109974
; PRIOR FILING DATE: 1997-04-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE:
; SEQ ID NO 23
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(29)
; OTHER INFORMATION: mixed synthetic primer described on pg. 98
; NAME/KEY: misc_feature
; LOCATION: (23)..(23)
; OTHER INFORMATION: A, G, C or T
US-10-044-592-23

Query Match 1.4%; Score 24; DB 1; Length 29;
Best Local Similarity 72.4%; Pred. No. 3.1e+02;
Matches 21; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 979 TTCGCATCTGCTGCTGCCCTTCACAT 1007
Db 29 TTCGATCTGCTGCTGCCCTTCACAT 1

RESULT 169
US-10-278-087A-61/c
; Sequence 61. Application US/10278087A
; Publication No. US20030138817A1
; GENERAL INFORMATION:
; APPLICANT: Shuji Hinuma
; YASUAKI ITO
; TITLE OF INVENTION: G Protein Coupled Receptor Protein,
; Production, And Use Thereof
```

```
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Edwards & Angel, LLP
; STREET: 101 Federal Street
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02209
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/278,087A
; FILING DATE: 31-Jan-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/461,436
; FILING DATE: 14-DEC-1999
; APPLICATION NUMBER: 09/038,572
; FILING DATE: 11-MAR-1998
; APPLICATION NUMBER: 08/513,974
; FILING DATE: 14-SEP-1995
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; APPLICATION NUMBER: 7-093989
; FILING DATE: 19-APR-1995
; APPLICATION NUMBER: 7-057186
; FILING DATE: 16-MAR-1995
; APPLICATION NUMBER: 7-007177
; FILING DATE: 20-JAN-1995
; APPLICATION NUMBER: 6-326611
; FILING DATE: 28-DEC-1994
; APPLICATION NUMBER: 6-270017
; FILING DATE: 02-NOV-1994
; APPLICATION NUMBER: 6-236357
; FILING DATE: 30-SEP-1994
; APPLICATION NUMBER: 6-236356
; FILING DATE: 30-SEP-1994
; APPLICATION NUMBER: 6-189274
; FILING DATE: 11-AUG-1994
; APPLICATION NUMBER: 6-189273
; FILING DATE: 11-AUG-1994
; APPLICATION NUMBER: 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, DAVID G.
; REGISTRATION NUMBER: <Unknown>
; REFERENCE/DOCKET NUMBER: 45753 DIV3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-439-4444
; TELEFAX: 617-439-4170
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA
; OTHER INFORMATION: /note = N is inosine, S is G or C; W is A or T;
; R is A or G; K is G or T; Y is C or T."
; SEQUENCE DESCRIPTION: SEQ ID NO: 61:
US-10-278-087A-61

Query Match 1.4%; Score 24; DB 1; Length 29;
Best Local Similarity 72.4%; Pred. No. 3.1e+02;
Matches 21; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 979 TTCGCATCTGCTGCTGCCCTTCACAT 1007
|||:::|||||
```

Db 29 TTCRYSNCTGCTGCTGCCCTWCTWCMT 1

```
RESULT 170
US-11-054-211-32/c
; Sequence 32, Application US/11054211
; Publication No. US20050170461A1
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
;          Habata, Yugo
;          Kawamata, Yuji
;          Hosoya, Masaki
;          Fujii, Ryo
;          Fukusumi, Shoji
;          Kitada, Chieko
; TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: DIXE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/054,211
; FILING DATE: 08-Feb-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/716,147
; FILING DATE: 17-Nov-2000
; APPLICATION NUMBER: US/08/776,971
; FILING DATE: 06-Feb-1997
; APPLICATION NUMBER: PCT/JP96/03821
; FILING DATE: 28-Dec-1996
; APPLICATION NUMBER: JP 7/343371
; FILING DATE: 28-Dec-1995
; APPLICATION NUMBER: JP 8/59419
; FILING DATE: 15-Mar-1996
; APPLICATION NUMBER: JP 8/211805
; FILING DATE: 12-Aug-1996
; APPLICATION NUMBER: JP 8/246573
; FILING DATE: 18-Sep-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Conlin, David G.
; REGISTRATION NUMBER: 27,026
; REFERENCE/DOCKET NUMBER: 47176
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-11-054-211-32
```

```
Query Match 1.4%; Score 24; DB 1; Length 29;
Best Local Similarity 72.4%; Pred. No. 3.1e+02;
Matches 21; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
```

QY 979 TTGCGCATCTGCTGCTGCCCTTCCACAT 1007
|||||
Db 29 TTCRYSNCTGCTGCTGCCCTWCTWCMT 1

```
RESULT 171
US-10-005-956-1215
; Sequence 1215, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1215
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-005-956-1215
```

```
Query Match 1.3%; Score 23.6; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 2.6e+02;
Matches 23; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

QY 1631 CTGTGCTGCTCAACCAATCACT 1654
|||||
Db 1 CTGTGCTGCTCAACCAATCACT 24

```
RESULT 172
US-10-719-900-67260
; Sequence 67260, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 67260
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-67260
```

```
Query Match 1.3%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 2.8e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 926 AAGTCTCTGCCAAGCGAAGTGT 950
|||||
Db 1 AAGTCTCTGCCAAGCGAAGTGT 25

```
RESULT 173
US-10-719-900-237659
; Sequence 237659, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
```

```
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 237659
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-719-900-237659

Query Match      1.3%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 2.8e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1027 ATCAACCCAGATCTCTACTGAGAGA 1051
Db      1 ATCAACCCAGATCTCTACTGAGAGA 25

RESULT 174
; US-10-719-900-247410
; Sequence 247410, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 247410
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-719-900-247410

Query Match      1.3%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 2.8e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1120 ATCTACTGCTGCTCAATGACAGGT 1144
Db      1 ATCTACTGCTGCTCAATGACAGGT 25

RESULT 175
; US-10-719-900-253859
; Sequence 253859, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 253859
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-719-900-253859

Query Match      1.3%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 2.8e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1136 ATGACAGTTCCTCTGCGCTTCA 1160
Db      1 ATGACAGTTCCTCTGCGCTTCA 25

RESULT 176
; US-10-719-900-890393
; Sequence 890393, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 890393
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-719-900-890393

Query Match      1.3%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 2.8e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      880 TGGGCGAGTGAGATCCCGGGGACT 904
Db      1 TGGGCGAGTGAGATCCCGGGGACT 25

RESULT 177
; US-10-809-189-67914
; Sequence 67914, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67914
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-809-189-67914

Query Match      1.3%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 2.8e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1255 TACAAAGTCAGCCGCTGAGACCA 1279
Db      1 TACAAAGTCAGCCGCTGAGACCA 25

RESULT 178
; US-10-809-189-67926
; Sequence 67926, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
```

```
/ APPLICANT: Michael Miltmann
/ APPLICANT: David Mack
/ APPLICANT: David Lockhart
/ APPLICANT: Affymetrix, Inc.
/ TITLE OF INVENTION: Methods of Genetic Analysis
/ FILE REFERENCE: 3101.1
/ CURRENT APPLICATION NUMBER: US/10/809,189
/ CURRENT FILING DATE: 2004-03-25
/ PRIOR APPLICATION NUMBER: US/09/396,196
/ PRIOR FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: 60/100,678
/ PRIOR FILING DATE: 1998-09-17
/ NUMBER OF SEQ ID NOS: 127806
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 67926
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: mus musculus
/ US-10-809-189-67926

Query Match
Best Local Similarity 1.3%; Score 23.4; DB 1; Length 25;
Pred. No. 2.8e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1147 CGTGGGCTTCAGCATGCTTCC 1171
Db 1 CGTGGGCTTCAGCATGCTTTC 25

RESULT 179
US-11-036-317-400602
/ Sequence 400602, Application US/11036317
/ Publication No. US20050214823A1
/ GENERAL INFORMATION:
/ APPLICANT: Williams, Alan
/ APPLICANT: Blume, John
/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
/ FILE REFERENCE: 3654.1
/ CURRENT APPLICATION NUMBER: US/11/036,317
/ CURRENT FILING DATE: 2005-01-13
/ PRIOR APPLICATION NUMBER: US 60/536,639
/ PRIOR FILING DATE: 2004-01-13
/ NUMBER OF SEQ ID NOS: 991174
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 400602
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
/ US-11-036-317-400602

Query Match
Best Local Similarity 1.3%; Score 23.4; DB 1; Length 25;
Pred. No. 2.8e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 302 AAATGCTCTTGGCAGCTGCTA 326
Db 1 AAATGCTCTTGGCAGCTGCTA 25

RESULT 180
US-11-036-317-444773
/ Sequence 444773, Application US/11036317
/ Publication No. US20050214823A1
/ GENERAL INFORMATION:
/ APPLICANT: Williams, Alan
/ APPLICANT: Blume, John
/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
/ FILE REFERENCE: 3654.1
/ CURRENT APPLICATION NUMBER: US/11/036,317
/ CURRENT FILING DATE: 2005-01-13
/ PRIOR APPLICATION NUMBER: US 60/536,639
/ PRIOR FILING DATE: 2004-01-13
/ NUMBER OF SEQ ID NOS: 991174
```

```
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 444773
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
/ US-11-036-317-444773

Query Match
Best Local Similarity 1.3%; Score 23.4; DB 1; Length 25;
Pred. No. 2.8e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1062 GCAGGTCTACTGCGCCATCATGTGG 1086
Db 1 GCAGGTCTACTGCGCCAGCATGTGG 25

RESULT 181
US-11-036-317-466837
/ Sequence 466837, Application US/11036317
/ Publication No. US20050214823A1
/ GENERAL INFORMATION:
/ APPLICANT: Williams, Alan
/ APPLICANT: Blume, John
/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
/ FILE REFERENCE: 3654.1
/ CURRENT APPLICATION NUMBER: US/11/036,317
/ CURRENT FILING DATE: 2005-01-13
/ PRIOR APPLICATION NUMBER: US 60/536,639
/ PRIOR FILING DATE: 2004-01-13
/ NUMBER OF SEQ ID NOS: 991174
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 466837
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
/ US-11-036-317-466837

Query Match
Best Local Similarity 1.3%; Score 23.4; DB 1; Length 25;
Pred. No. 2.8e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 567 TATCTACTCATGACGGCTGTGGCC 591
Db 1 TATCTACTCATGACGCTGTGGCC 25

RESULT 182
US-11-060-756-169932
/ Sequence 169932, Application US/11060756
/ Publication No. US20050221354A1
/ GENERAL INFORMATION:
/ APPLICANT: Wyeth
/ APPLICANT: Mounts, William Martin
/ TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
/ FILE REFERENCE: AM101083 (031896-042000)
/ CURRENT APPLICATION NUMBER: US/11/060,756
/ CURRENT FILING DATE: 2005-02-18
/ NUMBER OF SEQ ID NOS: 303284
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 169932
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: probe
/ US-11-060-756-169932

Query Match
Best Local Similarity 1.3%; Score 23.4; DB 1; Length 25;
Pred. No. 2.8e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1104 CATGACACCCCATCATCTACTGC 1128
Db 1 CATGACATCCCATCATCTACTGC 25
```


RESULT 183

```
US-09-930-512-4/c
; Sequence 4, Application US/09893512
; Publication No. US20030017530A1
; GENERAL INFORMATION:
; APPLICANT: OMAN, CHRISTER
; TITLE OF INVENTION: HEPHAELIX RECEPTOR AND ITS USE AS LEUKOTRIENE B4
; FILE REFERENCE: 07675.0001-03 SEQUENCE LISTING
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/061,789
; PRIOR FILING DATE: 1997-10-14
; PRIOR APPLICATION NUMBER: 60/081,958
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 09/170,069
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-930-512-4
```

Query Match

```
Best Local Similarity 1.3%; Score 23.4; DB 1; Length 29;
Matches 21; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 979 TTGGCCATTCGCTGCTGCTTCCACAT 1007
Db 29 TTCRYSTCTGCTGCTGCTTCCACAT 1
```

RESULT 184

```
US-10-799-736-4/c
; Sequence 4, Application US/10799736
; Publication No. US20050118675A1
; GENERAL INFORMATION:
; APPLICANT: OMAN, CHRISTER
; TITLE OF INVENTION: HEPHAELIX RECEPTOR AND ITS USE AS LEUKOTRIENE B4
; FILE REFERENCE: 07675.0001-03 SEQUENCE LISTING
; CURRENT FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US/10/799,736
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/061,789
; PRIOR FILING DATE: 1997-10-14
; PRIOR APPLICATION NUMBER: 60/081,958
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 09/170,069
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-799-736-4
```

Query Match

```
Best Local Similarity 1.3%; Score 23.4; DB 1; Length 29;
Matches 21; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 979 TTGGCCATTCGCTGCTGCTTCCACAT 1007
Db 29 TTCRYSTCTGCTGCTGCTTCCACAT 1
```

RESULT 185

US-10-005-956-1128/c

```
; Sequence 1128, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1128
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-005-956-1128
```

Query Match

```
Best Local Similarity 1.3%; Score 23; DB 1; Length 23;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1675 AATTAAGTTCGACGACGCTTTT 1697
Db 23 AATTAAGTTCGACGACGCTTTT 1
```

RESULT 186

```
US-10-310-914A-386270/c
; Sequence 386270, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kvuazac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 386270
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-386270
```

Query Match

```
Best Local Similarity 1.3%; Score 23; DB 1; Length 23;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1460 CCCCACCTGCTTGAACCTGCTT 1482
Db 23 CCCCACCTGCTTGAACCTGCTT 1
```

RESULT 187

```
US-10-310-914A-386274/c
; Sequence 386274, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kvuazac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
```

```

; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 386274
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-386274

Query Match      1.3%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      154 GACTCTGCTGACAGAGGGGGTTG 176
DB      23 GACTCTGCTGACAGAGGGGGTTG 1

RESULT 188
US-10-310-914A-386275/c
; Sequence 386275, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 386275
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-386275

Query Match      1.3%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      154 GACTCTGCTGACAGAGGGGGTTG 176
DB      23 GACTCTGCTGACAGAGGGGGTTG 1

RESULT 189
US-10-310-914A-386284/c
; Sequence 386284, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 386284
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-386284

Query Match      1.3%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1530 CTCACACTGGGAGCTGCAGAAAG 1552
DB      23 CTCACACTGGGAGCTGCAGAAAG 1
```

```

RESULT 190
US-10-310-914A-386298/c
; Sequence 386298, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 386298
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-386298

Query Match      1.3%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      187 GTAGCTTTACGCTAGCTTCGA 209
DB      23 GTAGCTTTACGCTAGCTTCGA 1

RESULT 191
US-09-930-503-34/c
; Sequence 34, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; FILE REFERENCE: 39245-173913
; CURRENT APPLICATION NUMBER: US/09/930,503
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 34
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-34

Query Match      1.3%; Score 23; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1105 ATGTACAAACCCCATCTACTG 1127
DB      24 ATGTACAAACCCCATCTACTG 2

RESULT 192
US-11-036-317-490648
; Sequence 490648, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
```

```
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 490648
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-490648

Query Match
Best Local Similarity 1.3%; Score 22.4; DB 1; Length 25;
Pred. No. 3.4e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 970 GTGTGACCTTGGCCATCTGCTGG 993
DB 2 GTGTGACCTTGGCCATCTGCTGG 25

RESULT 193
US-11-060-756-34830
Sequence 34830, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 34830
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-11-060-756-34830

Query Match
Best Local Similarity 1.3%; Score 22.4; DB 1; Length 25;
Pred. No. 3.4e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1102 ACCATGTACAACCCATCATCTAC 1125
DB 2 ACCATGTACAATCCCATCATCTAC 25

RESULT 194
US-10-005-956-1130/C
Sequence 1130, Application US/10005956
Publication No. US20030113726A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: D0053NP
CURRENT APPLICATION NUMBER: US/10/005,956
CURRENT FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: 60/251,015
PRIOR FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: 60/263,678
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 60/273,037
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 1579
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1130
LENGTH: 22
TYPE: DNA
ORGANISM: Homo sapiens
```

```
US-10-005-956-1130

Query Match
Best Local Similarity 1.2%; Score 22; DB 1; Length 22;
Pred. No. 3.1e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1373 CACGAGTGAAGTCCAGACCAT 1394
DB 22 CACGAGTGAAGTCCAGACCAT 1

RESULT 195
US-10-005-956-1301/C
Sequence 1301, Application US/10005956
Publication No. US20030113726A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: D0053NP
CURRENT APPLICATION NUMBER: US/10/005,956
CURRENT FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: 60/251,015
PRIOR FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: 60/263,678
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 60/273,037
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 1579
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1301
LENGTH: 22
TYPE: DNA
ORGANISM: Homo sapiens
US-10-005-956-1301

Query Match
Best Local Similarity 1.2%; Score 22; DB 1; Length 22;
Pred. No. 3.1e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 673 TGAGTCTGAGCTCTCTGCTGG 694
DB 22 TGAGTCTGAGCTCTCTGCTGG 1

RESULT 196
US-10-310-914A-386285/C
Sequence 386285, Application US/10310914A
Publication No. US2006000322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiller, Yvazac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 386285
LENGTH: 22
TYPE: RNA
ORGANISM: Human
US-10-310-914A-386285

Query Match
Best Local Similarity 1.2%; Score 22; DB 1; Length 22;
Pred. No. 3.1e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1535 ACTGGGACTTGCAAAAAGGCTC 1556
DB 22 ACTGGGACTTGCAAAAAGGCTC 1
```

```
RESULT 197
US-10-310-914A-386297/c
; Sequence 386297, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 386297
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-386297

Query Match          1.2%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      134 GCCCCAGCGCCGACCCACAGCA 155
Db      22 GCCCCAGCGCCGACCCACAGCA 1

RESULT 198
US-10-310-914A-386305/c
; Sequence 386305, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 386305
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-386305

Query Match          1.2%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1552 GGGTCAGTATGGGTAGGGAAA 1573
Db      22 GGGTCAGTATGGGTAGGGAAA 1

RESULT 199
US-10-809-189-67908
; Sequence 67908, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809.189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396.196
; PRIOR FILING DATE: 1999-09-15
```

```
; PRIOR APPLICATION NUMBER: 60/100.678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67908
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-67908

Query Match          1.2%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1051 AAGTTATCCAGCAGGCTTACC 1072
Db      4 AAGTTATCCAGCAGGCTTACC 25

RESULT 200
US-10-719-900-146775
; Sequence 146775, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719.900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427.808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 146775
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-146775

Query Match          1.2%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 3.9e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1388 AGACCATGACAGAGAGCTTCAGCTT 1412
Db      1 AGACCATGACAGAGAGCTTCAGCTT 25

RESULT 201
US-10-719-900-237660
; Sequence 237660, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719.900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427.808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 237660
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-237660

Query Match          1.2%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 3.9e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1027 ATCAACCAAGATCTCTACTGAAGA 1051
```

Db 1 ATCAACCCAGATGCTCTACCTTAAGA 25

RESULT 202

US-10-719-900-455081
; Sequence 455081, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 455081
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-455081

Query Match 1.2%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 3.9e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 910 GACCGCTACCAAGCAAGTCTCTG 934
Db 1 GACCGTTACCATGAGCAAGTCTCTG 25

RESULT 203

US-10-719-900-890394
; Sequence 890394, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 890394
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-890394

Query Match 1.2%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 3.9e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 880 TGGGCCAGTGAATCCCGGGGACT 904
Db 1 TGGGCCAGTGAATCCCGGGGACT 25

RESULT 204

US-10-809-189-67912
; Sequence 67912, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67912
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-67912

Query Match 1.2%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 3.9e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 907 TCTGACCGCTACCAAGCAAGTCT 931
Db 1 TCTGACCGTTACCATGAGCAAGTCT 25

RESULT 205

US-10-809-189-67913
; Sequence 67913, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67913
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-67913

Query Match 1.2%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 3.9e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 913 CGCTACCAAGCAAGTCTGCGCA 937
Db 1 CGTTACCATGAGCAAGTCTGCGCA 25

RESULT 206

US-11-060-756-34801
; Sequence 34801, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34801
; LENGTH: 25

TYPE: DNA
ORGANISM: probe
US-11-060-756-34801

Query Match 1.2%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 3.9e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1110 CAACCCATCATCTACTGCTGCTC 1134
DB 1 CAATCCATCATCTACTGCTGCTC 25

RESULT 207
US-11-060-756-34809

Sequence 34809, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:

APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REFERENCE: AM101083 (031896-042000)
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 34809
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-11-060-756-34809

Query Match 1.2%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 3.9e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1112 ACCCCATCATCTACTGCTGCTCAA 1136
DB 1 ATCCCATCATCTACTGCTGCTCAA 25

RESULT 208

US-11-060-756-34810
Sequence 34810, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:

APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REFERENCE: AM101083 (031896-042000)
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 34810
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-11-060-756-34810

Query Match 1.2%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 3.9e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1111 AACCCATCATCTACTGCTGCTCA 1135
DB 1 AATCCATCATCTACTGCTGCTCA 25

RESULT 209
US-11-060-756-34831

Sequence 34831, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:

APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REFERENCE: AM101083 (031896-042000)
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 34831
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-11-060-756-34831

Query Match 1.2%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 3.9e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1098 CTCACCATGTACACCCCATCATC 1122
DB 1 CTCACCATGTACATCCATCATC 25

RESULT 210
US-11-060-756-36931

Sequence 36931, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REFERENCE: AM101083 (031896-042000)
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 36931
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-11-060-756-36931

Query Match 1.2%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 3.9e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1105 ATGTACAACCCATCATCTACTGCT 1129
DB 1 ATCTACAATCCATCATCTACTGCT 25

RESULT 211
US-11-060-756-36932

Sequence 36932, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:

APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REFERENCE: AM101083 (031896-042000)
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 36932
LENGTH: 25
TYPE: DNA

ORGANISM: probe
US-11-060-756-36932

Query Match 1.2%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 3.9e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1104 CATGTACACCCCATCTCATCTACG 1128
DB 1 CATCTACATCCCATCTCATCTACG 25

RESULT 212
US-11-060-756-232071
Sequence 232071, Application US/11060756
Publication No. US20050221354A1

GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 232071
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-11-060-756-232071

Query Match 1.2%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 3.9e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1086 GCTGGCATTGAGCTCCACCATGTAC 1110
DB 1 GTTGGCATTGAGCTCTACCATGTAC 25

RESULT 213
US-11-060-756-260556
Sequence 260556, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 260556
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-11-060-756-260556

Query Match 1.2%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 3.9e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1085 GGCTGGCATTGAGCTCCACCATGT 1109
DB 1 GGCTGGCATTGAGCTCAACCATGT 25

RESULT 214
US-11-060-756-270235
Sequence 270235, Application US/11060756

Publication No. US20050221354A1
GENERAL INFORMATION:

APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 270235
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-11-060-756-270235

Query Match 1.2%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 3.9e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1094 TGAGCTCACCATTGATACACCCCAT 1118
DB 1 TGAGCTCACCATTGATACATCCCAT 25

RESULT 215
US-08-796-570A-8/c
Sequence 8, Application US/08796570A
Publication No. US20020009771A1

GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: G Protein Coupled Receptor Proteins,
TITLE OF INVENTION: Their Production And Use
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/796,570A
FILING DATE: 06-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: Japan 8-021562
FILING DATE: 2-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Eisenstein, Ronald I.
REFERENCE//DOCKET NUMBER: 30,628
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 27
TYPE: Nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Other nucleic acid Synthetic
MOLECULE TYPE: DNA
US-08-796-570A-8

Query Match 1.2%; Score 21.8; DB 1; Length 27;

Best Local Similarity 74.1%; Pred. No. 4.3e+02;
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 979 TTGGCATCTGCTGGCTGCCCTTCAC 1005
Db 27 TTGGCMTCTGCTGANTGCCYWCNAC 1

RESULT 216

US-09-929-752-6/c
; Sequence 6, Application US/09929752
; Publication No. US20030113909A1
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; Fujii, Ryo
; Kawamata, Yui
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; PRODUCTION AND USE THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/929.752
; FILING DATE: 14-Aug-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/555.905
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP 7-215798
; FILING DATE: 24-AUG-1995
; APPLICATION NUMBER: JP 6-326611
; FILING DATE: 28-DEC-1994
; APPLICATION NUMBER: JP 7-007177
; FILING DATE: 20-JAN-1995
; APPLICATION NUMBER: JP 7-057186
; FILING DATE: 16-MAR-1995
; APPLICATION NUMBER: JP 7-224544
; FILING DATE: 10-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Conlin, David G.
; REGISTRATION NUMBER: 27,026
; REFERENCE/DOCKET NUMBER: 1550/45836
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3
; OTHER INFORMATION: /product= "may be A, T, C or G"
; NAME/KEY: misc_feature
; LOCATION: 12
; OTHER INFORMATION: /product= "may be A, T, C or G"
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-929-752-6

Query Match 1.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 4.3e+02;
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 979 TTGGCATCTGCTGGCTGCCCTTCAC 1005
Db 27 TTGGCMTCTGCTGANTGCCYWCNAC 1

RESULT 217

US-10-044-592-21/c
; Sequence 21, Application US/10044592
; Publication No. US20020143152A1
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; Applicant: Fukusumi, Shoji
; TITLE OF INVENTION: Polypeptides, their Production and Use
; FILE REFERENCE: 2463US2P
; CURRENT APPLICATION NUMBER: US/10/044,592
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 09/403639
; PRIOR FILING DATE: 1999-25-10
; PRIOR APPLICATION NUMBER: PCT/JP98/01923
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: JP 9-109974
; PRIOR FILING DATE: 1997-04-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE:
; SEQ ID NO 21
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(27)
; OTHER INFORMATION: mixed synthetic primer described on pg. 95
; NAME/KEY: misc_feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: A, G, C or T
; NAME/KEY: misc_feature
; LOCATION: (12)..(12)
; OTHER INFORMATION: A, G, C or T
US-10-044-592-21

Query Match 1.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 4.3e+02;
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 979 TTGGCATCTGCTGGCTGCCCTTCAC 1005
Db 27 TTGGCMTCTGCTGANTGCCYWCNAC 1

RESULT 218

US-10-067-477-8/c
; Sequence 8, Application US/10067477
; Publication No. US20020168720A1
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: G Protein Coupled Receptor Proteins,
; TITLE OF INVENTION: Their Production And Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: dike, Bronstein, Roberts & Cushman, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/067,477
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/796,570
FILING DATE: 06-FEB-1997
APPLICATION NUMBER: Japan 8-021562
FILING DATE: 2-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Eisenstein, Ronald I.
REGISTRATION NUMBER: 30,628
REFERENCE/DOCKET NUMBER: 47147
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 27
TYPE: Nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Other nucleic acid Synthetic
US-10-067-477-8

Query Match 1.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 4.3e+02;
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 979 TTGGCATTCTGCTGCTGCCCTTCAC 1005
Db 27 TTGGCATTCTGCTGCTGCCCTTCAC 1

RESULT 219
US-10-090-569-8/c
Sequence 8, Application US/10090569
Publication No. US20030008329A1
GENERAL INFORMATION:
APPLICANT: HINUMA, Shuji
FUJII, Ryo
FUKUSUMI, Shoji
OHYAKI, Tetsuya
HOSOYA, Masaki
OHGI, Kazuhiko
ONDA, Haruo
TITLE OF INVENTION: GALANIN RECEPTOR PROTEIN, PRODUCTION AND USE THEREOF
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/090,569
FILING DATE: 04-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/540,650
FILING DATE: 11-OCT-1995
APPLICATION NUMBER: 7-134412
FILING DATE: 31-MAY-1995
APPLICATION NUMBER: 6-326610

FILING DATE: 28-DEC-1994
APPLICATION NUMBER: 6-247599
FILING DATE: 13-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45901
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 27
TYPE: Nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Other nucleic acid Synthetic DNA
OTHER INFORMATION: N is A, G, C, or T
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-090-569-8

Query Match 1.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 4.3e+02;
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 979 TTGGCATTCTGCTGCTGCCCTTCAC 1005
Db 27 TTGGCATTCTGCTGCTGCCCTTCAC 1

RESULT 220
US-10-184-722-6/c
Sequence 6, Application US/10184722
Publication No. US20030092618A1
GENERAL INFORMATION:
APPLICANT: HINUMA, SHUJI
TANEMOTO, KAZUHIKO
APPLICANT: HOSOYA, MASAKI
APPLICANT: HABATA, YUGO
APPLICANT: FUJII, RYO
APPLICANT: KITADA, CHIEKO
TITLE OF INVENTION: POLYPEPTIDES, THEIR PRODUCTION AND USE
FILE REFERENCE: 48970(342)
CURRENT APPLICATION NUMBER: US/10/184,722
CURRENT FILING DATE: 2002-06-27
PRIOR APPLICATION NUMBER: US/09/255,518
PRIOR FILING DATE: 1999-02-22
PRIOR APPLICATION NUMBER: PCT/JP98/05805
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 9-353955
PRIOR FILING DATE: 1997-12-24
PRIOR APPLICATION NUMBER: 10-032577
PRIOR FILING DATE: 1998-02-16
PRIOR APPLICATION NUMBER: 10-220853
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 10-271645
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 27
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
NAME/KEY: modified base
LOCATION: (1)..(27)
OTHER INFORMATION: "n" may be a, t, c, g
US-10-184-722-6

Query Match 1.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 4.3e+02;

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 27
TYPE: Nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
FEATURE:
OTHER INFORMATION: /note = "N is A, G, C, or T; w is A or T;
R is A or G; K is G or T."
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-278-087A-2

Query Match 1.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 4.3e+02;
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 979 TTGGCATTGCTGGTGGCTTCCAC 1005
DB 27 TTGGCATTGCTGGTGGCTTCCAC 1

RESULT 223
US-11-054-211-30/C
Sequence 30, Application US/11054211
Publication No. US20050170461A1
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
Fuji, Ryo
Fukusumi, Shoji
Kikada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESSES:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: PatsEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/054, 211
FILING DATE: 08-Feb-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/716, 147
FILING DATE: 17-Nov-2000
APPLICATION NUMBER: US/08/776, 971
FILING DATE: 06-Feb-1997
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-Dec-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-Dec-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-Mar-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-Aug-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-11-054-211-30

Query Match 1.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 4.3e+02;
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 979 TTGGCATTGCTGGTGGCTTCCAC 1005
DB 27 TTGGCATTGCTGGTGGCTTCCAC 1

RESULT 224
US-11-060-756-34818
Sequence 34818, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:
APPLICANT: Wyeth
Mounie, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REFERENCE: AM101083 (031896-042000)
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 34818
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-11-060-756-34818

Query Match 1.2%; Score 21.4; DB 1; Length 25;
Best Local Similarity 95.7%; Pred. No. 4.2e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1114 CCCATCATCTACTGCTGCTCAA 1136
DB 2 CCCATCATCTACTGCTGCTCAA 24

RESULT 225
US-09-930-503-23
Sequence 23, Application US/09930503
Publication No. US20030060438A1
GENERAL INFORMATION:
APPLICANT: HENRY, JAMES
CAHILL, CATHERINE
APPLICANT: YASHPAL, KIRAN
TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
TITLE OF INVENTION: THERAPEUTIC USES THEREOF
FILE REFERENCE: 39245-173913
CURRENT APPLICATION NUMBER: US/09/930, 503
CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 60/226,086
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 23
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-23

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 956 TGATGATTGCTGGTGTGCA 976
|||||
DB 1 TGATGATTGCTGGTGTGCA 21

RESULT 226
US-09-930-503-24

Sequence 24, Application US/09930503
Publication No. US20030060438A1
GENERAL INFORMATION:
APPLICANT: HENRY, JAMES
APPLICANT: CAHILL, CATHERINE
APPLICANT: YASHPAL, KIRAN
TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
TITLE OF INVENTION: THERAPEUTIC USES THEREOF
FILE REFERENCE: 39245-173913
CURRENT APPLICATION NUMBER: US/09/930,503
CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 60/226,086
PRIOR FILING DATE: 2000-08-18
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 24
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-24

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 924 GCAAGTCTCTGCCAGCGCAA 944
|||||
DB 1 GCAAGTCTCTGCCAGCGCAA 21

RESULT 227

US-09-930-503-26/c
Sequence 26, Application US/09930503
Publication No. US20030060438A1
GENERAL INFORMATION:
APPLICANT: HENRY, JAMES
APPLICANT: CAHILL, CATHERINE
APPLICANT: YASHPAL, KIRAN
TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
TITLE OF INVENTION: THERAPEUTIC USES THEREOF
FILE REFERENCE: 39245-173913
CURRENT APPLICATION NUMBER: US/09/930,503
CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 60/226,086
PRIOR FILING DATE: 2000-08-18
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 26
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-26

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 956 TGATGATTGCTGGTGTGCA 976
|||||
DB 21 TGATGATTGCTGGTGTGCA 1

RESULT 228
US-09-930-503-28/c

Sequence 28, Application US/09930503
Publication No. US20030060438A1
GENERAL INFORMATION:
APPLICANT: HENRY, JAMES
APPLICANT: CAHILL, CATHERINE
APPLICANT: YASHPAL, KIRAN
TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
TITLE OF INVENTION: THERAPEUTIC USES THEREOF
FILE REFERENCE: 39245-173913
CURRENT APPLICATION NUMBER: US/09/930,503
CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 60/226,086
PRIOR FILING DATE: 2000-08-18
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-28

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 836 TGCTGTGATTTGGCTATGAT 856
|||||
DB 21 TGCTGTGATTTGGCTATGAT 1

RESULT 229
US-09-930-503-31/c
Sequence 31, Application US/09930503
Publication No. US20030060438A1
GENERAL INFORMATION:
APPLICANT: HENRY, JAMES
APPLICANT: CAHILL, CATHERINE
APPLICANT: YASHPAL, KIRAN
TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
TITLE OF INVENTION: THERAPEUTIC USES THEREOF
FILE REFERENCE: 39245-173913
CURRENT APPLICATION NUMBER: US/09/930,503
CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 60/226,086
PRIOR FILING DATE: 2000-08-18
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 31
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-31

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 559 TTGGCCAGTATCTACTCATG 579
|||||
DB 21 TTGGCCAGTATCTACTCATG 1

```
RESULT 230
US-09-930-503-33/c
; Sequence 33, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; FILE REFERENCE: 39245-173913
; CURRENT APPLICATION NUMBER: US/09/930,503
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-33

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1567 AGGAAACATTCATCCTTG 1587
Db      21  AGGAAACATTCATCCTTG 1

RESULT 231
US-09-930-503-38/c
; Sequence 38, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; FILE REFERENCE: 39245-173913
; CURRENT APPLICATION NUMBER: US/09/930,503
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-38

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1567 AGGAAACATTCATCCTTG 1587
Db      21  AGGAAACATTCATCCTTG 1

RESULT 232
US-09-930-503-40
; Sequence 40, Application US/09930503
```

```
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; FILE REFERENCE: 39245-173913
; CURRENT APPLICATION NUMBER: US/09/930,503
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-40

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      205 TTGGAATGATTAACGTCCTC 225
Db      1  TTGGAATGATTAACGTCCTC 21

RESULT 233
US-09-930-503-42/c
; Sequence 42, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; FILE REFERENCE: 39245-173913
; CURRENT APPLICATION NUMBER: US/09/930,503
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-42

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      956 TGATGATTCGCGGTGTGCA 976
Db      21  TGATGATTCGCGGTGTGCA 1

RESULT 234
US-09-930-503-43/c
; Sequence 43, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
```

```
/ TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
/ FILE OF INVENTION: THERAPEUTIC USES THEREOF
/ FILE REFERENCE: 39245-173913
/ CURRENT APPLICATION NUMBER: US/09/930,503
/ CURRENT FILING DATE: 2001-08-16
/ PRIOR APPLICATION NUMBER: 60/226,086
/ PRIOR FILING DATE: 2000-08-18
/ NUMBER OF SEQ ID NOS: 59
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 43
/ LENGTH: 21
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-43

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      924 GCAAGTCTCTGCCAAGCCCA 944
Db      21 GCAAGTCTCTGCCAAGCCCA 1

RESULT 235
US-09-930-503-45
/ Sequence 45, Application US/09930503
/ Publication No. US20030060438A1
/ GENERAL INFORMATION:
/ APPLICANT: HENRY, JAMES
/ APPLICANT: CAHILL, CATHERINE
/ APPLICANT: YASHPAL, KIRAN
/ TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
/ FILE OF INVENTION: THERAPEUTIC USES THEREOF
/ FILE REFERENCE: 39245-173913
/ CURRENT APPLICATION NUMBER: US/09/930,503
/ CURRENT FILING DATE: 2001-08-16
/ PRIOR APPLICATION NUMBER: 60/226,086
/ PRIOR FILING DATE: 2000-08-18
/ NUMBER OF SEQ ID NOS: 59
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 45
/ LENGTH: 21
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-45

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      956 TGATGATTTGCTGCGTGTGCA 976
Db      1 TGATGATTTGCTGCGTGTGCA 21

RESULT 236
US-09-930-503-47
/ Sequence 47, Application US/09930503
/ Publication No. US20030060438A1
/ GENERAL INFORMATION:
/ APPLICANT: HENRY, JAMES
/ APPLICANT: CAHILL, CATHERINE
/ APPLICANT: YASHPAL, KIRAN
/ TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
/ FILE OF INVENTION: THERAPEUTIC USES THEREOF
/ FILE REFERENCE: 39245-173913
/ CURRENT APPLICATION NUMBER: US/09/930,503
/ CURRENT FILING DATE: 2001-08-16
```

```
/ PRIOR APPLICATION NUMBER: 60/226,086
/ PRIOR FILING DATE: 2000-08-18
/ NUMBER OF SEQ ID NOS: 59
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 47
/ LENGTH: 21
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-47

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      836 TGCTGTGATTTGCTATGTCAT 856
Db      1 TGCTGTGATTTGCTATGTCAT 21

RESULT 237
US-09-930-503-50
/ Sequence 50, Application US/09930503
/ Publication No. US20030060438A1
/ GENERAL INFORMATION:
/ APPLICANT: HENRY, JAMES
/ APPLICANT: CAHILL, CATHERINE
/ APPLICANT: YASHPAL, KIRAN
/ TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
/ FILE OF INVENTION: THERAPEUTIC USES THEREOF
/ FILE REFERENCE: 39245-173913
/ CURRENT APPLICATION NUMBER: US/09/930,503
/ CURRENT FILING DATE: 2001-08-16
/ PRIOR APPLICATION NUMBER: 60/226,086
/ PRIOR FILING DATE: 2000-08-18
/ NUMBER OF SEQ ID NOS: 59
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 50
/ LENGTH: 21
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-50

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      559 TTCGCAGTATCTACTCATG 579
Db      1 TTCGCAGTATCTACTCATG 21

RESULT 238
US-09-930-503-52
/ Sequence 52, Application US/09930503
/ Publication No. US20030060438A1
/ GENERAL INFORMATION:
/ APPLICANT: HENRY, JAMES
/ APPLICANT: CAHILL, CATHERINE
/ APPLICANT: YASHPAL, KIRAN
/ TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
/ FILE OF INVENTION: THERAPEUTIC USES THEREOF
/ FILE REFERENCE: 39245-173913
/ CURRENT APPLICATION NUMBER: US/09/930,503
/ CURRENT FILING DATE: 2001-08-16
/ PRIOR APPLICATION NUMBER: 60/226,086
/ PRIOR FILING DATE: 2000-08-18
/ NUMBER OF SEQ ID NOS: 59
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 52
```

LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-52

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1051 AGTTATCCAGCGGTCTAC 1071
1 AAGTTATCCAGCGGTCTAC 21

RESULT 239
US-09-930-503-53
Sequence 53, Application US/09930503
Publication No. US20030060438A1
GENERAL INFORMATION:
APPLICANT: HENRY, JAMES
APPLICANT: CAHILL, CATHERINE
APPLICANT: YASHPAL, KIRAN
TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
FILE REFERENCE: 39245-173913
CURRENT APPLICATION NUMBER: US/09/930,503
CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 60/226,086
PRIOR FILING DATE: 2000-08-18
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 53
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-53

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1105 ATGTACAACCCATCATCTAC 1125
1 ATGTACAACCCATCATCTAC 21

RESULT 240
US-09-930-503-57
Sequence 57, Application US/09930503
Publication No. US20030060438A1
GENERAL INFORMATION:
APPLICANT: HENRY, JAMES
APPLICANT: CAHILL, CATHERINE
APPLICANT: YASHPAL, KIRAN
TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
FILE REFERENCE: 39245-173913
CURRENT APPLICATION NUMBER: US/09/930,503
CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 60/226,086
PRIOR FILING DATE: 2000-08-18
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 57
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer

US-09-930-503-57

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1567 AGGAAAACATTCATCTTG 1587
1 AGGAAAACATTCATCTTG 21

RESULT 241
US-09-930-503-59/C
Sequence 59, Application US/09930503
Publication No. US20030060438A1
GENERAL INFORMATION:
APPLICANT: HENRY, JAMES
APPLICANT: CAHILL, CATHERINE
APPLICANT: YASHPAL, KIRAN
TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
FILE REFERENCE: 39245-173913
CURRENT APPLICATION NUMBER: US/09/930,503
CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 60/226,086
PRIOR FILING DATE: 2000-08-18
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 59
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-59

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 205 TTGGAATGATTAAGTCTTC 225
1 TTGGAATGATTAAGTCTTC 1

RESULT 242
US-10-005-956-347/C
Sequence 347, Application US/10005956
Publication No. US20030113726A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: D0053NP
CURRENT APPLICATION NUMBER: US/10/005,956
CURRENT FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: 60/251,015
PRIOR FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: 60/263,678
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 60/273,037
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 1579
SOFTWARE: PatentIn version 3.0
SEQ ID NO 347
LENGTH: 21
TYPE: DNA
ORGANISM: homo sapiens
US-10-005-956-347

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1545 GCAAAAAGGTCAGTANGGT 1565
 Db 21 GCAAAAAGGTCAGTANGGT 1

RESULT 243
 US-10-005-956-404
 ; Sequence 404, Application US/10005956
 ; Publication No. US20030113726A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
 ; FILE REFERENCE: D0053NP
 ; CURRENT APPLICATION NUMBER: US/10/005,956
 ; PRIOR FILING DATE: 2001-12-03
 ; PRIOR APPLICATION NUMBER: 60/251,015
 ; PRIOR FILING DATE: 2000-12-04
 ; PRIOR APPLICATION NUMBER: 60/263,678
 ; PRIOR FILING DATE: 2001-01-23
 ; PRIOR APPLICATION NUMBER: 60/273,037
 ; PRIOR FILING DATE: 2001-03-02
 ; NUMBER OF SEQ ID NOS: 1579
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 404
 ; LENGTH: 21
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 US-10-005-956-404

Query Match 1.2%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 CATCTCCACTAACAACCTCGGA 272
 Db 1 CATCTCCACTAACAACCTCGGA 21

RESULT 244
 US-10-005-956-407
 ; Sequence 407, Application US/10005956
 ; Publication No. US20030113726A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
 ; FILE REFERENCE: D0053NP
 ; CURRENT APPLICATION NUMBER: US/10/005,956
 ; PRIOR FILING DATE: 2001-12-03
 ; PRIOR APPLICATION NUMBER: 60/251,015
 ; PRIOR FILING DATE: 2000-12-04
 ; PRIOR APPLICATION NUMBER: 60/263,678
 ; PRIOR FILING DATE: 2001-01-23
 ; PRIOR APPLICATION NUMBER: 60/273,037
 ; PRIOR FILING DATE: 2001-03-02
 ; NUMBER OF SEQ ID NOS: 1579
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 407
 ; LENGTH: 21
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 US-10-005-956-407

Query Match 1.2%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1360 TCCAACTGCTCTTCACGAGT 1380
 Db 1 TCCAACTGCTCTTCACGAGT 21

RESULT 245
 US-10-005-956-408

; Sequence 408, Application US/10005956
 ; Publication No. US20030113726A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
 ; FILE REFERENCE: D0053NP
 ; CURRENT APPLICATION NUMBER: US/10/005,956
 ; PRIOR FILING DATE: 2001-12-03
 ; PRIOR APPLICATION NUMBER: 60/251,015
 ; PRIOR FILING DATE: 2000-12-04
 ; PRIOR APPLICATION NUMBER: 60/263,678
 ; PRIOR FILING DATE: 2001-01-23
 ; PRIOR APPLICATION NUMBER: 60/273,037
 ; PRIOR FILING DATE: 2001-03-02
 ; NUMBER OF SEQ ID NOS: 1579
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 408
 ; LENGTH: 21
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 US-10-005-956-408

Query Match 1.2%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1360 TCCAACTGCTCTTCACGAGT 1380
 Db 1 TCCAACTGCTCTTCACGAGT 21

RESULT 246
 US-10-005-956-409
 ; Sequence 409, Application US/10005956
 ; Publication No. US20030113726A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
 ; FILE REFERENCE: D0053NP
 ; CURRENT APPLICATION NUMBER: US/10/005,956
 ; PRIOR FILING DATE: 2001-12-03
 ; PRIOR APPLICATION NUMBER: 60/251,015
 ; PRIOR FILING DATE: 2000-12-04
 ; PRIOR APPLICATION NUMBER: 60/263,678
 ; PRIOR FILING DATE: 2001-01-23
 ; PRIOR APPLICATION NUMBER: 60/273,037
 ; PRIOR FILING DATE: 2001-03-02
 ; NUMBER OF SEQ ID NOS: 1579
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 409
 ; LENGTH: 21
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 US-10-005-956-409

Query Match 1.2%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1360 TCCAACTGCTCTTCACGAGT 1380
 Db 1 TCCAACTGCTCTTCACGAGT 21

RESULT 247
 US-10-005-956-467/c
 ; Sequence 467, Application US/10005956
 ; Publication No. US20030113726A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
 ; FILE REFERENCE: D0053NP
 ; CURRENT APPLICATION NUMBER: US/10/005,956

CURRENT FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: 60/251,015
PRIOR FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: 60/263,678
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 60/273,037
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 1579
SOFTWARE: PatentIn version 3.0
SEQ ID NO 467
LENGTH: 21
TYPE: DNA
ORGANISM: homo sapiens
US-10-005-956-467

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 372 GTGATCATCTTAGCCACAA 392
Db 21 GTGATCATCTTAGCCACAA 1

RESULT 248
US-10-005-956-473/C
Sequence 473, Application US/10005956
Publication No. US20030113726A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: D0053NP
CURRENT APPLICATION NUMBER: US/10/005,956
CURRENT FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: 60/251,015
PRIOR FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: 60/263,678
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 60/273,037
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 1579
SOFTWARE: PatentIn version 3.0
SEQ ID NO 473
LENGTH: 21
TYPE: DNA
ORGANISM: homo sapiens
US-10-005-956-473

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1499 ATTCCTTCATCTGGAACAT 1519
Db 21 ATTCCTTCATCTGGAACAT 1

RESULT 249
US-10-005-956-533
Sequence 533, Application US/10005956
Publication No. US20030113726A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: D0053NP
CURRENT APPLICATION NUMBER: US/10/005,956
CURRENT FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: 60/251,015
PRIOR FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: 60/263,678
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 60/273,037
PRIOR FILING DATE: 2001-03-02

NUMBER OF SEQ ID NOS: 1579
SOFTWARE: PatentIn version 3.0
SEQ ID NO 533
LENGTH: 21
TYPE: DNA
ORGANISM: homo sapiens
US-10-005-956-533

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1399 GAGAGCTTCAGCTTCCTCC 1419
Db 1 GAGAGCTTCAGCTTCCTCC 21

RESULT 250
US-10-005-956-534
Sequence 534, Application US/10005956
Publication No. US20030113726A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: D0053NP
CURRENT APPLICATION NUMBER: US/10/005,956
CURRENT FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: 60/251,015
PRIOR FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: 60/263,678
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 60/273,037
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 1579
SOFTWARE: PatentIn version 3.0
SEQ ID NO 534
LENGTH: 21
TYPE: DNA
ORGANISM: homo sapiens
US-10-005-956-534

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1399 GAGAGCTTCAGCTTCCTCC 1419
Db 1 GAGAGCTTCAGCTTCCTCC 21

RESULT 251
US-10-005-956-535
Sequence 535, Application US/10005956
Publication No. US20030113726A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: D0053NP
CURRENT APPLICATION NUMBER: US/10/005,956
CURRENT FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: 60/251,015
PRIOR FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: 60/263,678
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 60/273,037
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 1579
SOFTWARE: PatentIn version 3.0
SEQ ID NO 535
LENGTH: 21
TYPE: DNA
ORGANISM: homo sapiens
US-10-005-956-535

Query Match 1.2%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1399 GAGAGCTTCAGCTTCCTCC 1419
 |||||
 Db 1 GAGAGCTTCAGCTTCCTCC 21

RESULT 252
 US-10-005-956-1212
 ; Sequence 1212, Application US/10005956
 ; Publication No. US20030113726A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
 ; FILE REFERENCE: D0053NP
 ; CURRENT APPLICATION NUMBER: US/10/005,956
 ; PRIOR FILING DATE: 2001-12-03
 ; PRIOR APPLICATION NUMBER: 60/251,015
 ; PRIOR FILING DATE: 2000-12-04
 ; PRIOR APPLICATION NUMBER: 60/263,678
 ; PRIOR FILING DATE: 2001-01-23
 ; PRIOR APPLICATION NUMBER: 60/273,037
 ; PRIOR FILING DATE: 2001-03-02
 ; NUMBER OF SEQ ID NOS: 1579
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1212
 ; LENGTH: 21
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-005-956-1212

Query Match 1.2%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 493 CACAACGATGGTACTACGGC 513
 |||||
 Db 1 CACAACGATGGTACTACGGC 21

RESULT 253
 US-10-005-956-1217
 ; Sequence 1217, Application US/10005956
 ; Publication No. US20030113726A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
 ; FILE REFERENCE: D0053NP
 ; CURRENT APPLICATION NUMBER: US/10/005,956
 ; PRIOR FILING DATE: 2001-12-03
 ; PRIOR APPLICATION NUMBER: 60/251,015
 ; PRIOR FILING DATE: 2000-12-04
 ; PRIOR APPLICATION NUMBER: 60/263,678
 ; PRIOR FILING DATE: 2001-01-23
 ; PRIOR APPLICATION NUMBER: 60/273,037
 ; PRIOR FILING DATE: 2001-03-02
 ; NUMBER OF SEQ ID NOS: 1579
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1217
 ; LENGTH: 21
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-005-956-1217

Query Match 1.2%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1492 CATGGAATTCCTTCATCTG 1512
 |||||

Db 1 CATGGAATTCCTTCATCTG 21

RESULT 254
 US-10-310-914A-386280/c
 ; Sequence 386280, Application US/10310914A
 ; Publication No. US20060003322A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentwaych, Isaac
 ; APPLICANT: Shiller, Kuzat
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 ; FILE REFERENCE: 06087.0200.CPUS01
 ; CURRENT APPLICATION NUMBER: US/10/310,914A
 ; CURRENT FILING DATE: 2002-12-06
 ; NUMBER OF SEQ ID NOS: 1388402
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 386280
 ; LENGTH: 21
 ; TYPE: RNA
 ; ORGANISM: Human
 US-10-310-914A-386280

Query Match 1.2%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 GCCCCAGGCGCCGACGACGAG 154
 |||||
 Db 21 GCCCCAGGCGCCGACGACGAG 1

RESULT 255
 US-10-310-914A-386281/c
 ; Sequence 386281, Application US/10310914A
 ; Publication No. US20060003322A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentwaych, Isaac
 ; APPLICANT: Shiller, Kuzat
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 ; FILE REFERENCE: 06087.0200.CPUS01
 ; CURRENT APPLICATION NUMBER: US/10/310,914A
 ; CURRENT FILING DATE: 2002-12-06
 ; NUMBER OF SEQ ID NOS: 1388402
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 386281
 ; LENGTH: 21
 ; TYPE: RNA
 ; ORGANISM: Human
 US-10-310-914A-386281

Query Match 1.2%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1730 GTGACTTGGCTGCATGCGAG 1750
 |||||
 Db 21 GTGACTTGGCTGCATGCGAG 1

RESULT 256
 US-10-310-914A-386282/c
 ; Sequence 386282, Application US/10310914A
 ; Publication No. US20060003322A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentwaych, Isaac
 ; APPLICANT: Shiller, Kuzat
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 ; FILE REFERENCE: 06087.0200.CPUS01
 ; CURRENT APPLICATION NUMBER: US/10/310,914A
 ; CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO: 386282
LENGTH: 21
TYPE: RNA
ORGANISM: Human
US-10-310-914A-386282

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1439 CAGGCGCTTTGGCAGTGCAG 1459
Db 21 CAGGCGCTTTGGCAGTGCAG 1

RESULT 257
US-10-310-914A-386299/C
Sequence 386299, Application US/10310914A
Publication No. US2006003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shlier, Kuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087,0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO: 386299
LENGTH: 21
TYPE: RNA
ORGANISM: Human
US-10-310-914A-386299

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1682 GGTGCGACGAGCTTTCTCTCA 1702
Db 21 GGTGCGACGAGCTTTCTCTCA 1

RESULT 258
US-11-127-877-430
Sequence 430, Application US/11127877
Publication No. US20050287565A1
GENERAL INFORMATION:
APPLICANT: Merchiers, Pascal G.
APPLICANT: Hoffmann, Marcel
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
TITLE OF INVENTION: Amyloid-Beta Protein Production
FILE REFERENCE: P27,800-B USA
CURRENT APPLICATION NUMBER: US/11/127,877
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: 60/570,352
PRIOR FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: 60/603,948
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 590
SOFTWARE: PatentIn version 3.3
SEQ ID NO: 430
LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens
US-11-127-877-430

Query Match 1.2%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 290 AACCGCCTGGCAATTGTCC 310
Db 1 AACCGCCTGGCAATTGTCC 21

RESULT 259
US-11-127-877-431
Sequence 431, Application US/11127877
Publication No. US20050287565A1
GENERAL INFORMATION:
APPLICANT: Merchiers, Pascal G.
APPLICANT: Hoffmann, Marcel
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
TITLE OF INVENTION: Amyloid-Beta Protein Production
FILE REFERENCE: P27,800-B USA
CURRENT APPLICATION NUMBER: US/11/127,877
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: 60/570,352
PRIOR FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: 60/603,948
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 590
SOFTWARE: PatentIn version 3.3
SEQ ID NO: 431
LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens
US-11-127-877-431

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 303 AATTGTCCTTTGGGCGAGCTGC 323
Db 1 AATTGTCCTTTGGGCGAGCTGC 21

RESULT 260
US-11-127-877-432
Sequence 432, Application US/11127877
Publication No. US20050287565A1
GENERAL INFORMATION:
APPLICANT: Merchiers, Pascal G.
APPLICANT: Hoffmann, Marcel
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
TITLE OF INVENTION: Amyloid-Beta Protein Production
FILE REFERENCE: P27,800-B USA
CURRENT APPLICATION NUMBER: US/11/127,877
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: 60/570,352
PRIOR FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: 60/570,352
PRIOR FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: 60/603,948
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 590
SOFTWARE: PatentIn version 3.3
SEQ ID NO: 432
LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens
US-11-127-877-432

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 AACGTGTAGTGTGATC 378
|||||
Db 1 AACGTGTAGTGTGATC 21

RESULT 261
US-11-127-877-433
; Sequence 433, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27, 800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 433
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-433

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 AATACAGTGTGACTTCACC 483
|||||
Db 1 AATACAGTGTGACTTCACC 21

RESULT 262
US-11-127-877-434
; Sequence 434, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27, 800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 434
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-434

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 475 AACTTCACTATGCTGCCAC 495
|||||
Db 1 AACTTCACTATGCTGCCAC 21

RESULT 263
US-11-127-877-435
; Sequence 435, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27, 800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 435
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-435

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 494 ACAACGAATGTAACGGCC 514
|||||
Db 1 ACAACGAATGTAACGGCC 21

RESULT 264
US-11-127-877-436
; Sequence 436, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27, 800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 436
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-436

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 526 AAGTCCACAACCTTCTCC 546
|||||
Db 1 AAGTCCACAACCTTCTCC 21

RESULT 265

```
US-11-127-877-437
; Sequence 437, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Merckers, Pascal G.
; APPLICANT: Spittaels, Koentraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27, 800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 437
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-437

Query Match      1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      643 ACAGCCACCAAGTGTGTCATC 663
Db      1 ACAGCCACCAAGTGTGTCATC 21

RESULT 266
US-11-127-877-438
; Sequence 438, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merckers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koentraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27, 800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 438
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-438

Query Match      1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      649 ACCAAGTGTGTCATCTGTGTC 669
Db      1 ACCAAGTGTGTCATCTGTGTC 21

RESULT 267
US-11-127-877-439
; Sequence 439, Application US/11127877
; Publication No. US20050287565A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Merckers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koentraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27, 800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 439
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-439

Query Match      1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      652 AAAGTGTGTCATCTGTGTCATC 672
Db      1 AAAGTGTGTCATCTGTGTCATC 21

RESULT 268
US-11-127-877-440
; Sequence 440, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merckers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koentraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27, 800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 440
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-440

Query Match      1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      713 ACTCAACCAAGACGACATGTC 733
Db      1 ACTCAACCAAGACGACATGTC 21

RESULT 269
US-11-127-877-441
; Sequence 441, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merckers, Pascal G.
; APPLICANT: Hoffmann, Marcel
```

```
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: 60/603,948
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 441
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-441
```

```
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 797 ACCGATCTGTGTGACGTGCG 817
Db 1 ACCGATCTGTGTGACGTGCG 21
```

```
RESULT 270
US-11-127-877-442
; Sequence 442, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann, Pascal G.
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: 60/603,948
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 442
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-442
```

```
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 811 ACTGTGCTGATCTACTTCTCTC 831
Db 1 ACTGTGCTGATCTACTTCTCTC 21
```

```
RESULT 271
US-11-127-877-443
; Sequence 443, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merckers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
```

```
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT FILING DATE: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 443
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-443
```

```
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 857 ACACCGTAGTGGGATCAGCAGC 877
Db 1 ACACCGTAGTGGGATCAGCAGC 21
```

```
RESULT 272
US-11-127-877-444
; Sequence 444, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merckers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: 60/603,948
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 444
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-444
```

```
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 874 ACACATATGGGCGCAGTGAGATC 894
Db 1 ACACATATGGGCGCAGTGAGATC 21
```

```
RESULT 273
US-11-127-877-445
; Sequence 445, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merckers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
```

;; CURRENT FILING DATE: 2005-05-12
;; PRIOR APPLICATION NUMBER: 60/570,352
;; PRIOR FILING DATE: 2004-05-12
;; PRIOR APPLICATION NUMBER: 60/603,948
;; PRIOR FILING DATE: 2004-08-24
;; NUMBER OF SEQ ID NOS: 590
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 445
;; LENGTH: 21
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-11-127-877-445

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 876 ACTATGGGCGCAGTGGATCCC 896
Db 1 ACTATGGGCGCAGTGGATCCC 21

RESULT 274
US-11-127-877-446
;; Sequence 446, Application US/11127877
;; Publication No. US20050287565A1
;; GENERAL INFORMATION:
;; APPLICANT: Merchiers, Pascal G.
;; APPLICANT: Hoffmann, Marcel
;; APPLICANT: Spittaels, Koenraad F. F.
;; APPLICANT: Laenen, Wendy
;; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
;; TITLE OF INVENTION: Amyloid-Beta Protein Production
;; FILE REFERENCE: P27, 800-B USA
;; CURRENT FILING DATE: 2005-05-12
;; PRIOR APPLICATION NUMBER: US/11/127,877
;; PRIOR FILING DATE: 2004-05-12
;; PRIOR APPLICATION NUMBER: 60/570,352
;; PRIOR FILING DATE: 2004-08-24
;; PRIOR APPLICATION NUMBER: 60/603,948
;; NUMBER OF SEQ ID NOS: 590
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 446
;; LENGTH: 21
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-11-127-877-446

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 920 ACGAGCAAGTCTGCGCAGC 940
Db 1 ACGAGCAAGTCTGCGCAGC 21

RESULT 275
US-11-127-877-447
;; Sequence 447, Application US/11127877
;; Publication No. US20050287565A1
;; GENERAL INFORMATION:
;; APPLICANT: Merchiers, Pascal G.
;; APPLICANT: Hoffmann, Marcel
;; APPLICANT: Spittaels, Koenraad F. F.
;; APPLICANT: Laenen, Wendy
;; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
;; TITLE OF INVENTION: Amyloid-Beta Protein Production
;; FILE REFERENCE: P27, 800-B USA
;; CURRENT FILING DATE: 2005-05-12
;; PRIOR APPLICATION NUMBER: US/11/127,877
;; PRIOR FILING DATE: 2004-05-12
;; PRIOR APPLICATION NUMBER: 60/570,352
;; PRIOR FILING DATE: 2004-05-12

;; PRIOR APPLICATION NUMBER: 60/603,948
;; PRIOR FILING DATE: 2004-08-24
;; NUMBER OF SEQ ID NOS: 590
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 447
;; LENGTH: 21
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-11-127-877-447

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1025 ACATCAACCCAGATCTCTACC 1045
Db 1 ACATCAACCCAGATCTCTACC 21

RESULT 276
US-11-127-877-448
;; Sequence 448, Application US/11127877
;; Publication No. US20050287565A1
;; GENERAL INFORMATION:
;; APPLICANT: Merchiers, Pascal G.
;; APPLICANT: Hoffmann, Marcel
;; APPLICANT: Spittaels, Koenraad F. F.
;; APPLICANT: Laenen, Wendy
;; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
;; TITLE OF INVENTION: Amyloid-Beta Protein Production
;; FILE REFERENCE: P27, 800-B USA
;; CURRENT FILING DATE: 2005-05-12
;; PRIOR APPLICATION NUMBER: US/11/127,877
;; PRIOR FILING DATE: 2004-05-12
;; PRIOR APPLICATION NUMBER: 60/570,352
;; PRIOR FILING DATE: 2004-08-24
;; PRIOR APPLICATION NUMBER: 60/603,948
;; NUMBER OF SEQ ID NOS: 590
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 448
;; LENGTH: 21
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-11-127-877-448

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1043 ACCTGAAGAGTTTATCCAGC 1063
Db 1 ACCTGAAGAGTTTATCCAGC 21

RESULT 277
US-11-127-877-449
;; Sequence 449, Application US/11127877
;; Publication No. US20050287565A1
;; GENERAL INFORMATION:
;; APPLICANT: Merchiers, Pascal G.
;; APPLICANT: Hoffmann, Marcel
;; APPLICANT: Spittaels, Koenraad F. F.
;; APPLICANT: Laenen, Wendy
;; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
;; TITLE OF INVENTION: Amyloid-Beta Protein Production
;; FILE REFERENCE: P27, 800-B USA
;; CURRENT FILING DATE: 2005-05-12
;; PRIOR APPLICATION NUMBER: US/11/127,877
;; PRIOR FILING DATE: 2004-05-12
;; PRIOR APPLICATION NUMBER: 60/570,352
;; PRIOR FILING DATE: 2004-08-24
;; PRIOR APPLICATION NUMBER: 60/603,948
;; PRIOR FILING DATE: 2004-05-12
;; NUMBER OF SEQ ID NOS: 590

```
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 449
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-449

Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1048 AAGAAGTTATCCAGCAGGTC 1068
Db 1 AAGAAGTTATCCAGCAGGTC 21

RESULT 278
US-11-127-877-450
; Sequence 450, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27, 800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 450
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-450

Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1051 AAGTTATCCAGCAGGTCCTAC 1071
Db 1 AAGTTATCCAGCAGGTCCTAC 21

RESULT 279
US-11-127-877-451
; Sequence 451, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27, 800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 451
; LENGTH: 21
```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-451

Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1135 AATGACAGGTTCCGTCGTGGGC 1155
Db 1 AATGACAGGTTCCGTCGTGGGC 21

RESULT 280
US-11-127-877-452
; Sequence 452, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27, 800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 452
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-452

Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1214 AATGAATCCACCCGGTATC 1234
Db 1 AATGAATCCACCCGGTATC 21

RESULT 281
US-11-127-877-453
; Sequence 453, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27, 800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 453
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-453
```


Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1363 AACTGCTCTTCACGAGATGAC 1363
Db 1 AACTGCTCTTCACGAGATGAC 21

RESULT 282
US-11-127-877-454
; Sequence 454, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koentraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27, 800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 454
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-454

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1377 AAGTACTCCAGACATGAC 1397
Db 1 AAGTACTCCAGACATGAC 21

RESULT 283
US-11-127-877-455
; Sequence 455, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koentraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27, 800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 455
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-455

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1387 AAGACATGACAGAGCTTC 1407
Db 1 AAGACATGACAGAGCTTC 21

RESULT 284
US-11-127-877-456
; Sequence 456, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koentraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27, 800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 456
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-456

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1390 ACCATGACAGAGCTTCAGC 1410
Db 1 ACCATGACAGAGCTTCAGC 21

RESULT 285
US-11-127-877-457
; Sequence 457, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koentraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27, 800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 457
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-457

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1396 ACAGAGAGCTTCAGCTTC 1416

Db 1 ACAGAGGCTTCAAGCTTCTCC 21

```

RESULT 286
US-11-127-877-458
; Sequence 458, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spitlaels, Koentraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 458
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-458

```

Query Match 1.2%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02; Indels 0; Gaps 0;
 Matches 21; Conservative 0; Mismatches 0;

QY 1497 AATTCCTTCATCTGAACC 1517
 Db 1 AATTCCTTCATCTGAACC 21

```

RESULT 287
US-11-127-877-459
; Sequence 459, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spitlaels, Koentraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 459
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-459

```

Query Match 1.2%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02; Indels 0; Gaps 0;
 Matches 21; Conservative 0; Mismatches 0;

QY 1514 AACCATCAGAAACCCCTCAG 1534
 Db 1 AACCATCAGAAACCCCTCAG 21

```

RESULT 288
US-11-127-877-460
; Sequence 460, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spitlaels, Koentraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 460
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-460

```

Query Match 1.2%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02; Indels 0; Gaps 0;
 Matches 21; Conservative 0; Mismatches 0;

QY 1648 AATCAGTGAAGTTGCTGAGC 1668
 Db 1 AATCAGTGAAGTTGCTGAGC 21

```

RESULT 289
US-11-127-877-461
; Sequence 461, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spitlaels, Koentraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 461
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-461

```

Query Match 1.2%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02; Indels 0; Gaps 0;
 Matches 21; Conservative 0; Mismatches 0;

QY 1733 ACTTGCTGATGAGTGC 1753
 Db 1 ACTTGCTGATGAGTGC 21

RESULT 290
 US-11-127-877-462

```
; Sequence 462, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27, 800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 462
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-462
```

```
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 290 AACCAAGCTGCGCAATTGTCC 310
Db 1 AACCAAGCTGCGCAATTGTCC 21
```

```
RESULT 291
US-11-127-877-463
; Sequence 463, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27, 800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 463
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-463
```

```
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 303 AATTGTCTTTGGGACAGCTGC 323
Db 1 AATTGTCTTTGGGACAGCTGC 21
```

```
RESULT 292
US-11-127-877-464
; Sequence 464, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27, 800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 464
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-464
```

```
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 358 AACGTGTAGTAGTGTGATC 378
Db 1 AACGTGTAGTAGTGTGATC 21
```

```
RESULT 293
US-11-127-877-465
; Sequence 465, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27, 800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 465
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-465
```

```
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 463 AATACAGTGTGAACCTTACCC 483
Db 1 AATACAGTGTGAACCTTACCC 21
```

```
RESULT 294
US-11-127-877-466
; Sequence 466, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
```

```
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 466
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-466

Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 475 AACTTCACTATGCTGTCAC 495
Db 1 AACTTCACTATGCTGTCAC 21

RESULT 295
US-11-127-877-467
; Sequence 467, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 467
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-467

Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 494 ACAACGAATGGTACTACGACC 514
Db 1 ACAACGAATGGTACTACGACC 21

RESULT 296
US-11-127-877-468
; Sequence 468, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
```

```
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 468
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-468

Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 643 ACAGCCACCAAGTGTGATC 663
Db 1 ACAGCCACCAAGTGTGATC 21

RESULT 297
US-11-127-877-469
; Sequence 469, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 469
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-469

Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 649 ACCAAAGTGTATCTGTGTC 669
Db 1 ACCAAAGTGTATCTGTGTC 21

RESULT 298
US-11-127-877-470
; Sequence 470, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
```

;; PRIOR APPLICATION NUMBER: 60/570,352
;; PRIOR FILING DATE: 2004-05-12
;; PRIOR APPLICATION NUMBER: 60/603,948
;; PRIOR FILING DATE: 2004-08-24
;; NUMBER OF SEQ ID NOS: 590
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 470
;; LENGTH: 21
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-11-127-877-470

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 652 AAGTGTGATCTGTGTCATC 672
DB 1 AAGTGTGATCTGTGTCATC 21

RESULT 299
US-11-127-877-471
;; Sequence 471, Application US/11127877
;; Publication No. US20050287565A1
;; GENERAL INFORMATION:
;; APPLICANT: Merchiers, Pascal G.
;; APPLICANT: Hoffmann, Marcel
;; APPLICANT: Spittaels, Koenraad F. F.
;; APPLICANT: Laenen, Wendy
;; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
;; TITLE OF INVENTION: Amyloid-Beta Protein Production
;; FILE REFERENCE: P27,800-B USA
;; CURRENT APPLICATION NUMBER: US/11/127,877
;; PRIOR FILING DATE: 2005-05-12
;; PRIOR APPLICATION NUMBER: 60/570,352
;; PRIOR FILING DATE: 2004-05-12
;; PRIOR APPLICATION NUMBER: 60/603,948
;; PRIOR FILING DATE: 2004-08-24
;; NUMBER OF SEQ ID NOS: 590
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 471
;; LENGTH: 21
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-11-127-877-471

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 713 ACTCACCACAGAGACCATGC 733
DB 1 ACTCACCACAGAGACCATGC 21

RESULT 300
US-11-127-877-472
;; Sequence 472, Application US/11127877
;; Publication No. US20050287565A1
;; GENERAL INFORMATION:
;; APPLICANT: Merchiers, Pascal G.
;; APPLICANT: Hoffmann, Marcel
;; APPLICANT: Spittaels, Koenraad F. F.
;; APPLICANT: Laenen, Wendy
;; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
;; TITLE OF INVENTION: Amyloid-Beta Protein Production
;; FILE REFERENCE: P27,800-B USA
;; CURRENT APPLICATION NUMBER: US/11/127,877
;; PRIOR FILING DATE: 2005-05-12
;; PRIOR APPLICATION NUMBER: 60/570,352
;; PRIOR FILING DATE: 2004-05-12
;; PRIOR APPLICATION NUMBER: 60/603,948

;; PRIOR FILING DATE: 2004-08-24
;; NUMBER OF SEQ ID NOS: 590
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 472
;; LENGTH: 21
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-11-127-877-472

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 797 ACCACATCTGTGTACTTCCTC 817
DB 1 ACCACATCTGTGTACTTCCTC 21

RESULT 301
US-11-127-877-473
;; Sequence 473, Application US/11127877
;; Publication No. US20050287565A1
;; GENERAL INFORMATION:
;; APPLICANT: Merchiers, Pascal G.
;; APPLICANT: Hoffmann, Marcel
;; APPLICANT: Spittaels, Koenraad F. F.
;; APPLICANT: Laenen, Wendy
;; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
;; TITLE OF INVENTION: Amyloid-Beta Protein Production
;; FILE REFERENCE: P27,800-B USA
;; CURRENT APPLICATION NUMBER: US/11/127,877
;; PRIOR FILING DATE: 2005-05-12
;; PRIOR APPLICATION NUMBER: 60/570,352
;; PRIOR FILING DATE: 2004-05-12
;; PRIOR APPLICATION NUMBER: 60/603,948
;; PRIOR FILING DATE: 2004-08-24
;; NUMBER OF SEQ ID NOS: 590
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 473
;; LENGTH: 21
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-11-127-877-473

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 811 ACTGTGCTGATCTACTTCCTC 831
DB 1 ACTGTGCTGATCTACTTCCTC 21

RESULT 302
US-11-127-877-475
;; Sequence 475, Application US/11127877
;; Publication No. US20050287565A1
;; GENERAL INFORMATION:
;; APPLICANT: Merchiers, Pascal G.
;; APPLICANT: Hoffmann, Marcel
;; APPLICANT: Spittaels, Koenraad F. F.
;; APPLICANT: Laenen, Wendy
;; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
;; TITLE OF INVENTION: Amyloid-Beta Protein Production
;; FILE REFERENCE: P27,800-B USA
;; CURRENT APPLICATION NUMBER: US/11/127,877
;; PRIOR FILING DATE: 2005-05-12
;; PRIOR APPLICATION NUMBER: 60/570,352
;; PRIOR FILING DATE: 2004-05-12
;; PRIOR APPLICATION NUMBER: 60/603,948
;; PRIOR FILING DATE: 2004-08-24
;; NUMBER OF SEQ ID NOS: 590
;; SOFTWARE: PatentIn version 3.3

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; SEQ ID NO 475
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-475

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      874  ACATATGGCCAGTGAGATC 894
Db      1  ACATATGGCCAGTGAGATC 21

RESULT 303
US-11-127-877-476
; Sequence 476, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 476
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-476

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      876  ACTATGGCCAGTGAGATCCC 896
Db      1  ACTATGGCCAGTGAGATCCC 21

RESULT 304
US-11-127-877-477
; Sequence 477, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 477
; LENGTH: 21
; TYPE: DNA
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; ORGANISM: Homo sapiens
US-11-127-877-477

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      920  ACAGCAAGCTCTTGCCAAAC 940
Db      1  ACAGCAAGCTCTTGCCAAAC 21

RESULT 305
US-11-127-877-478
; Sequence 478, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 478
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-478

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1025 ACATCAACCCAGATCTCTACC 1045
Db      1  ACATCAACCCAGATCTCTACC 21

RESULT 306
US-11-127-877-479
; Sequence 479, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 479
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-479
```

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1043 ACCTGAAGAGTTATCCAGC 1063
DB 1 ACCTGAAGAGTTATCCAGC 21

RESULT 307
US-11-127-877-480
; Sequence 480, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 480
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-480

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1048 AAGAACTTATCCAGCAGTC 1068
DB 1 AAGAACTTATCCAGCAGTC 21

RESULT 308
US-11-127-877-481
; Sequence 481, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 481
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-481

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1051 AAGTTATCCAGCAGCTTAC 1071
DB 1 AAGTTATCCAGCAGCTTAC 21

RESULT 309
US-11-127-877-484
; Sequence 484, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 484
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-484

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 290 AACGAGCTGCAATGTCC 310
DB 1 AACGAGCTGCAATGTCC 21

RESULT 310
US-11-127-877-485
; Sequence 485, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 485
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-485

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 AATGTCCTTGGCAGCTGC 323
|||||

Db 1 AATTGTCCTTGGGACAGCTGC 21

RESULT 311

US-11-127-877-486
; Sequence 486, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 486
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-486

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 AACGTGGTAGTGATGATC 378
Db 1 AACCTGCTAGTGTGATC 21

RESULT 312

US-11-127-877-487
; Sequence 487, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 487
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-487

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 AATACAGTGTGACTTACCC 483
Db 1 AATACAGTGTGACTTACCC 21

RESULT 313

US-11-127-877-488
; Sequence 488, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 488
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-488

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 475 AACTTCACCTATGCTGCAC 495
Db 1 AACTTCACCTATGCTGCAC 21

RESULT 314

US-11-127-877-489
; Sequence 489, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 489
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-489

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 494 ACAACGAATGTACTACGCC 514
Db 1 ACAACGAATGTACTACGCC 21

RESULT 315

US-11-127-877-490
; Sequence 490, Application US/11127877


```
/ Publication No. US2005028756SA1
/ GENERAL INFORMATION:
/ APPLICANT: Merchiers, Pascal G.
/ APPLICANT: Hoffmann, Marcel
/ APPLICANT: Spittaels, Koenraad F. F.
/ APPLICANT: Laenen, Wendy
/ TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
/ FILE REFERENCE: P27,800-B USA
/ CURRENT APPLICATION NUMBER: US/11/127,877
/ PRIOR FILING DATE: 2005-05-12
/ PRIOR APPLICATION NUMBER: 60/570,352
/ PRIOR FILING DATE: 2004-05-12
/ PRIOR APPLICATION NUMBER: 60/603,948
/ PRIOR FILING DATE: 2004-08-24
/ NUMBER OF SEQ ID NOS: 590
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 490
/ LENGTH: 21
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-11-127-877-490

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No.3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      526 AAGTTCACAACTCTTCCC 546
DB      1 AAGTTCACAACTCTTCCC 21

RESULT 316
US-11-127-877-491
/ Sequence 491, Application US/11127877
/ Publication No. US2005028756SA1
/ GENERAL INFORMATION:
/ APPLICANT: Merchiers, Pascal G.
/ APPLICANT: Hoffmann, Marcel
/ APPLICANT: Spittaels, Koenraad F. F.
/ APPLICANT: Laenen, Wendy
/ TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
/ FILE REFERENCE: P27,800-B USA
/ CURRENT APPLICATION NUMBER: US/11/127,877
/ PRIOR FILING DATE: 2005-05-12
/ PRIOR APPLICATION NUMBER: 60/570,352
/ PRIOR FILING DATE: 2004-05-12
/ PRIOR APPLICATION NUMBER: 60/603,948
/ PRIOR FILING DATE: 2004-08-24
/ NUMBER OF SEQ ID NOS: 590
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 491
/ LENGTH: 21
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-11-127-877-491

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No.3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      643 ACAGCCACCAAGTGTATC 663
DB      1 ACAGCCACCAAGTGTATC 21

RESULT 317
US-11-127-877-492
/ Sequence 492, Application US/11127877
/ Publication No. US2005028756SA1
/ GENERAL INFORMATION:
/ APPLICANT: Merchiers, Pascal G.
```

```
/ APPLICANT: Hoffmann, Marcel
/ APPLICANT: Spittaels, Koenraad F. F.
/ APPLICANT: Laenen, Wendy
/ TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
/ FILE REFERENCE: P27,800-B USA
/ CURRENT APPLICATION NUMBER: US/11/127,877
/ PRIOR FILING DATE: 2005-05-12
/ PRIOR APPLICATION NUMBER: 60/570,352
/ PRIOR FILING DATE: 2004-05-12
/ PRIOR APPLICATION NUMBER: 60/603,948
/ PRIOR FILING DATE: 2004-08-24
/ NUMBER OF SEQ ID NOS: 590
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 492
/ LENGTH: 21
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-11-127-877-492

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No.3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      649 ACCAAGTGCATCTGTGC 669
DB      1 ACCAAGTGCATCTGTGC 21

RESULT 318
US-11-127-877-493
/ Sequence 493, Application US/11127877
/ Publication No. US2005028756SA1
/ GENERAL INFORMATION:
/ APPLICANT: Merchiers, Pascal G.
/ APPLICANT: Hoffmann, Marcel
/ APPLICANT: Spittaels, Koenraad F. F.
/ APPLICANT: Laenen, Wendy
/ TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
/ FILE REFERENCE: P27,800-B USA
/ CURRENT APPLICATION NUMBER: US/11/127,877
/ PRIOR FILING DATE: 2005-05-12
/ PRIOR APPLICATION NUMBER: 60/570,352
/ PRIOR FILING DATE: 2004-05-12
/ PRIOR APPLICATION NUMBER: 60/603,948
/ PRIOR FILING DATE: 2004-08-24
/ NUMBER OF SEQ ID NOS: 590
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 493
/ LENGTH: 21
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-11-127-877-493

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No.3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      652 AAGTGTATCTGTGTATC 672
DB      1 AAGTGTATCTGTGTATC 21

RESULT 319
US-11-127-877-494
/ Sequence 494, Application US/11127877
/ Publication No. US2005028756SA1
/ GENERAL INFORMATION:
/ APPLICANT: Merchiers, Pascal G.
/ APPLICANT: Hoffmann, Marcel
/ APPLICANT: Spittaels, Koenraad F. F.
/ APPLICANT: Laenen, Wendy
```

```

; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27, 800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 494
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-494

```

Query Match	1.2%;	Score 21;	DB 1;	Length 21;
Best Local Similarity	100.0%;	Pred. No. 3.6e+02;		
Matches 21; Conservative	0;	Mismatches	0;	Indels 0;
QY	713	ACTGACCAACGAGACCCATGC	733	
Db	1	ACTGACCAACGAGACCCATGC	21	

```

RESULT 320
US-11-127-877-495
? Sequence 495, Application US/11127877
? Publication No. US20050287565A1
? GENERAL INFORMATION:
? APPLICANT: Merchiers, Pascal G.
? APPLICANT: Hoffmann, Marcel
? APPLICANT: Spiltsaels, Koenraad F. F.
? APPLICANT: Laenen, Wendy
? TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
? TITLE OF INVENTION: Amyloid-Beta Protein Production
? FILE REFERENCE: P27, 800-B USA
? CURRENT APPLICATION NUMBER: US/11/127,877
? CURRENT FILING DATE: 2005-05-12
? PRIOR APPLICATION NUMBER: 60/570,352
? PRIOR FILING DATE: 2004-05-12
? PRIOR APPLICATION NUMBER: 60/603,948
? PRIOR FILING DATE: 2004-08-24
? NUMBER OF SEQ ID NOS: 590
? SOFTWARE: PatentIn version 3.3
? SEQ ID NO 495
? LENGTH: 21
? TYPE: DNA
? ORGANISM: Homo sapiens
US-11-127-877-495

```

Query Match	1.2%	Score 21;	DB 1;	Length 21;
Best Local Similarity	100.0%	Pred. No. 3.6e+02;		
Matches	21;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0
QY	797	ACCACATCTGTGTACTGTGC	817	
Db	1	ACCACATCTGTGTACTGTGC	21	

```

RESULT 321
US-11-127-877-496
; Sequence 496, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spiltsaels, Koenraad F. F.
; APPLICANT: laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA

```

```

; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 496
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-496

```

	Query Match	Score 21; DB 1; Length 21;
	Best Local Similarity	100.0%; Pred. No. 3,6e+02;
Matches	21; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	811 ACTGTGCTGATCTACTTCCTC	831
Db	1 ACTGTGCTGATCTACTTCCTC	21

```

RESULT 322
US-11-127-877-497
; Sequence 497, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27, 800-B USA
; CURRENT APPLICATION NUMBER: US/11/127, 877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 497
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-497

```

Query Match	1.2%	Score 21;	DB 1;	Length 21;
Best Local Similarity	100.0%	Pred. No. 3.6e+02;		
Matches	21;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;
QY	857	ACACCGTGTGGGATCAAC	877	
Db	1	ACACCGTGTGGGATCAAC	21	

```

RESULT 323
US-11-127-877-498
; Sequence 498, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127, 877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352

```

;; PRIOR FILING DATE: 2004-05-12
;; PRIOR APPLICATION NUMBER: 60/603,948
;; PRIOR FILING DATE: 2004-08-24
;; NUMBER OF SEQ ID NOS: 590
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 498
;; LENGTH: 21
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-11-127-877-498

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 874 ACATATGGCCAGTGATGC 894
DB 1 ACATATGGCCAGTGATGC 21

RESULT 324
US-11-127-877-499
;; Sequence 499, Application US/11127877
;; Publication No. US20050287565A1
;; GENERAL INFORMATION:
;; APPLICANT: Merchiers, Pascal G.
;; APPLICANT: Hoffmann, Marcel
;; APPLICANT: Spittaels, Koenraad F. F.
;; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
;; FILE REFERENCE: P27, 800-B USA
;; CURRENT APPLICATION NUMBER: US/11/127,877
;; PRIOR FILING DATE: 2005-05-12
;; PRIOR APPLICATION NUMBER: 60/570,352
;; PRIOR FILING DATE: 2004-05-12
;; PRIOR APPLICATION NUMBER: 60/603,948
;; PRIOR FILING DATE: 2004-08-24
;; NUMBER OF SEQ ID NOS: 590
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 499
;; LENGTH: 21
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-11-127-877-499

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 876 ACTATGGCCAGTGATCCC 896
DB 1 ACTATGGCCAGTGATCCC 21

RESULT 325
US-11-127-877-500
;; Sequence 500, Application US/11127877
;; Publication No. US20050287565A1
;; GENERAL INFORMATION:
;; APPLICANT: Merchiers, Pascal G.
;; APPLICANT: Hoffmann, Marcel
;; APPLICANT: Spittaels, Koenraad F. F.
;; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
;; FILE REFERENCE: P27, 800-B USA
;; CURRENT APPLICATION NUMBER: US/11/127,877
;; PRIOR FILING DATE: 2005-05-12
;; PRIOR APPLICATION NUMBER: 60/570,352
;; PRIOR FILING DATE: 2004-05-12
;; PRIOR APPLICATION NUMBER: 60/603,948
;; PRIOR FILING DATE: 2004-08-24

;; NUMBER OF SEQ ID NOS: 590
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 500
;; LENGTH: 21
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-11-127-877-500

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 920 ACAGCAAGTCTGCGAAGC 940
DB 1 ACAGCAAGTCTGCGAAGC 21

RESULT 326
US-11-127-877-501
;; Sequence 501, Application US/11127877
;; Publication No. US20050287565A1
;; GENERAL INFORMATION:
;; APPLICANT: Merchiers, Pascal G.
;; APPLICANT: Hoffmann, Marcel
;; APPLICANT: Spittaels, Koenraad F. F.
;; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
;; FILE REFERENCE: P27, 800-B USA
;; CURRENT APPLICATION NUMBER: US/11/127,877
;; PRIOR FILING DATE: 2005-05-12
;; PRIOR APPLICATION NUMBER: 60/570,352
;; PRIOR FILING DATE: 2004-05-12
;; PRIOR APPLICATION NUMBER: 60/603,948
;; PRIOR FILING DATE: 2004-08-24
;; NUMBER OF SEQ ID NOS: 590
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 501
;; LENGTH: 21
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-11-127-877-501

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1025 ACATCAACCGATCTTACC 1045
DB 1 ACATCAACCGATCTTACC 21

RESULT 327
US-11-127-877-502
;; Sequence 502, Application US/11127877
;; Publication No. US20050287565A1
;; GENERAL INFORMATION:
;; APPLICANT: Merchiers, Pascal G.
;; APPLICANT: Hoffmann, Marcel
;; APPLICANT: Spittaels, Koenraad F. F.
;; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
;; FILE REFERENCE: P27, 800-B USA
;; CURRENT APPLICATION NUMBER: US/11/127,877
;; PRIOR FILING DATE: 2005-05-12
;; PRIOR APPLICATION NUMBER: 60/570,352
;; PRIOR FILING DATE: 2004-05-12
;; PRIOR APPLICATION NUMBER: 60/603,948
;; PRIOR FILING DATE: 2004-08-24
;; NUMBER OF SEQ ID NOS: 590
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 502

LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens
US-11-127-877-502

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1043 ACCTGAAGAAGTTATCCAGC 1063
Db 1 ACCTGAAGAAGTTATCCAGC 21

RESULT 328
US-11-127-877-503
Sequence 503, Application US/11127877
Publication No. US20050287565A1
GENERAL INFORMATION:
APPLICANT: Merchiers, Pascal G.
APPLICANT: Hoffmann, Marcel
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
TITLE OF INVENTION: Amyloid-Beta Protein Production
FILE REFERENCE: P27,800-B USA
CURRENT APPLICATION NUMBER: US/11/127,877
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: 60/570,352
PRIOR FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: 60/603,948
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 590
SOFTWARE: PatentIn version 3.3
SEQ ID NO 503
LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens
US-11-127-877-503

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1048 AAGAAGTTATCCAGCAGGTC 1068
Db 1 AAGAAGTTATCCAGCAGGTC 21

RESULT 329
US-11-127-877-504
Sequence 504, Application US/11127877
Publication No. US20050287565A1
GENERAL INFORMATION:
APPLICANT: Merchiers, Pascal G.
APPLICANT: Hoffmann, Marcel
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
TITLE OF INVENTION: Amyloid-Beta Protein Production
FILE REFERENCE: P27,800-B USA
CURRENT APPLICATION NUMBER: US/11/127,877
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: 60/570,352
PRIOR FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: 60/603,948
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 590
SOFTWARE: PatentIn version 3.3
SEQ ID NO 504
LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens

US-11-127-877-504

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1051 AAGTTATCCAGCAGGTCCTAC 1071
Db 1 AAGTTATCCAGCAGGTCCTAC 21

RESULT 330
US-11-127-877-505
Sequence 505, Application US/11127877
Publication No. US20050287565A1
GENERAL INFORMATION:
APPLICANT: Merchiers, Pascal G.
APPLICANT: Hoffmann, Marcel
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
TITLE OF INVENTION: Amyloid-Beta Protein Production
FILE REFERENCE: P27,800-B USA
CURRENT APPLICATION NUMBER: US/11/127,877
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: 60/570,352
PRIOR FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: 60/603,948
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 590
SOFTWARE: PatentIn version 3.3
SEQ ID NO 505
LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens
US-11-127-877-505

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1135 AATGACAGGTTCCGCTCGGC 1155
Db 1 AATGACAGGTTCCGCTCGGC 21

RESULT 331
US-11-127-877-506
Sequence 506, Application US/11127877
Publication No. US20050287565A1
GENERAL INFORMATION:
APPLICANT: Merchiers, Pascal G.
APPLICANT: Hoffmann, Marcel
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
TITLE OF INVENTION: Amyloid-Beta Protein Production
FILE REFERENCE: P27,800-B USA
CURRENT APPLICATION NUMBER: US/11/127,877
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: 60/570,352
PRIOR FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: 60/603,948
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 590
SOFTWARE: PatentIn version 3.3
SEQ ID NO 506
LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens
US-11-127-877-506

Query Match 1.2%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1214 AATGAATCCACCCGGTATC 1234
Db 1 AATGAATCCACCCGGTATC 21

RESULT 332

US-11-127-877-507
; Sequence 507, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 507
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-507

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1363 AACTGCTCTTCACGAGTGAC 1383
Db 1 AACTGCTCTTCACGAGTGAC 21

RESULT 333

US-11-127-877-508
; Sequence 508, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 508
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-508

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1377 AAGTACTCCAAGACATGAC 1397
Db 1 AAGTACTCCAAGACATGAC 21

RESULT 334

US-11-127-877-509
; Sequence 509, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 509
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-509

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1387 AAGCATGACAGAGCTTC 1407
Db 1 AAGCATGACAGAGCTTC 21

RESULT 335

US-11-127-877-510
; Sequence 510, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 510
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-510

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1390 ACCATGACAGAGCTTCAC 1410
Db 1 ACCATGACAGAGCTTCAC 21

```
RESULT 336
US-11-127-877-511
; Sequence 511, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27, 800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 511
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-511
```

```
Query Match
Best Local Similarity 1.2%; Score 21; DB 1; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1396 ACAGAGAGCTTCAGCTTCTCC 1416
Db 1 ACAGAGAGCTTCAGCTTCTCC 21
```

```
RESULT 337
US-11-127-877-512
; Sequence 512, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27, 800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: 60/603,948
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 512
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-512
```

```
Query Match
Best Local Similarity 1.2%; Score 21; DB 1; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1497 AAATTCCTCATCTGGAACC 1517
Db 1 AAATTCCTCATCTGGAACC 21
```

RESULT 338

```
US-11-127-877-513
; Sequence 513, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27, 800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 513
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-513
```

```
Query Match
Best Local Similarity 1.2%; Score 21; DB 1; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1514 AACCATCAGAAACACCTCTAC 1534
Db 1 AACCATCAGAAACACCTCTAC 21
```

```
RESULT 339
US-11-127-877-514
; Sequence 514, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27, 800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: 60/603,948
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 514
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-514
```

```
Query Match
Best Local Similarity 1.2%; Score 21; DB 1; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1648 AATCAGTGAACCTTGCTGAGC 1668
Db 1 AATCAGTGAACCTTGCTGAGC 21
```

RESULT 340
US-11-127-877-515
; Sequence 515, Application US/11127877
; Publication No. US20050287565A1

```

; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 515
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-515

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1733 ACTTTGGCTGCATGCGAGTGC 1753
Db      1 ACTTTGGCTGCATGCGAGTGC 21

RESULT 341
US-11-127-877-516
; Sequence 516, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 516
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-516

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      290 AACCAAGCTGGCAAAATGTCC 310
Db      1 AACCAAGCTGGCAAAATGTCC 21

RESULT 342
US-11-127-877-517
; Sequence 517, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
```

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; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 517
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-517

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      303 AATTGCTTTGGGAGCTGC 323
Db      1 AATTGCTTTGGGAGCTGC 21

RESULT 343
US-11-127-877-518
; Sequence 518, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 518
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-518

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      358 AACGTGTAAGTATGTGATC 378
Db      1 AACGTGTAAGTATGTGATC 21

RESULT 344
US-11-127-877-519
; Sequence 519, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
```

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; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 519
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-519

Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 AATCAGTGGTGAAGTCTCACC 483
DB 1 AATCAGTGGTGAAGTCTCACC 21

RESULT 345
US-11-127-877-520
; Sequence 520, Application US/11/127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 520
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-520

Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 475 AACTTCACCTATGCTGTGCAC 495
DB 1 AACTTCACCTATGCTGTGCAC 21

RESULT 346
US-11-127-877-521
; Sequence 521, Application US/11/127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
```

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; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 521
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-521

Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 494 ACAACGAATGATCTACGCGCC 514
DB 1 ACAACGAATGATCTACGCGCC 21

RESULT 347
US-11-127-877-522
; Sequence 522, Application US/11/127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 522
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-522

Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 643 ACAGCCACCAAGTGTGATC 663
DB 1 ACAGCCACCAAGTGTGATC 21

RESULT 348
US-11-127-877-523
; Sequence 523, Application US/11/127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
```


PRIOR APPLICATION NUMBER: 60/603,948
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 590
SOFTWARE: PatentIn version 3.3
SEQ ID NO 523
LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens
US-11-127-877-523

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 649 ACCAAGTGTCTGTCTGTC 669
Db 1 ACCAAGTGTCTGTCTGTC 21

RESULT 349
US-11-127-877-524
Sequence 524, Application US/11127877
Publication No. US20050287565A1
GENERAL INFORMATION:
APPLICANT: Merchiers, Pascal G.
APPLICANT: Hoffmann, Marcel
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
FILE REFERENCE: P27,800-B USA
CURRENT APPLICATION NUMBER: US/11/127,877
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: 60/570,352
PRIOR FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: 60/603,948
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 590
SOFTWARE: PatentIn version 3.3
SEQ ID NO 524
LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens
US-11-127-877-524

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 652 AAAGTGTCTGTCTGTCTGTC 672
Db 1 AAAGTGTCTGTCTGTCTGTC 21

RESULT 350
US-11-127-877-525
Sequence 525, Application US/11127877
Publication No. US20050287565A1
GENERAL INFORMATION:
APPLICANT: Merchiers, Pascal G.
APPLICANT: Hoffmann, Marcel
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
FILE REFERENCE: P27,800-B USA
CURRENT APPLICATION NUMBER: US/11/127,877
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: 60/570,352
PRIOR FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: 60/603,948
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 590

SOFTWARE: PatentIn version 3.3
SEQ ID NO 525
LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens
US-11-127-877-525

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 713 ACTCACACAGAGACCATGC 733
Db 1 ACTCACACAGAGACCATGC 21

RESULT 351
US-11-127-877-526
Sequence 526, Application US/11127877
Publication No. US20050287565A1
GENERAL INFORMATION:
APPLICANT: Merchiers, Pascal G.
APPLICANT: Hoffmann, Marcel
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
FILE REFERENCE: P27,800-B USA
CURRENT APPLICATION NUMBER: US/11/127,877
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: 60/570,352
PRIOR FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: 60/603,948
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 590
SOFTWARE: PatentIn version 3.3
SEQ ID NO 526
LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens
US-11-127-877-526

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 797 ACCACATCTGTGTGACTGTGC 817
Db 1 ACCACATCTGTGTGACTGTGC 21

RESULT 352
US-11-127-877-527
Sequence 527, Application US/11127877
Publication No. US20050287565A1
GENERAL INFORMATION:
APPLICANT: Merchiers, Pascal G.
APPLICANT: Hoffmann, Marcel
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
FILE REFERENCE: P27,800-B USA
CURRENT APPLICATION NUMBER: US/11/127,877
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: 60/570,352
PRIOR FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: 60/603,948
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 590
SOFTWARE: PatentIn version 3.3
SEQ ID NO 527
LENGTH: 21

TYPE: DNA
ORGANISM: Homo sapiens
US-11-127-877-527

Query Match
Best Local Similarity 1.2%; Score 21; DB 1; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 811 ACTGTGCTGATCTACTTCTC 831
DB 1 ACTGTGCTGATCTACTTCTC 21

RESULT 353
US-11-127-877-528
Sequence 528, Application US/11127877
Publication No. US20050287565A1
GENERAL INFORMATION:
APPLICANT: Merchiers, Pascal G.
APPLICANT: Hoffmann, Marcel
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
FILE REFERENCE: P27, 800-B USA
CURRENT APPLICATION NUMBER: US/11/127, 877
PRIOR FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: 60/570,352
PRIOR FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: 60/603,948
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 590
SOFTWARE: Patentin version 3.3
SEQ ID NO 528
LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens
US-11-127-877-528

Query Match
Best Local Similarity 1.2%; Score 21; DB 1; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 857 ACACCGTAGTGGGATCAGAC 877
DB 1 ACACCGTAGTGGGATCAGAC 21

RESULT 354
US-11-127-877-529
Sequence 529, Application US/11127877
Publication No. US20050287565A1
GENERAL INFORMATION:
APPLICANT: Merchiers, Pascal G.
APPLICANT: Hoffmann, Marcel
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
FILE REFERENCE: P27, 800-B USA
CURRENT APPLICATION NUMBER: US/11/127, 877
PRIOR FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: 60/570,352
PRIOR FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: 60/603,948
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 590
SOFTWARE: Patentin version 3.3
SEQ ID NO 529
LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens
US-11-127-877-529

Query Match
Best Local Similarity 1.2%; Score 21; DB 1; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 874 ACACTATGGGCCAGTAGATC 894
DB 1 ACACTATGGGCCAGTAGATC 21

RESULT 355
US-11-127-877-530
Sequence 530, Application US/11127877
Publication No. US20050287565A1
GENERAL INFORMATION:
APPLICANT: Merchiers, Pascal G.
APPLICANT: Hoffmann, Marcel
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
FILE REFERENCE: P27, 800-B USA
CURRENT APPLICATION NUMBER: US/11/127, 877
PRIOR FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: 60/570,352
PRIOR FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: 60/603,948
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 590
SOFTWARE: Patentin version 3.3
SEQ ID NO 530
LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens
US-11-127-877-530

Query Match
Best Local Similarity 1.2%; Score 21; DB 1; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 876 ACTATGGGCCAGTAGATCCC 896
DB 1 ACTATGGGCCAGTAGATCCC 21

RESULT 356
US-11-127-877-531
Sequence 531, Application US/11127877
Publication No. US20050287565A1
GENERAL INFORMATION:
APPLICANT: Merchiers, Pascal G.
APPLICANT: Hoffmann, Marcel
APPLICANT: Spittaels, Koenraad F. F.
APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
FILE REFERENCE: P27, 800-B USA
CURRENT APPLICATION NUMBER: US/11/127, 877
PRIOR FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: 60/570,352
PRIOR FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: 60/603,948
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 590
SOFTWARE: Patentin version 3.3
SEQ ID NO 531
LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens
US-11-127-877-531

Query Match
Best Local Similarity 1.2%; Score 21; DB 1; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 920 ACGAGCAAGTCTGCGCAAGC 940

Db 1 ACGAGCAAGTCTGCGCAAGC 21

RESULT 357

US-11-127-877-532

Sequence 532, Application US/11127877

Publication No. US20050287565A1

GENERAL INFORMATION:

APPLICANT: Merchiers, Pascal G.

APPLICANT: Hoffmann, Marcel

APPLICANT: Spittaels, Koenraad F. F.

APPLICANT: Laenen, Wendy

TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting

FILE REFERENCE: P27,800-B USA

CURRENT FILING DATE: 2005-05-12

PRIOR FILING DATE: 2004-05-12

PRIOR APPLICATION NUMBER: 60/570,352

PRIOR FILING DATE: 2004-08-24

NUMBER OF SEQ ID NOS: 590

SOFTWARE: PatentIn version 3.3

SEQ ID NO 532

LENGTH: 21

TYPE: DNA

ORGANISM: Homo sapiens

US-11-127-877-532

Query Match 1.2%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 3.6e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1025 ACATCAACCCGATCTCTACC 1045

Db 1 ACATCAACCCGATCTCTACC 21

RESULT 358

US-11-127-877-533

Sequence 533, Application US/11127877

Publication No. US20050287565A1

GENERAL INFORMATION:

APPLICANT: Merchiers, Pascal G.

APPLICANT: Hoffmann, Marcel

APPLICANT: Spittaels, Koenraad F. F.

APPLICANT: Laenen, Wendy

TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting

FILE REFERENCE: P27,800-B USA

CURRENT FILING DATE: 2005-05-12

PRIOR FILING DATE: 2004-05-12

PRIOR APPLICATION NUMBER: 60/570,352

PRIOR FILING DATE: 2004-08-24

NUMBER OF SEQ ID NOS: 590

SOFTWARE: PatentIn version 3.3

SEQ ID NO 533

LENGTH: 21

TYPE: DNA

ORGANISM: Homo sapiens

US-11-127-877-533

Query Match 1.2%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 3.6e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1043 ACCTGAAGAAGTTATCCAGC 1063

Db 1 ACCTGAAGAAGTTATCCAGC 21

RESULT 359

US-11-127-877-534

Sequence 534, Application US/11127877

Publication No. US20050287565A1

GENERAL INFORMATION:

APPLICANT: Merchiers, Pascal G.

APPLICANT: Hoffmann, Marcel

APPLICANT: Spittaels, Koenraad F. F.

APPLICANT: Laenen, Wendy

TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting

FILE REFERENCE: P27,800-B USA

CURRENT FILING DATE: 2005-05-12

PRIOR FILING DATE: 2004-05-12

PRIOR APPLICATION NUMBER: 60/570,352

PRIOR FILING DATE: 2004-08-24

NUMBER OF SEQ ID NOS: 590

SOFTWARE: PatentIn version 3.3

SEQ ID NO 534

LENGTH: 21

TYPE: DNA

ORGANISM: Homo sapiens

US-11-127-877-534

Query Match 1.2%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 3.6e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1048 AAGAAGTTATCCAGCAGTC 1068

Db 1 AAGAAGTTATCCAGCAGTC 21

RESULT 360

US-11-127-877-535

Sequence 535, Application US/11127877

Publication No. US20050287565A1

GENERAL INFORMATION:

APPLICANT: Merchiers, Pascal G.

APPLICANT: Hoffmann, Marcel

APPLICANT: Spittaels, Koenraad F. F.

APPLICANT: Laenen, Wendy

TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting

FILE REFERENCE: P27,800-B USA

CURRENT FILING DATE: 2005-05-12

PRIOR FILING DATE: 2004-05-12

PRIOR APPLICATION NUMBER: 60/570,352

PRIOR FILING DATE: 2004-08-24

NUMBER OF SEQ ID NOS: 590

SOFTWARE: PatentIn version 3.3

SEQ ID NO 535

LENGTH: 21

TYPE: DNA

ORGANISM: Homo sapiens

US-11-127-877-535

Query Match 1.2%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 3.6e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1051 AAGTTATCCAGCAGGTCTAC 1071

Db 1 AAGTTATCCAGCAGGTCTAC 21

```
RESULT 361
US-10-310-914A-386286/C
; Sequence 386286, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 386286
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-386286

Query Match          1.2%; Score 21; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      116 GCTTTAGAGAGACCTGAGCC 136
DB      21 GCTTTAGAGAGACCTGAGCC 1

RESULT 362
US-10-809-189-67919
; Sequence 67919, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809.189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396.196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67919
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-67919

Query Match          1.2%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 4.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1382 ACTCGAGACATGACAGAGAGCT 1405
DB      2 ACTCGAGACATGACAGAGAGCT 25

RESULT 363
US-11-036-317-443229
; Sequence 443229, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
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; CURRENT APPLICATION NUMBER: US/11/036.317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536.639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 443229
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-443229

Query Match          1.2%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 4.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      843 GATTGGCTATGATACACCGTAGT 866
DB      1 GATTGGCTATGATACACCTGTGCT 24

RESULT 364
US-11-060-756-34802
; Sequence 34802, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060.756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34802
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34802

Query Match          1.2%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 4.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1051 AAGTTATCCAGCAGGTCTACCTG 1074
DB      2 AAGTTATCCAGCAGGTCTACCTG 25

RESULT 365
US-11-060-756-36930
; Sequence 36930, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060.756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36930
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-36930

Query Match          1.2%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 4.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 1108 TACACCCCATCTACTGCTGC 1131
Db 2 TACATCCCATCTACTGCTTC 25

RESULT 366
US-11-060-756-36933
; Sequence 36933, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounes, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36933
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-36933

Query Match 1.2%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 4.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1104 CATGTACACCCCATCTACTG 1127
Db 2 CATCTACATCCCATCTACTG 25

RESULT 367
US-11-060-756-36934
; Sequence 36934, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounes, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36934
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-36934

Query Match 1.2%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 4.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1106 TGTACACCCCATCTACTGCT 1129
Db 1 TCTACATCCCATCTACTGCT 24

RESULT 368
US-11-060-756-36935
; Sequence 36935, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounes, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes

FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36935
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-36935

Query Match 1.2%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 4.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1108 TACACCCCATCTACTGCTGC 1131
Db 1 TACATCCCATCTACTGCTTC 24

RESULT 369
US-11-060-756-233624
; Sequence 233624, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounes, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 233624
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-233624

Query Match 1.2%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 4.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1053 GTTATCCAGCAGCTTACTGCTGC 1076
Db 1 GTTCATCCAGCAAGTCTACTGCTGC 24

RESULT 370
US-11-060-756-233625
; Sequence 233625, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounes, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 233625
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-233625

Query Match 1.2%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 4.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1053 GTTATCCAGAGTCTACTGSC 1076
Db 1 GTTCATCCAGCAGTCTACTGSC 24

RESULT 371
US-10-005-956-1129/c
; Sequence 1129, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1129
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-005-956-1129

Query Match 1.2%; Score 20.6; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 3.8e+02;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1624 CCTCATGCTGTGACTCAAA 1644
Db 21 CCTCATGCTGTGACTCAAA 1

RESULT 372
US-10-278-087A-15/c
; Sequence 15, Application US/10278087A
; Publication No. US20030138817A1
; GENERAL INFORMATION:
; APPLICANT: Shuji Hinuma
; Yasuaki Ito
; Ryo Fujii
; TITLE OF INVENTION: G Protein Coupled Receptor Protein,
; Production, And Use Thereof
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Edwards & Angell, LLP
; STREET: 101 Federal Street
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02209
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/278,087A
; FILING DATE: 31-Jan-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/461,436
; FILING DATE: 14-DEC-1999
; APPLICATION NUMBER: 09/038,572
; FILING DATE: 11-MAR-1998
; APPLICATION NUMBER: 08/513,974
; FILING DATE: 14-SEP-1995
; APPLICATION NUMBER: PCT/JP95/01599

; FILING DATE: 10-AUG-1995
; APPLICATION NUMBER: 7-093989
; FILING DATE: 19-APR-1995
; APPLICATION NUMBER: 7-057186
; FILING DATE: 16-MAR-1995
; APPLICATION NUMBER: 7-007177
; FILING DATE: 20-JAN-1995
; APPLICATION NUMBER: 6-326611
; FILING DATE: 28-DEC-1994
; APPLICATION NUMBER: 6-270017
; FILING DATE: 02-NOV-1994
; APPLICATION NUMBER: 6-236357
; FILING DATE: 30-SEP-1994
; APPLICATION NUMBER: 6-236356
; FILING DATE: 30-SEP-1994
; APPLICATION NUMBER: 6-189274
; FILING DATE: 11-AUG-1994
; APPLICATION NUMBER: 6-189273
; FILING DATE: 11-AUG-1994
; APPLICATION NUMBER: 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, DAVID G.
; REGISTRATION NUMBER: <Unknown>
; REFERENCE/DOCKET NUMBER: 45753 DIV3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-439-4444
; TELEFAX: 617-439-4170
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24
; TYPE: Nucleic acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA
; FEATURE:
; OTHER INFORMATION: /note= N is inosine; W is A or T;
; S is G or C; K is G or T; I is A or G."
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
; US-10-278-087A-15

Query Match 1.2%; Score 20.6; DB 1; Length 24;
Best Local Similarity 70.8%; Pred. No. 4.6e+02;
Matches 17; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 979 TTGCGCATCTGCTGCTGCCCTTC 1002
Db 24 TTGCGCATCTGCTGCTGCCCTTC 1

RESULT 373
US-11-060-756-34807
; Sequence 34807, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TARGET GENES
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34807
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
; US-11-060-756-34807

Query Match 1.2%; Score 20.4; DB 1; Length 25;
Best Local Similarity 95.5%; Pred. No. 5e+02;

```
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1115 CCATCATCTACTGCTGCTCA 1136
Db 1 CCATCATCTACTGCTGCTCA 22

RESULT 374
US-10-719-956-382728
; Sequence 382728, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 382728
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-382728

Query Match 1.1%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 5.2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1376 GAAGTACTCCAAACCATGACAGA 1400
Db 1 GCAGCAACTCCAAACCATGACAGA 25

RESULT 375
US-10-719-900-33169
; Sequence 33169, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 33169
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-33169

Query Match 1.1%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 5.2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1111 AACCCATCATCTACTGCTGCTCA 1135
Db 1 AACCCATCATCTACTGCTGCTCA 25

RESULT 376
US-10-719-900-146776
; Sequence 146776, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
```

```
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 146776
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-146776

Query Match 1.1%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 5.2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1388 AGACCATGACGTAAGCTCCAGCTT 1412
Db 1 AGACCATGACGTAAGCTCCAGCTT 25

RESULT 377
US-10-719-900-152541
; Sequence 152541, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 152541
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-152541

Query Match 1.1%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 5.2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1244 AGGCGAGTGTGTACAAGTCAGCG 1268
Db 1 AGGCGAGTGTGTACAAGTCAGCG 25

RESULT 378
US-10-719-900-455080
; Sequence 455080, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 455080
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-455080

Query Match 1.1%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 5.2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

Qy 910 GACCGTACGACGACGAGTCTCTG 934
 |||||
 Db 1 GACCGTACCATGACGAAAGTCTCTG 25

RESULT 379
 US-10-809-189-67918
 ; Sequence 67918, Application US/10809189
 ; Publication No. US20050048531A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Michael Miltmann
 ; APPLICANT: David Mack
 ; APPLICANT: David Lockhart
 ; APPLICANT: Affymetrix, Inc.
 ; TITLE OF INVENTION: Methods of Genetic Analysis
 ; FILE REFERENCE: 3101.1
 ; CURRENT APPLICATION NUMBER: US/10/809,189
 ; CURRENT FILING DATE: 2004-03-25
 ; PRIOR APPLICATION NUMBER: US/09/396,196
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: 60/100,678
 ; PRIOR FILING DATE: 1998-09-17
 ; NUMBER OF SEQ ID NOS: 127806
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 67918
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: mus musculus
 US-10-809-189-67918

Query Match 1.1%; Score 20.2; DB 1; Length 25;
 Best Local Similarity 88.0%; Pred. No. 5.2e+02;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1375 CGAGTGACTCCAGACCATGACG 1399
 |||||
 Db 1 CGAGGCAACTCGAAGACCATGACG 25

RESULT 380
 US-10-809-189-67927
 ; Sequence 67927, Application US/10809189
 ; Publication No. US20050048531A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Michael Miltmann
 ; APPLICANT: David Mack
 ; APPLICANT: David Lockhart
 ; APPLICANT: Affymetrix, Inc.
 ; TITLE OF INVENTION: Methods of Genetic Analysis
 ; FILE REFERENCE: 3101.1
 ; CURRENT APPLICATION NUMBER: US/10/809,189
 ; CURRENT FILING DATE: 2004-03-25
 ; PRIOR APPLICATION NUMBER: US/09/396,196
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: 60/100,678
 ; PRIOR FILING DATE: 1998-09-17
 ; NUMBER OF SEQ ID NOS: 127806
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 67927
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: mus musculus
 US-10-809-189-67927

Query Match 1.1%; Score 20.2; DB 1; Length 25;
 Best Local Similarity 88.0%; Pred. No. 5.2e+02;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1165 GCCTTCGCGTGCCTTCATCA 1189
 |||||
 Db 1 GCCTTCGCTGCTGCCCTTCATCA 25

RESULT 381
 US-10-809-189-67930
 ; Sequence 67930, Application US/10809189
 ; Publication No. US20050048531A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Michael Miltmann
 ; APPLICANT: David Mack
 ; APPLICANT: David Lockhart
 ; APPLICANT: Affymetrix, Inc.
 ; TITLE OF INVENTION: Methods of Genetic Analysis
 ; FILE REFERENCE: 3101.1
 ; CURRENT APPLICATION NUMBER: US/10/809,189
 ; CURRENT FILING DATE: 2004-03-25
 ; PRIOR APPLICATION NUMBER: US/09/396,196
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: 60/100,678
 ; PRIOR FILING DATE: 1998-09-17
 ; NUMBER OF SEQ ID NOS: 127806
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 67930
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: mus musculus
 US-10-809-189-67930

Query Match 1.1%; Score 20.2; DB 1; Length 25;
 Best Local Similarity 88.0%; Pred. No. 5.2e+02;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1231 TATCTCAGACCCGAGGAGTGT 1255
 |||||
 Db 1 TACTTCAGACCCGAGGAGTGT 25

RESULT 382
 US-10-809-189-67931
 ; Sequence 67931, Application US/10809189
 ; Publication No. US20050048531A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Michael Miltmann
 ; APPLICANT: David Mack
 ; APPLICANT: David Lockhart
 ; APPLICANT: Affymetrix, Inc.
 ; TITLE OF INVENTION: Methods of Genetic Analysis
 ; FILE REFERENCE: 3101.1
 ; CURRENT APPLICATION NUMBER: US/10/809,189
 ; CURRENT FILING DATE: 2004-03-25
 ; PRIOR APPLICATION NUMBER: US/09/396,196
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: 60/100,678
 ; PRIOR FILING DATE: 1998-09-17
 ; NUMBER OF SEQ ID NOS: 127806
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 67931
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: mus musculus
 US-10-809-189-67931

Query Match 1.1%; Score 20.2; DB 1; Length 25;
 Best Local Similarity 88.0%; Pred. No. 5.2e+02;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1237 CAGACCCAGGCGAGTGTACAAAG 1261
 |||||
 Db 1 CAGACCCAGAGCAGCGTGTACAAAG 25

RESULT 383
 US-10-956-157-170659
 ; Sequence 170659, Application US/10956157
 ; Publication No. US20050118625A1


```
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: Patent version 3.2
; SEQ ID NO 170659
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-956-157-170659

Query Match
Best Local Similarity 1.1%; Score 20.2; DB 1; Length 25;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1386 CACAGCCATGACAGAGCTTCAGC 1410
Db 1 CACACCGCTCACAGAGCTTCAGC 25

RESULT 384
US-11-036-317-411229
; Sequence 411229, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 411229
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-411229

Query Match
Best Local Similarity 1.1%; Score 20.2; DB 1; Length 25;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 493 CACACGATGCTACTACGGCTCT 517
Db 1 CACACGCTGTGCTACTACGGCTCT 25

RESULT 385
US-11-036-317-413994
; Sequence 413994, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 413994
; LENGTH: 25
; TYPE: DNA
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```
; ORGANISM: Mus musculus
US-11-036-317-413994

Query Match
Best Local Similarity 1.1%; Score 20.2; DB 1; Length 25;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1243 CAGGCGCTGTCTCAAGTCAGCC 1267
Db 1 CAGAGCAGCGTGTCAAGTCAGCC 25

RESULT 386
US-11-060-756-27267
; Sequence 27267, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: Patent version 3.2
; SEQ ID NO 27267
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-060-756-27267

Query Match
Best Local Similarity 1.1%; Score 20.2; DB 1; Length 25;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1005 CATCTTCTCTCTCTGCTCCATC 1029
Db 1 CATCTTCTCTCTCTGCTCCATC 25

RESULT 387
US-11-060-756-34789
; Sequence 34789, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: Patent version 3.2
; SEQ ID NO 34789
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-060-756-34789

Query Match
Best Local Similarity 1.1%; Score 20.2; DB 1; Length 25;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1116 CATCATCTACTGCTGCTCAATGAC 1140
Db 1 CATCATCTACTGCTGCTCAATGAC 25

RESULT 388
US-11-060-756-34795
; Sequence 34795, Application US/11060756
```

```
/ Publication No. US20050221354A1
/ GENERAL INFORMATION:
/ APPLICANT: Wyeth
/ APPLICANT: Mounts, William Martin
/ TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
/ TITLE OF INVENTION: Target Genes
/ FILE REFERENCE: AM101083 (031896-042000)
/ CURRENT APPLICATION NUMBER: US/11/060,756
/ CURRENT FILING DATE: 2005-02-18
/ NUMBER OF SEQ ID NOS: 303284
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 34795
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: probe
US-11-060-756-34795

Query Match      1.1%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 5.2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy      1049 AGAAGTTATCCACAGGCTTACCT 1073
Db      1 ACAAGTTCATCCACAGGCTTACCT 25

RESULT 389
US-11-060-756-34800
/ Sequence 34800, Application US/11060756
/ Publication No. US20050221354A1
/ GENERAL INFORMATION:
/ APPLICANT: Wyeth
/ APPLICANT: Mounts, William Martin
/ TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
/ TITLE OF INVENTION: Target Genes
/ FILE REFERENCE: AM101083 (031896-042000)
/ CURRENT APPLICATION NUMBER: US/11/060,756
/ CURRENT FILING DATE: 2005-02-18
/ NUMBER OF SEQ ID NOS: 303284
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 34800
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: probe
US-11-060-756-34800

Query Match      1.1%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 5.2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy      1117 ATCATCTACTGCTGCTCAATGACA 1141
Db      1 ATCATCTACTGCTGCTCAACACACA 25

RESULT 390
US-11-060-756-34880
/ Sequence 34880, Application US/11060756
/ Publication No. US20050221354A1
/ GENERAL INFORMATION:
/ APPLICANT: Wyeth
/ APPLICANT: Mounts, William Martin
/ TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
/ TITLE OF INVENTION: Target Genes
/ FILE REFERENCE: AM101083 (031896-042000)
/ CURRENT APPLICATION NUMBER: US/11/060,756
/ CURRENT FILING DATE: 2005-02-18
/ NUMBER OF SEQ ID NOS: 303284
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 34880
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: probe
```

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US-11-060-756-34880

Query Match      1.1%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 5.2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy      1115 CCATCATCTACTGCTGCTCAATGA 1139
Db      1 CCATCATCTACTGCTGCTCAATGA 25

RESULT 391
US-11-060-756-36619
/ Sequence 36619, Application US/11060756
/ Publication No. US20050221354A1
/ GENERAL INFORMATION:
/ APPLICANT: Wyeth
/ APPLICANT: Mounts, William Martin
/ TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
/ TITLE OF INVENTION: Target Genes
/ FILE REFERENCE: AM101083 (031896-042000)
/ CURRENT APPLICATION NUMBER: US/11/060,756
/ CURRENT FILING DATE: 2005-02-18
/ NUMBER OF SEQ ID NOS: 303284
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 36619
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: probe
US-11-060-756-36619

Query Match      1.1%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 5.2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy      1110 CAACCCCATCATCTACTGCTGCTC 1134
Db      1 CAACCCCATCATCTACTGCTGCTC 25

RESULT 392
US-11-060-756-36624
/ Sequence 36624, Application US/11060756
/ Publication No. US20050221354A1
/ GENERAL INFORMATION:
/ APPLICANT: Wyeth
/ APPLICANT: Mounts, William Martin
/ TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
/ TITLE OF INVENTION: Target Genes
/ FILE REFERENCE: AM101083 (031896-042000)
/ CURRENT APPLICATION NUMBER: US/11/060,756
/ CURRENT FILING DATE: 2005-02-18
/ NUMBER OF SEQ ID NOS: 303284
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 36624
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: probe
US-11-060-756-36624

Query Match      1.1%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 5.2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy      1111 AACCCCATCATCTACTGCTGCTCA 1135
Db      1 AACCCCATCATCTAACAATTCTCTCA 25

RESULT 393
US-11-060-756-36940
/ Sequence 36940, Application US/11060756
/ Publication No. US20050221354A1
```

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; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36940
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-36940

Query Match
Best Local Similarity 1.1%; Score 20.2; DB 1; Length 25;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1109 ACAACCCATCATCTACTGCTGCTTCA 1133
Db 1 ACAATCCATCATCTACTGCTTCA 25

RESULT 394
US-11-060-756-56876
; Sequence 56876, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56876
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-56876

Query Match
Best Local Similarity 1.1%; Score 20.2; DB 1; Length 25;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1110 CAACCCATCATCTACTGCTGCTTC 1134
Db 1 CAACCCATCATCTACGGCTACTTC 25

RESULT 395
US-11-060-756-56877
; Sequence 56877, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56877
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-56877

Query Match
Best Local Similarity 1.1%; Score 20.2; DB 1; Length 25;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1112 ACCCCATCATCTACTGCTGCTCA 1136
Db 1 ACCCCATCATCTACGGCTACTTCA 25

RESULT 396
US-11-060-756-56878
; Sequence 56878, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56878
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-56878

Query Match
Best Local Similarity 1.1%; Score 20.2; DB 1; Length 25;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1111 AACCCATCATCTACTGCTGCTCA 1135
Db 1 AACCCATCATCTACGGCTACTTCA 25

RESULT 397
US-11-060-756-122999
; Sequence 122999, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 122999
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-122999

Query Match
Best Local Similarity 1.1%; Score 20.2; DB 1; Length 25;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1120 ATCTACTGCTGCTCAATGACAGT 1144
Db 1 ATCTACTGCTGCTCAACACACAGT 25

RESULT 398
US-11-060-756-123000
; Sequence 123000, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
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; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 123000
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-123000

Query Match
Best Local Similarity 1.1%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 5.2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1120 ATCTACTGCTGCTCAATGACAGGT 1144
Db 1 ATCTACTGCTGCTCAACACAGGT 25

RESULT 399
US-11-060-756-146971
; Sequence 146971, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 146971
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-146971

Query Match
Best Local Similarity 1.1%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 5.2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1049 AGAAGTTATCCAGCAGGTCTACCT 1073
Db 1 ACAAGTCAATCCAGCAAGTCTACCT 25

RESULT 400
US-11-060-756-146972
; Sequence 146972, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 146972
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-146972
```

```

Query Match
Best Local Similarity 1.1%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 5.2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1049 AGAAGTTATCCAGCAGGTCTACCT 1073
Db 1 ACAAGTCAATCCAGCAAGTCTACCT 25

RESULT 401
US-11-136-527-151571
; Sequence 151571, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 151571
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-151571

Query Match
Best Local Similarity 1.1%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 5.2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1101 CACCATGTACACCCCATCATCTAC 1125
Db 1 CTCATCTACACCCCATCATCTAC 25

RESULT 402
US-11-136-527-151582
; Sequence 151582, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 151582
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-151582

Query Match
Best Local Similarity 1.1%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 5.2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1100 CCACATGTACACCCCATCATCTA 1124
Db 1 CTCATCTACACCCCATCATCTA 25
```

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RESULT 403
US-09-930-503-22
; Sequence 22, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; FILE REFERENCE: 39245-173913
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-22

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1000 TTCCACATCTTCTCTCTCTCT 1019
DB      1 TTCCACATCTTCTCTCTCTCT 20

RESULT 404
US-09-930-503-25/c
; Sequence 25, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; FILE REFERENCE: 39245-173913
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-25

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1012 TTCTCTGCTGCTTCATCA 1031
DB      20 TTCTCTGCTGCTTCATCAA 1

RESULT 405
US-09-930-503-27/c
; Sequence 27, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; FILE REFERENCE: 39245-173913
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-27
```

```
APPLICANT: HENRY, JAMES
APPLICANT: CAHILL, CATHERINE
APPLICANT: YASHPAL, KIRAN
TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
FILE REFERENCE: 39245-173913
CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 60/226,086
PRIOR FILING DATE: 2000-08-18
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 27
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-27

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      862 GTAGTGGGATCAGCTATG 881
DB      20 GTAGTGGGATCAGCTATG 1

RESULT 406
US-09-930-503-29/c
; Sequence 29, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; FILE REFERENCE: 39245-173913
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-29

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      637 TCAGCCAGCCAGCAAGT 656
DB      20 TCAGCCAGCCAGCAAGT 1

RESULT 407
US-09-930-503-30/c
; Sequence 30, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; FILE REFERENCE: 39245-173913
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-30
```

```
; FILE REFERENCE: 39245-173913
; CURRENT APPLICATION NUMBER: US/09/930,503
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-30

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      601 TACATGGCCATCATCATCC 620
Db      20 TACATGGCCATCATCATCC 1

RESULT 408
US-09-930-503-41/c
; Sequence 41, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; FILE REFERENCE: 39245-173913
; CURRENT APPLICATION NUMBER: US/09/930,503
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-41

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1000 TTCGACATCTCTCTCTCT 1019
Db      20 TTCGACATCTCTCTCTCT 1

RESULT 409
US-09-930-503-44
; Sequence 44, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; FILE REFERENCE: 39245-173913
; CURRENT APPLICATION NUMBER: US/09/930,503
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
```

```
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-44

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1012 TTCCTCTGCGCCCTACATCA 1031
Db      1 TTCCTCTGCGCCCTACATCA 20

RESULT 410
US-09-930-503-46
; Sequence 46, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; FILE REFERENCE: 39245-173913
; CURRENT APPLICATION NUMBER: US/09/930,503
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-46

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      862 GTAGTGGGAATCACACTATG 881
Db      1 GTAGTGGGAATCACACTATG 20

RESULT 411
US-09-930-503-48
; Sequence 48, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; FILE REFERENCE: 39245-173913
; CURRENT APPLICATION NUMBER: US/09/930,503
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 20
; TYPE: DNA
```

```
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-48
```

```
Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      637 TCAGCCACAGCCACCAAGT 656
Db      1 TCAGCCACAGCCACCAAGT 20
```

RESULT 412

```
US-09-930-503-49
Sequence 49, Application US/09930503
Publication No. US20030060438A1
GENERAL INFORMATION:
```

APPLICANT: HENRY, JAMES

APPLICANT: CAHILL, CATHERINE

APPLICANT: VASHPAL, KIRAN

TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND

FILE REFERENCE: 39245-173913

CURRENT APPLICATION NUMBER: US/09/930,503

CURRENT FILING DATE: 2001-08-16

PRIOR APPLICATION NUMBER: 60/226,086

PRIOR FILING DATE: 2000-08-18

NUMBER OF SEQ ID NOS: 59

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 49

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Primer

US-09-930-503-49

```
Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      601 TACATGCCATCATCATCC 620
Db      1 TACATGCCATCATCATCC 20
```

RESULT 413

```
US-10-146-354A-34/C
Sequence 34, Application US/10146354A
Publication No. US20030054381A1
GENERAL INFORMATION:
```

APPLICANT: Pfizer Inc.

APPLICANT: Seymour, Albert B.

APPLICANT: Nelson, Darcy L.

APPLICANT: Webb, Suzin M.

TITLE OF INVENTION: GENETIC POLYMORPHISMS IN THE HUMAN NEUROKININ 1 RECEPTOR GENE AND

FILE REFERENCE: PC10461AGPR

CURRENT APPLICATION NUMBER: US/10/146,354A

CURRENT FILING DATE: 2002-08-15

PRIOR APPLICATION NUMBER: 60/293,425

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 48

SOFTWARE: PatentIn version 3.1

SEQ ID NO 34

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Primer

```
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)..(20)
OTHER INFORMATION: artificial / primer
US-10-146-354A-34
```

```
Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      355 GGCACCTGTGTAGTGTG 374
Db      20 GGCACCTGTGTAGTGTG 1
```

RESULT 414

```
US-10-146-354A-46/C
Sequence 46, Application US/10146354A
Publication No. US20030054381A1
GENERAL INFORMATION:
```

APPLICANT: Pfizer Inc.

APPLICANT: Seymour, Albert B.

APPLICANT: Nelson, Darcy L.

APPLICANT: Webb, Suzin M.

TITLE OF INVENTION: GENETIC POLYMORPHISMS IN THE HUMAN NEUROKININ 1 RECEPTOR GENE AND

FILE REFERENCE: PC10461AGPR

CURRENT APPLICATION NUMBER: US/10/146,354A

CURRENT FILING DATE: 2002-08-15

PRIOR APPLICATION NUMBER: 60/293,425

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 48

SOFTWARE: PatentIn version 3.1

SEQ ID NO 46

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Primer

FEATURE:

NAME/KEY: misc.feature

LOCATION: (1)..(20)

OTHER INFORMATION: artificial / primer

US-10-146-354A-46

```
Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1483 CCCTTCATGCATGGAATTC 1502
Db      20 CCCTTCATGCATGGAATTC 1
```

RESULT 415

```
US-10-146-354A-47
Sequence 47, Application US/10146354A
Publication No. US20030054381A1
GENERAL INFORMATION:
```

APPLICANT: Pfizer Inc.

APPLICANT: Seymour, Albert B.

APPLICANT: Nelson, Darcy L.

APPLICANT: Webb, Suzin M.

TITLE OF INVENTION: GENETIC POLYMORPHISMS IN THE HUMAN NEUROKININ 1 RECEPTOR GENE AND

FILE REFERENCE: PC10461AGPR

CURRENT APPLICATION NUMBER: US/10/146,354A

CURRENT FILING DATE: 2002-08-15

PRIOR APPLICATION NUMBER: 60/293,425

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 48

```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; NAME/KEY: misc_feature
; LOCATION: (1)..(20)
; OTHER INFORMATION: artificial / primer
US-10-146-354A-47
```

```
Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1417 TCCAAATGCTCTCTAGGC 1436
          |||||
Db       1 TCCAAATGCTCTCTAGGC 20
```

```
RESULT 416
US-10-146-354A-48/C
; Sequence 48, Application US/10146354A
; Publication No. US20030054381A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Seymour, Albert B.
; APPLICANT: Nelson, Darcy L.
; APPLICANT: Webb, Suzin M.
; APPLICANT: Affcoult, Jason P.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS IN THE HUMAN NEUROKININ 1 RECEPTOR GENE AND
; FILE REFERENCE: PCI0461AGPR
; CURRENT APPLICATION NUMBER: US/10/146,354A
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/293,425
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; NAME/KEY: misc_feature
; LOCATION: (1)..(20)
; OTHER INFORMATION: artificial / primer
US-10-146-354A-48
```

```
Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1746 GCGAGTGTCTATTCAGCAT 1765
          |||||
Db       20 GCGAGTGTCTATTCAGCAT 1
```

```
RESULT 417
US-10-005-956-1213
; Sequence 1213, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
```

```
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1213
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-005-956-1213
```

```
Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      609 CATCATATACATCCCTCCAGC 628
          |||||
Db       1 CATCATATACATCCCTCCAGC 20
```

```
RESULT 418
US-10-005-956-1214
; Sequence 1214, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1214
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-005-956-1214
```

```
Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      915 CTACACGAGCAAGTCTCTG 934
          |||||
Db       1 CTACACGAGCAAGTCTCTG 20
```

```
RESULT 419
US-10-310-914A-386277/C
; Sequence 386277, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087,0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 138402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 386277
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
```


US-10-310-914A-386277

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1720 ATTCTGAGAGTGCCTTGG 1739
DB 20 ATTCTGAGAGTGCCTTGG 1

RESULT 420

US-10-310-914A-386290/c
; Sequence 386290, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzae
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 386290
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-386290

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1715 ATTCATTCTCGAGAGTAC 1734
DB 20 ATTCATTCTCGAGAGTAC 1

RESULT 421
US-10-310-914A-386294/c
; Sequence 386294, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzae
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 386294
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-386294

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1552 GGGTCAGTATGGGTTAGGA 1571
DB 20 GGGTCAGTATGGGTTAGGA 1

RESULT 422
US-09-930-503-32/c
; Sequence 32, Application US/09930503
; Publication No. US20030060438A1

GENERAL INFORMATION:
APPLICANT: HENRY, JAMES
APPLICANT: CAHILL, CATHERINE
APPLICANT: YASHPAL, KIRAN

TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
TITLE OF INVENTION: THERAPEUTIC USES THEREOF
FILE REFERENCE: 39245-173913
CURRENT APPLICATION NUMBER: US/09/930.503
CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 60/226,086
PRIOR FILING DATE: 2000-08-18
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 32
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-32

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 523 TGCAGTCCACAACTTCTT 542
DB 21 TGCAGTCCACAACTTCTT 2

RESULT 423
US-09-930-503-51
; Sequence 51, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREOF
; FILE REFERENCE: 39245-173913
; CURRENT APPLICATION NUMBER: US/09/930.503
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-51

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 523 TGCAGTCCACAACTTCTT 542
DB 1 TGCAGTCCACAACTTCTT 20

RESULT 424
US-10-451-304-11
; Sequence 11, Application US/10451304
; Publication No. US20050079495A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company LLC
; APPLICANT: Hall, Matthew D.
; APPLICANT: McNulty, Shaun
; APPLICANT: Murray, James H.

```

; APPLICANT: Suman-Chauhan, Nirmala
; TITLE OF INVENTION: Modified Tachykinin Receptors
; FILE REFERENCE: A0000197
; CURRENT APPLICATION NUMBER: US/10/451,304
; CURRENT FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: PCT/GB01/05404
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: UK 0031148.0
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Oligonucleotide
US-10-451-304-11

```

```

Query Match      1.1%; Score 19.8; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 5.1e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      438 CGCGAGGCTCTCCATGCGTGCAT 460
Db      1 CGCGAGGCTTCTATGCGTGCAT 23

```

```

RESULT 425
US-09-931-700-13/C
; Sequence 13, Application US/09931700
; Patent No. US20020055615A1
; GENERAL INFORMATION:
; APPLICANT: CUTTITTA, FRANK
; APPLICANT: MARTINEZ, ALFREDO
; APPLICANT: MILLER, MAE JEAN
; APPLICANT: UNSWORTH, EDWARD J.
; APPLICANT: HOOK, WILLIAM
; APPLICANT: WALSH, THOMAS
; APPLICANT: GREY, KAREN
; APPLICANT: MACRI, CHARLES
; TITLE OF INVENTION: Functional Role of Adrenomedullin (AM) and the
; TITLE OF INVENTION: Gene-Related Product (RAMP) in Human Pathology and
; TITLE OF INVENTION: Physiology
; FILE REFERENCE: 2026-4202U4
; CURRENT APPLICATION NUMBER: US/09/931,700
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 09/011,922
; PRIOR FILING DATE: 1998-02-17
; PRIOR APPLICATION NUMBER: PCT/US96/13286
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US/60/013,172
; PRIOR FILING DATE: 1996-03-12
; PRIOR APPLICATION NUMBER: US60/002,936
; PRIOR FILING DATE: 1995-08-30
; PRIOR APPLICATION NUMBER: US/60/002,514
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid,
; OTHER INFORMATION: AM-R antisense probe (nucleotides 788-811)
US-09-931-700-13

```

```

Query Match      1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 6e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

QY 980 TCGCATCTGCTGCTGCCCTTCC 1003

```

Db      24 TTGTACATCTGCTGCGCTTACC 1

```

```

RESULT 426
US-09-930-503-35
; Sequence 35, Application US/09930503
; Publication No. US20030060458A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREOF
; FILE REFERENCE: 39245-173913
; CURRENT APPLICATION NUMBER: US/09/930,503
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-35

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      176 GTGTACGATAGTAGGCTT 194
Db      1 GTGTACGATAGTAGGCTT 19

```

```

RESULT 427
US-09-930-503-37/C
; Sequence 37, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREOF
; FILE REFERENCE: 39245-173913
; CURRENT APPLICATION NUMBER: US/09/930,503
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-37

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1548 AAAAGGTCAGTAGGCTT 1566
Db      19 AAAAGGTCAGTAGGCTT 1

```

RESULT 428

```
US-09-930-503-54/c
; Sequence 54, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; FILE REFERENCE: 39245-173913
; CURRENT APPLICATION NUMBER: US/09/930,503
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-54

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      176 GTGTACAGATAGTAGGCTT 194
Db      19 GTGTACAGATAGTAGGCTT 1

RESULT 429
US-09-930-503-56
; Sequence 56, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; FILE REFERENCE: 39245-173913
; CURRENT APPLICATION NUMBER: US/09/930,503
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-56

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1548 AAAAGGTCAGTATGGCTT 1566
Db      1 AAAAGGTCAGTATGGCTT 19

RESULT 430
US-10-005-956-81
; Sequence 81, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
```

```
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 81
; LENGTH: 19
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-005-956-81

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      534 CAACTCTTCCCATCGCC 552
Db      1 CAACTCTTCCCATCGCC 19

RESULT 431
US-10-005-956-85/c
; Sequence 85, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 85
; LENGTH: 19
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-005-956-85

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1626 TCATGCTGTGTGACTCAA 1644
Db      19 TCATGCTGTGTGACTCAA 1

RESULT 432
US-10-005-956-87/c
; Sequence 87, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
```

```

; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 87
; LENGTH: 19
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-005-956-87

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1335 CACACCTCGTCCCTGGAC 1353
Db      19 CACACCTCGTCCCTGGAC 1

```

```

RESULT 433
US-10-005-956-145/c
; Sequence 145, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 145
; LENGTH: 19
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-005-956-145

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      663 CTGTGTCATCTGGGTCTCG 681
Db      19 CTGTGTCATCTGGGTCTCG 1

```

```

RESULT 434
US-10-005-956-149/c
; Sequence 149, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 149
; LENGTH: 19

```

```

; TYPE: DNA
; ORGANISM: homo sapiens
US-10-005-956-149

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1529 CCTCAGCTGGAGCTTGCA 1547
Db      19 CCTCAGCTGGAGCTTGCA 1

```

```

RESULT 435
US-10-310-914A-386272/c
; Sequence 386272, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kravut
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 386272
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-386272

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      167 AGGGGGTGTGTACAGAT 185
Db      19 AGGGGGTGTGTACAGAT 1

```

```

RESULT 436
US-10-310-914A-386273/c
; Sequence 386273, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kravut
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 386273
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-386273

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      167 AGGGGGTGTGTACAGAT 185
Db      19 AGGGGGTGTGTACAGAT 1

```

```

RESULT 437
US-10-310-914A-386300/c

```

```
; Sequence 386300, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 386300
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-386300

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1475 ACCTGCTCCTTCATGCA 1493
Db      19  ACCTGCTCCTTCATGCA 1

RESULT 438
US-10-310-914A-386304/C
; Sequence 386304, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 386304
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-386304

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      134 GCCCGAGCGCCAGCCACA 152
Db      19  GCCCGAGCGCCAGCCACA 1

RESULT 439
US-11-083-784-491124
; Sequence 491124, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083.784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714.333
; PRIOR FILING DATE: 2003-11-14
```

```
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491124
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491124

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      401 GGACAGTGACGAAGTATT 419
Db      1  GGACAGTGACGAAGTATT 19

RESULT 440
US-11-083-784-491125
; Sequence 491125, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083.784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714.333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491125
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491125

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      1655 GAACCTTGCTGAGCCTGTA 1673
Db      1  GAACCTTGCTGAGCCTGTA 19

RESULT 441
US-11-083-784-491126
; Sequence 491126, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083.784
```

```
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491126
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491126

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      247 CCAAACTCTCCACTAAC 265
Db      1 CCAAACTCTCCACTAAC 19

RESULT 442
US-11-083-784-491127
; Sequence 491127, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491127
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491127

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      773 CGAACAGATTATGAGA 791
Db      1 CGAACAGATTATGAGA 19

RESULT 443
US-11-083-784-491128
; Sequence 491128, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
```

```
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491128
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491128

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      76 AAAGAGTGTGCCCATAA 94
Db      1 AAAGAGTGTGCCCATAA 19

RESULT 444
US-11-083-784-491129
; Sequence 491129, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491129
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491129

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      789 GAAAGTGATCCATCTGT 807
Db      1 GAAAGTGATCCATCTGT 19

RESULT 445
US-11-083-784-491130
; Sequence 491130, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
```

```

; APPLICANT: Leeke, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491130
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491130
```

```

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy 178 GTACAGATACGAGCTTTA 196
Db 1 GUACAGAUAGUGGCUUUA 19
```

```

RESULT 446
US-11-083-784-491131
; Sequence 491131, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leeke, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491131
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491131
```

```

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 11; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy 809 TGACTGTCTGATCTACTT 827
Db 1 UGACUGUGCUGAUCUACU 19
```

```

RESULT 447
US-11-083-784-491132
; Sequence 491132, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leeke, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491132
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491132
```

```

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy 1033 CCAGATCTCTACGCTGAGA 1051
Db 1 CCAGATCTCTACGCTGAGA 19
```

```

RESULT 448
US-11-083-784-491133
; Sequence 491133, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leeke, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491133
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491133
```

```

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy 650 CCAAGTGTCTGATCTGCT 668
Db 1 CCAAGTGTCTGATCTGCT 19
```

```

RESULT 449
US-11-083-784-491134
```

```

Sequence 491134, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khavrova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OR INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 134990US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIORITY APPLICATION NUMBER: US/10/714,333
PRIORITY FILING DATE: 2003-11-14
PRIORITY APPLICATION NUMBER: 60/502,050
PRIORITY FILING DATE: 2003-09-10
PRIORITY APPLICATION NUMBER: 60/426,137
PRIORITY FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 491134
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-491134

```

```
Query Match Similarity      1.1% Score 19; DB 1; Length 19;
Best Local Similarity      68.4% Pred. No. 4.6e+02;
Matches    13; Conservative   6; Mismatches    0; Indels    0; Gaps    0;
```

```

RESULT 450
US-11-083-784-491135
; Sequence 491135, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 1349905
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491135
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491135

```

	Query Match	1.1%	Score 19;	DB 1;	length 19;
	Best Local Similarity	73.78%	Pred. No.	4.6e+02;	
	Matches	14;	Conservative	5;	Mismatches 0; Indels 0; Gaps 0
OY	600	GTACATGGCCATCATACAT	618		
	: : : :				
Dd	1	GTACAUGGCCAUCAUCAU	19		

```

RESULT 451
US-11-083-784-491136
; Sequence 491136, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083.784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491136
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491136

```

Query Match Similarity	1.1%	Score 19;	DB 1;	Length 19;
Best Local Similarity	84.2%	Pred. No. 4,6e+02;		
Matches	16;	Conservative	3;	Mismatches 0;
				Indels 0;
				Gaps 0;
QY	398	TGAGGACAGTGACGACACTA	416	
	:			:
DB	1	UGAGGACAGUGACGACACTA	19	

```

RESULT 452
US-11-083-784-491137
; Sequence 491137, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Pharmaco, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491137
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491137

```

Query Match	1.1%	Score 19	DB 1	Length 19
Best Local Similarity	78.9%	Pred. NO. 4.6e+02		
Matches 15; Conservative	4	Mismatches 0	Indels 0	Gaps 0

Db 1 GAGAAAGUGAACCAUCU 19

RESULT 453

US-11-083-784-491138
; Sequence 491138, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491138
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491138

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 578 TGACGGCTGGGCTTGA 596
Db 1 GAGCGCGUGGCCUUGA 19

RESULT 454

US-11-083-784-491139
; Sequence 491139, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491139
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491139

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;

Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 777 CAAGATTATGAGAAAGTG 795
Db 1 CAAGATUUAUGAGAAAGUG 19

RESULT 455

US-11-083-784-491140
; Sequence 491140, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491140
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491140

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 766 GAGCATCCGAACAATTT 784
Db 1 GAGCAUCCGACACAAAUU 19

RESULT 456

US-11-083-784-491141
; Sequence 491141, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491141
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491141

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 761 GGCCAGAGCATCCGACAA 779
Db 1 GGCCAGAGCAUCCGACAA 19

RESULT 457
US-11-083-784-491142
; Sequence 491142, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491142
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491142

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 4.6e+02;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 106 CCTCTGCTGCTTTGAA 124
Db 1 CCTCCUGUCGUUAGAA 19

RESULT 458
US-11-083-784-491143
; Sequence 491143, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491143
; LENGTH: 19

; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491143

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1473 TGACTGCTCCCTTCATG 1491
Db 1 UGACUGCCUCCUCCUUG 19

RESULT 459
US-11-083-784-491144
; Sequence 491144, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491144
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491144

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 47.4%; Pred. No. 4.6e+02;
Matches 9; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY 1600 TCAATTCTTCCCTTCTTT 1618
Db 1 UCAUUCUCCUCCUUCUU 19

RESULT 460
US-11-083-784-491145
; Sequence 491145, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911

```
; SOFTWARE: Proprietary
; SEQ ID NO 491145
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491145
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 576 CATGACGGCTGTGCGCTTT 594
||:|||||:|||||:
Db 1 CAUGACGGCTUGGCGCTUU 19
```

```
RESULT 461
US-11-083-784-491146
; Sequence 491146, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491146
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491146
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 4.6e+02;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 395 GAATGACGACACTGACGAA 413
||:|||||:|||||:
Db 1 GAATGACGACAGGACGAA 19
```

```
RESULT 462
US-11-083-784-491147
; Sequence 491147, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
```

```
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491147
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491147
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 375 GATCATCTTAGCCGACAA 393
||:|||||:|||||:
Db 1 GAUCAUCUAGCCGACAA 19
```

```
RESULT 463
US-11-083-784-491148
; Sequence 491148, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491148
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491148
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1641 CAATCAATCTGTAAGT 1659
||:|||||:|||||:
Db 1 CAATCAATCACTGTAAGT 19
```

```
RESULT 464
US-11-083-784-491149
; Sequence 491149, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
```

```

; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491149
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491149

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY      447 CTCGATGCGTCGATTCAT 465
Db      1 CUCCAGGCGGCAUCCAU 19

```

```

RESULT 465
US-11-083-784-491150
; Sequence 491150, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491150
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491150

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY      1742 GCAGCGAGTGTCTCTTC 1760
Db      1 GCAUGCGAGUCGCAUUC 19

```

```

RESULT 466
US-11-083-784-491151
; Sequence 491151, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US

```

```

; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491151
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491151

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY      1415 CCTGCAATGCTCTCTCTA 1433
Db      1 CCUCCAUUGGCUCCUCA 19

```

```

RESULT 467
US-11-083-784-491152
; Sequence 491152, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491152
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491152

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 52.6%; Pred. No. 4.6e+02;
Matches 10; Conservative 9; Mismatches 0; Indels 0; Gaps 0;
QY      1598 TCTCAATCTTCTCTCTCT 1616
Db      1 UCUCAUUCUUCUCCUUCU 19

```

```

RESULT 468
US-11-083-784-491153
; Sequence 491153, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William

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; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491153
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-083-784-491153

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      1242 CCAGGCGCATGTGTACAA 1260
Db      1 CCAGGCGCATGTGTACAA 19

RESULT 469
; Sequence 491154, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491154
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-083-784-491154

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1031 ACCCAGTCTCTACCTGAA 1049
Db      1 ACCCAGTCTCTACCTGAA 19

RESULT 470
; Sequence 491155, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
```

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; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491155
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-083-784-491155

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy      55 GAGGCGCATGTTC 73
Db      1 GAGGCGCATGTTC 19

RESULT 471
; Sequence 491156, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491156
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-083-784-491156

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy      356 GCAACGTGTGTATGATGTG 374
Db      1 GCAACGTGTGTATGATGTG 19

RESULT 472
; Sequence 491157, Application US/11083784
; Publication No. US20050245475A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ CURRENT FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491157
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-491157
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

QY 266 CCTCGAAGCCCAATGCAGT 284

Db 1 CCUCGAAGCCCAUCCAGU 19

RESULT 473

```
US-11-083-784-491158
/ Sequence 491158, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ CURRENT FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491158
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-491158
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

QY 1699 CTCAGAGCCCAATGCATT 1717

Db 1 CUCAGAGCCCAUCCAGU 19

RESULT 474

```
US-11-083-784-491159
/ Sequence 491159, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ CURRENT FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491159
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-491159
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

QY 1570 GAAACATTCCACCTTGA 1588

Db 1 GAAAGACUCCAUCCUGA 19

RESULT 475

```
US-11-083-784-491160
/ Sequence 491160, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ CURRENT FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491160
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-491160
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

QY 1376 GAAGTACTCCAGAGCCAT 1394

Db 1 GAAGGACUCCAGAGCCAU 19

RESULT 476
US-11-083-784-491161
; Sequence 491161, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491161
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491161

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 4.6e+02;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
Qy 35 TCCAGAGCGTTATATTC 53
Db 1 UCCAGAGCGUUAUUC 19

RESULT 477
US-11-083-784-491162
; Sequence 491162, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491162
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491162

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 4.6e+02;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 102 CCACCTCTCTCTCTTT 120
Db 1 CCACCCCTCGCTCGCTT 19

RESULT 478
US-11-083-784-491163
; Sequence 491163, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491163
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491163

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 4.6e+02;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 764 CAGAGCATCCGACAGAT 782
Db 1 CAGAGCAUCCGACAGAU 19

RESULT 479
US-11-083-784-491164
; Sequence 491164, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491164
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491164

Query Match 1.1%; Score 19; DB 1; Length 19;


```

; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491168

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      737 GCAGAGTCGTGTCATGAT 755
Db      1 GCAGAGUCGUGGCAUGAU 19

RESULT 484
US-11-083-784-491169
; Sequence 491169, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491169
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491169

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      1660 TTGCTGAGCCTGTAAATA 1678
Db      1 UUGCUGAGCCUGUAAAUA 19

RESULT 485
US-11-083-784-491170
; Sequence 491170, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2002-11-14
```

```

; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491170
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491170

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1638 ACTCAACCAATCATCTGA 1656
Db      1 ACUCAAACCAAUCCUGA 19

RESULT 486
US-11-083-784-491171
; Sequence 491171, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491171
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491171

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 4.6e+02;
Matches 11; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY      1596 AATCTCAATTCCTCCAT 1614
Db      1 AAUCUCAUUCUCCUUAU 19

RESULT 487
US-11-083-784-491172
; Sequence 491172, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2002-11-14
```

```

; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491172
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491172
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 941 GCAAGGTGTCGCAAAATGAT 959
Db 1 GCAAGGUGGUCAAAAGAU 19
```

```
RESULT 488
US-11-083-784-491173
; Sequence 491173, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491173
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491173
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 245 CCCCAACATCTCCACTAA 263
Db 1 CCCCAACACUCCACCUAA 19
```

```
RESULT 489
US-11-083-784-491174
; Sequence 491174, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
```

```

; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491174
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491174
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 109 CCTGTCGCTTTAGAAAGA 127
Db 1 CCUGUCUGCUUAGAAAGA 19
```

```
RESULT 490
US-11-083-784-491175
; Sequence 491175, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491175
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491175
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 32 GCATCAGAAAGCTTTATA 50
Db 1 GCAUCCAGAAAGCGUUAUA 19
```

```
RESULT 491
US-11-083-784-491176
; Sequence 491176, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
```

```
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491176
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491176

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 4.6e+02;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
```

QY 583 GCTGTGCGCTTGTGATGACT 601
||:|||||:|||||:
1 GCUGGCGCCTUGCAUAGGU 19

Db 1 GCUGGCGCCTUGCAUAGGU 19

```
RESULT 492
US-11-083-784-491177
; Sequence 491177, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491177
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491177
```

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 482 CCAATGCTGTCACACGA 500
||:|||||:|||||:
1 CCUAGCUGUCACACGA 19

Db 1 CCUAGCUGUCACACGA 19

```
RESULT 493
US-11-083-784-491178
; Sequence 491178, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
```

```
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491178
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491178

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

QY 261 TAACACCTCGAACCAGT 279
:|||||:|||||:
1 UAACACCTCGAACCAGU 19

Db 1 UAACACCTCGAACCAGU 19

```
RESULT 494
US-11-083-784-491179
; Sequence 491179, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491179
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491179
```

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1407 CAGCTTCTCTCCAGATGTG 1425
||||:||||:||||:
1 CAGCUCUCUCCCAUGUG 19

Db 1 CAGCUCUCUCCCAUGUG 19

```
RESULT 495
US-11-083-784-491180
; Sequence 491180, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
```

```

; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491180
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491180

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1360 TCCAACTGCTCTTTCACGAA 1378
      :||||:|:|:|:|:|:|
Db      1 UCCAACTGCTCTTTCACGAA 19

RESULT 496
US-11-083-784-491181
; Sequence 491181, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491181
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491181

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```

; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491182
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491182

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      652 AAAGTGTCATCTGTCTCA 670
      |||||:|:|:|:|:|:|
Db      1 AAAGTGTCACTGTGTCA 19

RESULT 498
US-11-083-784-491183
; Sequence 491183, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491183
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491183
```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      354 GGGCACTGTAGTATG 372
      |||||:|:|:|:|:|:|
Db      1 GGGCACTGTAGTATG 19

RESULT 497
US-11-083-784-491182
; Sequence 491182, Application US/11083784
```

```
RESULT 499
US-11-083-784-491184
; Sequence 491184, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491184
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491184

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. NO. 4.6e+02;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1517 CATCAGAAACACCTCACA 1535
Db      1 CAUCAGAAACACCCUCACA 19

RESULT 500
US-11-083-784-491185
; Sequence 491185, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491185
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491185

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. NO. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
Db      1 CAUCAGAAACAGUUCUAC 19

RESULT 501
US-11-083-784-491186
; Sequence 491186, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491186
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491186

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. NO. 4.6e+02;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY      806 GTGAGACTGTCGATCTCA 824
Db      1 GUGGACUGGUGUACUAC 19

RESULT 502
US-11-083-784-491187
; Sequence 491187, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491187
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491187

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. NO. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      1620 CCACCCATGCTGTGTGA 1638
          |||||:|:|:|:|:|
Db      1 CCACCCUCAUGCUUGUGA 19

```

```

RESULT 503
US-11-083-784-491188
; Sequence 491188, Application US/11083764
; Publication No. US20050245475X1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scarside, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491188
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491188

```

Query Match	1.1%	Score 19	DB 1	Length 19
Best Local Similarity	68.4%	Pred No. 4.6e+02		
Matches 13	Conservative 6	Mismatches 0	Indels 0	Gaps 0
QY	1572	AAACATTCATCTTGACT	1590	
DB	1	AAACATTCATCTTGAGU	19	

```

RESULT 504-491189
US-11-083-784-491189
/ Sequence 491189, Application US/11083784
/ Publication NO. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacom, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ CURRENT FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491189
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-491189

```

Query Match	1.1%	Score 19	DB 1	Length 19
Best Local Similarity	94.7%	Pred. No. 4.6e+02		
Matches 18	Conservative 1	Mismatches 0	Indels 0	Gaps 0
OY	763	CCAGAGCATCCGAAACAGA	781	
DB	1	CCAGAGCATCCGAAACAGA	19	

```

RESULT 505
US-11-083-784-491190
; Sequence 491190, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khavrova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491190
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491190

```

Query Match	Similarity	Score	DB	Length
Best Local	Similarity	68.4%	Pred. No.	4.6e+02
Matches	13	Conservative	6	Mismatches
			0	Indels
			0	Gaps
QY	503	GGTACTACGGCTGTCTTA	521	
		: : : : : : : : :		
DB	1	GGUACUACGGCCUGUUCUA	19	

```

RESULT 506
US-11-083-784-491191
Sequence 491191, Application US/11083784
Publication No. US2005024575M1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 1349905
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 491191
LENGTH: 19
TYPE: RNA

```

ORGANISM: Homo sapiens
US-11-083-784-491191

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1215 AATGAATCCACCCGGTAT 1233
DB 1 AAGGAAUCCACCCGGUAT 19

RESULT 507
US-11-083-784-491192

Sequence 491192, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:

APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 491192
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-491192

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 196 ACCGCTAGCTTGAATG 214
DB 1 ACCGCTAGCTTGAATG 19

RESULT 508
US-11-083-784-491193

Sequence 491193, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:

APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary

SEQ ID NO 491193
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-491193

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 772 CCGACACAGATTATGAGA 790
DB 1 CCGACACAGATTATGAGA 19

RESULT 509
US-11-083-784-491194

Sequence 491194, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:

APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 491194
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-491194

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 4.6e+02;
Matches 11; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 332 TCATGTCGTGACTCTGT 350
DB 1 UCAUUGUGUGACCTCUGU 19

RESULT 510
US-11-083-784-491195

Sequence 491195, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:

APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137

```

; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491195
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491195

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy      33 CATCCAGAGCGTTATAT 51
Db      1 CAUCCAGAGCGUUUAU 19

RESULT 511
US-11-083-784-491196
; Sequence 491196, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491196
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491196

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1631 CTGTGTGACTCAACCAAA 1649
Db      1 CUGUGUACUCAACCAAA 19

RESULT 512
US-11-083-784-491197
; Sequence 491197, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
```

```

; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491197
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491197

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy      1036 GATCTCTACCTGAAGAAGT 1054
Db      1 GAUCCUCUACCUCAAGAAGU 19

RESULT 513
US-11-083-784-491198
; Sequence 491198, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491198
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491198

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy      991 TGCGTCCCTTCACATCT 1009
Db      1 UGGCTGCCCTUCCACACUCU 19

RESULT 514
US-11-083-784-491199
; Sequence 491199, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
```



```
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491199
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491199
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 769 CATCGAACAAGATTATG 787
Db 1 CAUCCGAACAGAUUUAUG 19
```

```
RESULT 515
US-11-083-784-491200
; Sequence 491200, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491200
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491200
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 753 GATCGAATGCCGACGAT 771
Db 1 GAUCCGAUGCCAGAGCAU 19
```

```
RESULT 516
US-11-083-784-491201
; Sequence 491201, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
```

```
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491201
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491201
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 550 GCCGCTGCTTCGCCAGTA 568
Db 1 GCCGCTGCTTCGCCAGTA 19
```

```
RESULT 517
US-11-083-784-491202
; Sequence 491202, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491202
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491202
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 480 CACCTATGCTGTCCACAC 498
Db 1 CACCTATGCTGTCCACAC 19
```

```
RESULT 518
US-11-083-784-491203
; Sequence 491203, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
```

```

; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491203
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491203

```

```

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 479 TCACCTATGCTGTCACAA 497
DB 1 UCACCUAUGCUGCCACAA 19

```

```

RESULT 519
US-11-083-784-491204
; Sequence 491204, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491204
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491204

```

```

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 4.6e+02;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1384 TCACAACCATCAGACAGA 1402
DB 1 UCACAACCATCAGACAGA 19

```

```

RESULT 520
US-11-083-784-491205
; Sequence 491205, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491205
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491205

```

```

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1218 GAAATCCACCCGGATCTC 1236
DB 1 GAAATCCACCCGGATCTC 19

```

```

RESULT 521
US-11-083-784-491206
; Sequence 491206, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491206
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491206

```

```

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1119 CATCTACTGCTGCTCAAT 1137
DB 1 CAUCUACUGCUGCCUCAU 19

```

```

RESULT 522
US-11-083-784-491207

```

```
; Sequence 491207, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491207
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491207
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 504 GTACTACGCGCTCTGTTCTNC 522
Db 1 GUACUACGCGCCUCUCCUAC 19
```

```
RESULT 523
US-11-083-784-491208
; Sequence 491208, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491208
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491208
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 52.6%; Pred. No. 4.6e+02;
Matches 10; Conservative 9; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1601 CAATTCTTCCCTATCTTTG 1619
Db 1 CAATUCUCCUCCUACUUCUUG 19
```

```
RESULT 524
US-11-083-784-491209
; Sequence 491209, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491209
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491209
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 233 ACTGACACTCTCCCAAA 251
Db 1 ACUCAGACUCUCCCAAA 19
```

```
RESULT 525
US-11-083-784-491210
; Sequence 491210, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491210
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491210
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1747 CGAGTGCTCATTTACAGAT 1765
```

Db 1 CGAGUGCUCAUUUCAGAGAU 19

RESULT 526

US-11-083-784-491211
; Sequence 491211, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491211
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491211

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1687 GACCAAGCTTTCCTCAGA 1705
Db 1 GACCAAGCTTTCCTCAGA 19

RESULT 527

US-11-083-784-491212
; Sequence 491212, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491212
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491212

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;

Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1642 AAACCAATCACTGAACTT 1660
Db 1 AAACCAATCACTGAACTT 19

RESULT 528

US-11-083-784-491213
; Sequence 491213, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491213
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491213

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1519 TCAGAAACACCTCTACACT 1537
Db 1 UCAGAAACACCTCTACACT 19

RESULT 529

US-11-083-784-491214
; Sequence 491214, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491214
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491214

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Oy 840 GGTGATGCTGATCATAC 858
Db 1 GGUGAUGGCUAUGCAUAC 19

RESULT 530

US-11-083-784-491215
; Sequence 491215, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491215
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491215

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Oy 203 GCTTGAATGATGATAC 221
Db 1 GCUUGAAUGAUAACGU 19

RESULT 531

US-11-083-784-491216
; Sequence 491216, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491216
; LENGTH: 19

; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491216

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Oy 543 TCCCATGCCGCTGCTTC 561
Db 1 UCCCAUGCCGCGUCUUC 19

RESULT 532

US-11-083-784-491217
; Sequence 491217, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491217
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491217

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 492 CCACACGAATGATCTAC 510
Db 1 CCACACGAUGGUCUAC 19

RESULT 533

US-11-083-784-491218
; Sequence 491218, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911

```

; SOFTWARE: Proprietary
; SEQ ID NO 491218
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491218

```

```

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1274 AGACCACCATCTCCACAGT 1292
Db      1 AGACCACCATCTCCACAGU 19

```

```

RESULT 534
US-11-083-784-491219
; Sequence 491219, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491219
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491219

```

```

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      401 GGACAGTGCAGACTATT 419
Db      1 GGACAGUGACGACUUAUU 19

```

```

RESULT 535
US-11-083-784-491220
; Sequence 491220, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10

```

```

; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491220
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491220

```

```

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      247 CCAACATCTCCACTACA 265
Db      1 CCAACATCTCCACTACA 19

```

```

RESULT 536
US-11-083-784-491221
; Sequence 491221, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491221
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491221

```

```

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      773 CGAACAGATTATGAGA 791
Db      1 CGAACAGAUUUAGAGAA 19

```

```

RESULT 537
US-11-083-784-491224
; Sequence 491224, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333

```

;; PRIOR FILING DATE: 2003-11-14
;; PRIOR APPLICATION NUMBER: 60/502,050
;; PRIOR FILING DATE: 2003-09-10
;; PRIOR APPLICATION NUMBER: 60/426,137
;; PRIOR FILING DATE: 2002-11-14
;; NUMBER OF SEQ ID NOS: 1591911
;; SOFTWARE: Proprietary
;; SEQ ID NO: 491224
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-11-083-784-491224

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 789 GAAAGTGTACCATCTGT 807
Db 1 GAAAGUGUCCACUUCUGU 19

RESULT 538
US-11-083-784-491225
; Sequence 491225, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 491225
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491225

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 4.6e+02;
Matches 11; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 809 TGACTGCTACTACTT 827
Db 1 UGACUGGUCUACUUCUGU 19

RESULT 539
US-11-083-784-491226
; Sequence 491226, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US

;; CURRENT APPLICATION NUMBER: US/11/083,784
;; CURRENT FILING DATE: 2005-03-18
;; PRIOR APPLICATION NUMBER: US/10/714,333
;; PRIOR FILING DATE: 2003-11-14
;; PRIOR APPLICATION NUMBER: 60/502,050
;; PRIOR FILING DATE: 2003-09-10
;; PRIOR APPLICATION NUMBER: 60/426,137
;; PRIOR FILING DATE: 2002-11-14
;; NUMBER OF SEQ ID NOS: 1591911
;; SOFTWARE: Proprietary
;; SEQ ID NO: 491226
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-11-083-784-491226

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1033 CCAGATCTTACTGAAGA 1051
Db 1 CCAGUUCUUCUACUGAGA 19

RESULT 540
US-11-083-784-491227
; Sequence 491227, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 491227
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491227

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 650 CCAAGTGTCTACTGTGT 668
Db 1 CCAAGUGUCCUACUUCUGU 19

RESULT 541
US-11-083-784-491229
; Sequence 491229, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William


```

; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491234
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491234
```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      578 TGACGGCTGTGCGCTTGA 596
Db      1  UGACGGCTUGGCGCCUUGA 19
```

```

RESULT 546
US-11-083-784-491236
; Sequence 491236, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491236
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491236
```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      777 CAAGATTATGCAAGG 795
Db      1  CAAGAUUUAUGAAGG 19
```

RESULT 547

```

US-11-083-784-491237
; Sequence 491237, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491237
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491237
```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      766 GAGCATCGAACAAGATT 784
Db      1  GAGCAUCCGAACAAGAUU 19
```

```

RESULT 548
US-11-083-784-491238
; Sequence 491238, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491238
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491238
```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      761 GGCAGAGCATCCGAACA 779
Db      1  GGCAGAGCAUCCGAACA 19
```

```
RESULT 549
US-11-083-784-491241
; Sequence 491241, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491241
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491244

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      576 CATGACGGCTGTGGCCTTT 594
      ||:|||||:|||||:|||||:
Db      1 CAUGACGGCTGUGGCCUUD 19

RESULT 550
US-11-083-784-491244
; Sequence 491244, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491244
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491244

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 4.6e+02;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      395 GAATGAGCAGCTGACGAA 413
      ||:|||||:|||||:|||||:
Db      1 GAUGAGGACAGUGACGAA 19

RESULT 551
US-11-083-784-491245
; Sequence 491245, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491245
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491245

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      375 GATCATCTTAGCCACGAAA 393
      ||:|||||:|||||:|||||:
Db      1 GAUCAUUCUAGCCACGAAA 19

RESULT 552
US-11-083-784-491248
; Sequence 491248, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491248
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491248

Query Match      1.1%; Score 19; DB 1; Length 19;
```

Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

OY 447 CTCGATGGCTGATTCAT 465
Db 1 CUCCAGGCGUCGACUACAU 19

RESULT 553

US-11-083-784-491251
; Sequence 491251, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491251
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491251

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1031 ACCGAGTCTTACTGTA 1049
Db 1 ACCGAGUCCUACUCUGA 19

RESULT 554

US-11-083-784-491252
; Sequence 491252, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491252
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens

US-11-083-784-491252

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 356 GCAACGTGCTAGTATGTCG 374
Db 1 GCAACGUGGUGAGUGAGUG 19

RESULT 555

US-11-083-784-491256
; Sequence 491256, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491256
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491256

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 266 CTCGGAACCCATCAGTT 284
Db 1 CCUGGAACCCAAUCAGUU 19

RESULT 556

US-11-083-784-491262
; Sequence 491262, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491262

```

; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491262

```

```

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 4.6e+02;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      764 CAGAGCATCCGACACAGAT 782
          |||||:|||||:|||||:
Db      1 CAGAGCAUCCGACACAGAU 19

```

```

RESULT 557
US-11-083-784-491263
; Sequence 491263, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491263
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491263

```

```

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      841 GTGATTGGCTATGCATACA 859
          |||||:|||||:|||||:
Db      1 GUGAUGGCUAUGCAUACA 19

```

```

RESULT 558
US-11-083-784-491264
; Sequence 491264, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14

```

```

; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491264
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491264

```

```

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      737 GCAGAGTGTGTGCATGAT 755
          |||||:|||||:|||||:
Db      1 GCAGAGUCGUGUCAUGAU 19

```

```

RESULT 559
US-11-083-784-491265
; Sequence 491265, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491265
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491265

```

```

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      245 CCCGAAACATCTCCACTAA 263
          |||||:|||||:|||||:
Db      1 CCCGAAACAUCCGACAUAA 19

```

```

RESULT 560
US-11-083-784-491268
; Sequence 491268, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050

```

```
;; PRIOR FILING DATE: 2003-09-10
;; PRIOR APPLICATION NUMBER: 60/426,137
;; PRIOR FILING DATE: 2002-11-14
;; NUMBER OF SEQ ID NOS: 1591911
;; SOFTWARE: Proprietary
;; SEQ ID NO: 491268
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-11-083-784-491268
```

```
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      941 GCAAGTGTCGCAAAATGAT 959
Db      1 GCAAGUGUGUCAAAAUAGAU 19
```

```
RESULT 561
US-11-083-784-491269
; Sequence 491269, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 491269
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491269
```

```
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      261 TAACACTCGAACCACAT 279
Db      1 UAACACCCUGCAACCCAAU 19
```

```
RESULT 562
US-11-083-784-491270
; Sequence 491270, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
```

```
;; PRIOR APPLICATION NUMBER: US/10/714,333
;; PRIOR FILING DATE: 2003-11-14
;; PRIOR APPLICATION NUMBER: 60/502,050
;; PRIOR FILING DATE: 2003-09-10
;; PRIOR APPLICATION NUMBER: 60/426,137
;; PRIOR FILING DATE: 2002-11-14
;; NUMBER OF SEQ ID NOS: 1591911
;; SOFTWARE: Proprietary
;; SEQ ID NO: 491270
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-11-083-784-491270
```

```
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 4.6e+02;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      583 GCTGTGGCTTGTGATAGT 601
Db      1 GCTUGGCGCCUUGAUGAU 19
```

```
RESULT 563
US-11-083-784-491271
; Sequence 491271, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 491271
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491271
```

```
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      482 CCTATGCTGTCCACACGA 500
Db      1 CCUAGUGUGCCACACGA 19
```

```
RESULT 564
US-11-083-784-491272
; Sequence 491272, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
```

```

; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491272
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491272

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      786 TGAGAAAGTGTACCAATC 804
Db      1 UGAGAAAGUGAACCAATC 19

```

```

RESULT 565
US-11-083-784-491273
; Sequence 491273, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491273
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491273

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      652 AAAGTGTATCTGTCTCA 670
Db      1 AAAGUGUACUUCUGUCA 19

```

```

RESULT 566
US-11-083-784-491274
; Sequence 491274, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin

```

```

; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491274
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491274

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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Qy      354 GGGCAACGTGTGTATGATG 372
Db      1 GGGCAACGTGTGTATGATG 19

```

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RESULT 567
US-11-083-784-491275
; Sequence 491275, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491275
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491275

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1026 CATCAACCAATCTCTAC 1044
Db      1 CAUCAAACCAATCTCTAC 19

```

```

RESULT 568
US-11-083-784-491276
; Sequence 491276, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin

```

```

; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491276
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491276

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 806 GTGTACTGTGCTGATCTA 824
DB 1 GUGUGACUGUGUCGACUUA 19

RESULT 569
US-11-083-784-491278
; Sequence 491278, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491278
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491278

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 763 CCAGAGCATCCGACACAGA 781
DB 1 CCAGAGCATCCGACACAGA 19

RESULT 570
US-11-083-784-491279
; Sequence 491279, Application US/11083784

```

```

; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491279
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491279

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 503 GGTACTACGGCCGCTTCTA 521
DB 1 GGUACUACGGCCGCUUCUA 19

RESULT 571
US-11-083-784-491280
; Sequence 491280, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491280
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491280

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 11; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 332 TCATTGTGTCGACTCTCT 350
DB 1 UCAUUGUGUGACCUUCU 19

```

```

RESULT 572
US-11-083-784-491281
; Sequence 491281, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491281
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491281

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY      772 CCGAACAGATTATGAGA 790
          |||||:::|||||
Db      1 CCGAACAGAUUUNAGAGA 19

```

```

RESULT 573
US-11-083-784-491282
; Sequence 491282, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491282
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491282

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY      1036 GATCTTACTCTGAAGAGT 1054
          ||:::|||||:

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Db 1 GAUCCUACCCGAGAGAGU 19

```

RESULT 574
US-11-083-784-491283
; Sequence 491283, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491283
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491283

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY      991 TGGCTGCCCTTCACATCT 1009
          :||:::|||||:
Db      1 UGGCTGCCUCCACACATCU 19

```

```

RESULT 575
US-11-083-784-491284
; Sequence 491284, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491284
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491284

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```


QY 769 CATCCGAACAGATTATG 787
|||:|||||:|||||:
Db 1 CACCGAAGCAGAUUUAUG 19

RESULT 576

US-11-083-784-491285
; Sequence 491285, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491285
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491285

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 753 GATCGAATGCCACAGCAT 771
|||:|||||:|||||:
Db 1 GAUCGAUUGCCACAGCAU 19

RESULT 577
US-11-083-784-491286
; Sequence 491286, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491286
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491286

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 550 GCCGCTGTTCGCCAGTA 568
|||:|||||:|||||:
Db 1 GCCCGUCUCUCCGCAUA 19

RESULT 578

US-11-083-784-491287
; Sequence 491287, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491287
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491287

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 480 CACCTATGCTTCACAC 498
|||:|||||:|||||:
Db 1 CACCUAUGCUGCCACAC 19

RESULT 579
US-11-083-784-491288
; Sequence 491288, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491288
; LENGTH: 19
; TYPE: RNA

```

: ORGANISM: Homo sapiens
US-11-083-784-491288

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      479 TCACCTATGCTGTCACAA 497
      :||||:|:|:|:|:|:|
Db      1 UCACCUAGCUCGUCACAA 19

RESULT 580
US-11-083-784-491291
; Sequence 491291, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491291
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491291

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      1119 CATCTACTGCTGCTCAAT 1137
      :|:|:|:|:|:|:|:|:|:|
Db      1 CAUCUACUCUCGUCUCAAU 19

RESULT 581
US-11-083-784-491292
; Sequence 491292, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary

: SEQ ID NO 491292
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491294

RESULT 582
US-11-083-784-491294
; Sequence 491294, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491294
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491294

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      233 ACTGAGACCTGCTCCCAA 251
      :|:|:|:|:|:|:|:|:|:|
Db      1 ACUCAGACUCUCUCCCAA 19

RESULT 583
US-11-083-784-491296
; Sequence 491296, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary

```

;; PRIOR FILING DATE: 2002-11-14
;; NUMBER OF SEQ ID NOS: 1591911
;; SOFTWARE: Proprietary
;; SEQ ID NO 491296
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-11-083-784-491296

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 840 GGTATTGGCTATGCTATAC 858
Db 1 GGUGAUGGCUAUGCAUAC 19

RESULT 584

US-11-083-784-491297
; Sequence 491297, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:

;; APPLICANT: Dharmacon, Inc.
;; APPLICANT: Khvorova, Anastasia
;; APPLICANT: Reynolds, Angela
;; APPLICANT: Leake, Devin
;; APPLICANT: Marshall, William
;; APPLICANT: Scaringe, Stephen
;; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;; FILE REFERENCE: 134990S
;; CURRENT APPLICATION NUMBER: US/11/083,784
;; CURRENT FILING DATE: 2005-03-18
;; PRIOR APPLICATION NUMBER: US/10/714,333

;; PRIOR FILING DATE: 2003-11-14
;; PRIOR APPLICATION NUMBER: 60/502,050
;; PRIOR FILING DATE: 2003-09-10
;; PRIOR APPLICATION NUMBER: 60/426,137
;; PRIOR FILING DATE: 2002-11-14
;; NUMBER OF SEQ ID NOS: 1591911
;; SOFTWARE: Proprietary
;; SEQ ID NO 491297
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-11-083-784-491297

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 492 CCACACGATGCTACTAC 510
Db 1 CCACACGACGAUGGACUAC 19

RESULT 585

US-11-083-784-491298
; Sequence 491298, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:

;; APPLICANT: Dharmacon, Inc.
;; APPLICANT: Khvorova, Anastasia
;; APPLICANT: Reynolds, Angela
;; APPLICANT: Leake, Devin
;; APPLICANT: Marshall, William
;; APPLICANT: Scaringe, Stephen
;; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;; FILE REFERENCE: 134990S
;; CURRENT APPLICATION NUMBER: US/11/083,784
;; CURRENT FILING DATE: 2005-03-18
;; PRIOR APPLICATION NUMBER: US/10/714,333
;; PRIOR FILING DATE: 2003-11-14

;; PRIOR APPLICATION NUMBER: 60/502,050
;; PRIOR FILING DATE: 2003-09-10
;; PRIOR APPLICATION NUMBER: 60/426,137
;; PRIOR FILING DATE: 2002-11-14
;; NUMBER OF SEQ ID NOS: 1591911
;; SOFTWARE: Proprietary
;; SEQ ID NO 491298
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-11-083-784-491298

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 203 GCTTCGAATGATATACGT 221
Db 1 GCUCGAAUGGACUACGU 19

RESULT 586

US-11-101-244-491124
; Sequence 491124, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:

;; APPLICANT: Dharmacon, Inc.
;; APPLICANT: Khvorova, Anastasia
;; APPLICANT: Reynolds, Angela
;; APPLICANT: Leake, Devin
;; APPLICANT: Marshall, William
;; APPLICANT: Scaringe, Stephen
;; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;; FILE REFERENCE: 134990S
;; CURRENT APPLICATION NUMBER: US/11/101,244
;; CURRENT FILING DATE: 2005-04-07
;; PRIOR APPLICATION NUMBER: 60/502,050
;; PRIOR FILING DATE: 2003-09-10
;; PRIOR APPLICATION NUMBER: 60/426,137
;; PRIOR FILING DATE: 2002-11-14
;; NUMBER OF SEQ ID NOS: 1591911
;; SOFTWARE: Proprietary
;; SEQ ID NO 491124
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-11-101-244-491124

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 401 GGACAGTACGAATATTT 419
Db 1 GGACAGGACGACGACUACU 19

RESULT 587

US-11-101-244-491125
; Sequence 491125, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:

;; APPLICANT: Dharmacon, Inc.
;; APPLICANT: Khvorova, Anastasia
;; APPLICANT: Reynolds, Angela
;; APPLICANT: Leake, Devin
;; APPLICANT: Marshall, William
;; APPLICANT: Scaringe, Stephen
;; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;; FILE REFERENCE: 134990S
;; CURRENT APPLICATION NUMBER: US/11/101,244
;; CURRENT FILING DATE: 2005-04-07
;; PRIOR APPLICATION NUMBER: 60/502,050

```

; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491125
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491125

```

```

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1655 GAACTTGTCTGAGCCTGTA 1673
Db 1 GAACUUCGUGAGCCUGUA 19

```

```

RESULT 588
US-11-101-244-491126
; Sequence 491126, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491126
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491126

```

```

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 247 CCAACATCTCCACTACA 265
Db 1 CCAACATCTCCACTACA 19

```

```

RESULT 589
US-11-101-244-491127
; Sequence 491127, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10

```

```

; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491127
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491127

```

```

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 773 CGAACAGATTATGAGAA 791
Db 1 CGAACAGAUUUAUGAGAA 19

```

```

RESULT 590
US-11-101-244-491128
; Sequence 491128, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491128
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491128

```

```

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 76 AAAGAGTGTGCCCATAA 94
Db 1 AAAGAGUGUGCCCAUAAA 19

```

```

RESULT 591
US-11-101-244-491129
; Sequence 491129, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137

```

```
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491129
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491129
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 789 GAAGTGTACCACTCTGT 807
Db 1 GAAGUGUACCAUCUCGU 19
```

RESULT 592

```
US-11-101-244-491130
; Sequence 491130, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Khavrova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491130
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491130
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 178 GTACAGTACGAGCTTTA 196
Db 1 GUACAGUAGUGGCUUUA 19
```

RESULT 593

```
US-11-101-244-491131
; Sequence 491131, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacoin, Inc.
; APPLICANT: Khavrova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
```

```
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491131
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491131
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 4.6e+02;
Matches 11; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 809 TGACTGTGCTACTACTT 827
Db 1 UGACUGUCUGAUCUACU 19
```

RESULT 594

```
US-11-101-244-491132
; Sequence 491132, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacoin, Inc.
; APPLICANT: Khavrova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491132
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491132
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1033 CCAGATCTTACCTGAGGA 1051
Db 1 CGAGUCUCUACCTGAGGA 19
```

RESULT 595

```
US-11-101-244-491133
; Sequence 491133, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacoin, Inc.
; APPLICANT: Khavrova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
```

```
; SOFTWARE: Proprietary
; SEQ ID NO 491133
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491133
```

```
Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
```

```
QY          650 CCAAGTGTATCTGTGT 668
Db          1 CCAAGTGTATCTGTGT 19
```

```
RESULT 596
US-11-101-244-491134
; Sequence 491134, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491134
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491134
```

```
Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
```

```
QY          461 TCATATCAGTGTGGAATT 479
Db          1 UCACUACAGUGGUGAACUU 19
```

```
RESULT 597
US-11-101-244-491135
; Sequence 491135, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
```

```
; SEQ ID NO 491135
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491135
```

```
Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
QY          600 GTACATGCCATCATCATCAT 618
Db          1 GTACATGCCATCATCATCAT 19
```

```
RESULT 598
US-11-101-244-491136
; Sequence 491136, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491136
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491136
```

```
Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY          398 TGAGCAGTGCAGCACTA 416
Db          1 TGAGCAGTGCAGCACTA 19
```

```
RESULT 599
US-11-101-244-491137
; Sequence 491137, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491137
```

```
LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491137
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 787 GAGAAAGTGTACCAATCT 805
Db 1 GAGAAAGTGTACCAATCT 19
```

```
RESULT 600
US-11-101-244-491138
; Sequence 491138, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491138
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491138
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 578 TGACGGCTGTGCGCTTTGA 596
Db 1 TGACGGCTGTGCGCTTTGA 19
```

```
RESULT 601
US-11-101-244-491139
; Sequence 491139, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491139
; LENGTH: 19
```

```
TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491139
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 777 CAAGATTATGCAAGAGTG 795
Db 1 CAAGATTATGCAAGAGTG 19
```

```
RESULT 602
US-11-101-244-491140
; Sequence 491140, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491140
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491140
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 766 GAGCATCCGAACAAGATT 784
Db 1 GAGCATCCGAACAAGATT 19
```

```
RESULT 603
US-11-101-244-491141
; Sequence 491141, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491141
; LENGTH: 19
; TYPE: RNA
```

```
; ORGANISM: Homo sapiens
US-11-101-244-491141
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      761 GGGCAGAGCATCCGACAA 779
      ||| ||| ||| ||| ||| |||
Db      1 GGGCAGAGCAUCCGACAA 19

RESULT 604
US-11-101-244-491142
; Sequence 491142, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491142
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491142

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 4.6e+02;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY      106 CCTCTGTCTGCTTAGAA 124
      ||| ||| ||| ||| ||| |||
Db      1 CCUCCUGUCGUUAGAA 19

RESULT 605
US-11-101-244-491143
; Sequence 491143, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491143
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
```

```
US-11-101-244-491143
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      1473 TGACCTGCCTCCCTTCATG 1491
      : ||| ||| ||| ||| |||
Db      1 UGACCCUGCCUCCUUCUUG 19

RESULT 606
US-11-101-244-491144
; Sequence 491144, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491144
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491144

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 47.4%; Pred. No. 4.6e+02;
Matches 9; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY      1600 TCAATTCCTCCATCTTT 1618
      : ||| ||| ||| ||| |||
Db      1 UCAATUCUCCUUCUUCUU 19

RESULT 607
US-11-101-244-491145
; Sequence 491145, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491145
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491145
```


Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 576 CATGACGGCTGTGGCTTT 594
||:|||||:|||||:
Db 1 CAUGACGGCUGGCGCUU 19

RESULT 608
US-11-101-244-491146
; Sequence 491146, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491146
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491146

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 4.6e+02;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 395 GAATGAGACAGTCGCGAA 413
||:|||||:|||||:
Db 1 GAATGAGACAGTCGCGAA 19

RESULT 609
US-11-101-244-491147
; Sequence 491147, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491147
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491147

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 375 GATCATCTTAGCCACCAA 393
||:|||||:|||||:
Db 1 GAUCATCTTAGCCACCAA 19

RESULT 610
US-11-101-244-491148
; Sequence 491148, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491148
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491148

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1641 CAAACCAATCAGTCACT 1659
||:|||||:|||||:
Db 1 CAAACCAATCAGTCACT 19

RESULT 611
US-11-101-244-491149
; Sequence 491149, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491149
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491149

Query Match 1.1%; Score 19; DB 1; Length 19;

Oy 1242 CCAGGCGAGTGTACAA 1260
Db 1 CCAGGCGAGUGUGACAA 19

RESULT 616

US-11-101-244-491154
; Sequence 491154, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491154
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491154

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Oy 1031 ACCGAGTCTTACTGAA 1049
Db 1 ACCGAGUCUCUACCTGAA 19

RESULT 617

US-11-101-244-491155
; Sequence 491155, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491155
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491155

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Oy 55 GAGCGCGAGTTCAGCTTC 73
Db 1 GAGCGCGAGUGUGACUUC 19

RESULT 618

US-11-101-244-491156
; Sequence 491156, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491156
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491156

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Oy 356 GCAACGCGTAGCATGTC 374
Db 1 GCAACGUGUGAGUGUG 19

RESULT 619

US-11-101-244-491157
; Sequence 491157, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491157
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491157

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 1 CCUCGGAACCCCAUCCAGUU 19

```
RESULT 620
US-11-101-244-491158
; Sequence 491158, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491158
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491158
```

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1699 CTCAGAGCCCATCTGATT 1717
Db 1 CUCAGAGCCCAUCCAGUU 19

```
RESULT 621
US-11-101-244-491159
; Sequence 491159, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491159
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491159
```

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1570 GAAACATTCATCTCTTGA 1588
Db 1 GAAACATTCATCTCTTGA 1588

Db 1 GAAACAUUCCAUCCUUGA 19

```
RESULT 622
US-11-101-244-491160
; Sequence 491160, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491160
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491160
```

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1376 GAAGTGACTCCAGACCAT 1394
Db 1 GAAGUGACUCCAGACCAU 19

```
RESULT 623
US-11-101-244-491161
; Sequence 491161, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491161
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491161
```

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 4.6e+02;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 35 TCACGAGCGTTTATATC 53
Db 1 UCCAGAGCGUUAUUAUC 19

```
RESULT 624
US-11-101-244-491162
; Sequence 491162, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491162
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491162

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 4.6e+02;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy      102 CCACCTCTCTGTCGCTT 120
Db      1 CCACCCUCCUGUCUGCUU 19

RESULT 625
US-11-101-244-491163
; Sequence 491163, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491163
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491163

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 4.6e+02;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      764 CAGAGCATCCGAAACAGAT 782
Db      1 CAGAGCAUCCGAAACAGAU 19
```

```
RESULT 626
US-11-101-244-491164
; Sequence 491164, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491164
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491164

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy      1643 AACCAATCACTGACTTT 1661
Db      1 AACCAAUCAUCGAAACUU 19

RESULT 627
US-11-101-244-491165
; Sequence 491165, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491165
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491165

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1246 GGCAGTGTGTACAAATCA 1264
Db      1 GGCAGUGUGUACAAAGUCA 19
```

```
RESULT 628
US-11-101-244-491166
; Sequence 491166, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491166
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491166

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 841 GTGATTGGCTATGCATACA 859
Db 1 GUGAUGGCUAUGCAUCA 19

RESULT 629
US-11-101-244-491167
; Sequence 491167, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491167
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491167

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1700 TCAAGAGCCCAATGATTC 1718
Db 1 UCAAGAGCCCAATGCAUUC 19

RESULT 630

US-11-101-244-491168
; Sequence 491168, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491168
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491168

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 737 GCAGAGTCGTGTCATGAT 755
Db 1 GCAGAGTCGTGTCATGAT 19

RESULT 631
US-11-101-244-491169
; Sequence 491169, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491169
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491169

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1660 TTGCTGAGCCCTGTAAATA 1678
Db 1 UUGCTGAGCCCTGUAAAATA 19

RESULT 632
US-11-101-244-491170
```

```
; Sequence 491170, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491170
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491170

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1638 ACTCAACCAATCATCTGA 1656
Db      1 ACUCAACCAAUCACTGUA 19
      |||:|||||:|||||:|

RESULT 633
US-11-101-244-491171
; Sequence 491171, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491171
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491171

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 4.6e+02;
Matches 11; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY      1596 AATCTCAATCTTCCTAT 1614
Db      1 AAUCUCAUUCUCCUUAU 19
      |||:|||||:|||||:|

RESULT 634
US-11-101-244-491172
; Sequence 491172, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491172
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491172

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      941 GCAAGTGTCGCAAAATGAT 959
Db      1 GCAAGUGUGUCAAUAUGAU 19
      |||:|||||:|||||:|

RESULT 635
US-11-101-244-491173
; Sequence 491173, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491173
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491173

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      245 CCCCAACATCTCCACTAA 263
Db      1 CCCCAACAUUCUCCACUAA 19
      |||:|||||:|||||:|

RESULT 636
US-11-101-244-491174
; Sequence 491174, Application US/11101244
; Publication No. US20050246794A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491174
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491174

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      109 CCTGCTGCTTTAGAGGA 127
      |||:|||||:|||||
Db      1 CCUGUCUCUUAGAGGA 19

RESULT 637
US-11-101-244-491175
; Sequence 491175, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491175
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491175

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491176
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491176

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 4.6e+02;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      583 GCTGTGCGCTTGATAGT 601
      |||:|||||:|||||
Db      1 GCUGUGCCUUGAUNAGGU 19
```

```
RESULT 639
US-11-101-244-491177
; Sequence 491177, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491177
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491177
```

```
Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      482 CCTATGCTGTCCACACGA 500
      |||:|||||:|||||
Db      1 CCUAVGCUUCACACACGA 19
```

```
RESULT 640
US-11-101-244-491178
; Sequence 491178, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
```



```

; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491178
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491178
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 261 TAACACCTCGGAACCAAT 279
Db 1 UAACACCTCGGAACCAAT 19
```

```

RESULT 641
US-11-101-244-491179
; Sequence 491179, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491179
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491179
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1407 CAGCTCTCTCCCAATG 1425
Db 1 CAGCTCTCTCCCAATG 19
```

```

RESULT 642
US-11-101-244-491180
; Sequence 491180, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
```

```

; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491180
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491180
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1360 TCACACTGCTCTCAGAA 1378
Db 1 UCCAACTGCTCTCAGAA 19
```

```

RESULT 643
US-11-101-244-491181
; Sequence 491181, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491181
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491181
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 786 TGAGAAAGTGATACCATC 804
Db 1 UGAGAAAGTGATACCATC 19
```

```

RESULT 644
US-11-101-244-491182
; Sequence 491182, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
```

```

; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491182
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491182

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      652 AAAGTGTCTATCTGTCTCA 670
Db      1 AAAGUGUCACUCUGUGUCA 19

RESULT 645
US-11-101-244-491183
; Sequence 491183, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491183
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491183

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      354 GGGCAACGTGTAGTAGTATG 372
Db      1 GGGCAACGUGGUGAUGUGAUG 19

RESULT 646
US-11-101-244-491184
; Sequence 491184, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
```

```

; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491184
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491184

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 4.6e+02;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1517 CATCAGAAACACCCCTCACA 1535
Db      1 CAUCAGAAACACCCCTCACA 19

RESULT 647
US-11-101-244-491185
; Sequence 491185, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491185
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491185

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1026 CATCAACCCAGATCTCTAC 1044
Db      1 CAUCACCCAGAUUCUCAC 19

RESULT 648
US-11-101-244-491186
; Sequence 491186, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
```

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; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491186
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491186

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 4.6e+02;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY      806 GTGTGACTGTGCTGATCTA 824
Db      1 GUGGACUGGUGCUGAUCUA 19

RESULT 649
US-11-101-244-491187
; Sequence 491187, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491187
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491187

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1620 CCACCTCATGCTGTGTGA 1638
Db      1 CCACCCUACUGCUGUGA 19

RESULT 650
US-11-101-244-491188
; Sequence 491188, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
```

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; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491188
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491188

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      1572 AACATTCATCTCTTGACT 1590
Db      1 AAACATUCCAUCCUGAGU 19

RESULT 651
US-11-101-244-491189
; Sequence 491189, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491189
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491189

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      763 CCAGAGCATCGAACAAGA 781
Db      1 CCAGAGCAUCCGAACAAGA 19

RESULT 652
US-11-101-244-491190
; Sequence 491190, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
```

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; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491190
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491190

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.4%; Pred. No. 4.6e+02;
Matches 15; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      503 GGTACTACGGCCTGTCTA 521
Db      1 GGUACUACGCCCTGUCUUA 19

RESULT 653
US-11-101-244-491191
; Sequence 491191, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491191
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491191

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1215 AATGAATCCACCGGTAT 1233
Db      1 AAUGAAUCCACCCGGUADU 19

RESULT 654
US-11-101-244-491192
; Sequence 491192, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
```

```

; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491192
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491192

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      196 ACGCTAGCTTCGAATGC 214
Db      1 ACGCTAGCTUCCGAATGCG 19

RESULT 655
US-11-101-244-491193
; Sequence 491193, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491193
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491193

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      772 CCGAACAGATTATGAGA 790
Db      1 CCGAACAGAUUUAUGAGA 19

RESULT 656
US-11-101-244-491194
; Sequence 491194, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
```

```
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491194
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491194
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 4.6e+02;
Matches 11; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 332 TCATTGTGTCGCTCTGT 350
Db 1 UCAGUGGUGGACCCUGU 19
```

```
RESULT 657
US-11-101-244-491195
; Sequence 491195, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491195
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491195
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 33 CATCCAGAGCGTTATAT 51
Db 1 CAUCGAGAGCGUUUAU 19
```

```
RESULT 658
US-11-101-244-491196
; Sequence 491196, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
```

```
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491196
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491196
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1631 CTGTGTACTCAACCAA 1649
Db 1 CUGUGGACUCGAAACCAA 19
```

```
RESULT 659
US-11-101-244-491197
; Sequence 491197, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491197
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491197
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1036 GATCTCTACTGAAGAAGT 1054
Db 1 GAUCUCUACCCUGAAGAU 19
```

```
RESULT 660
US-11-101-244-491198
; Sequence 491198, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
```

```

; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491198
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491198

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy      991 TGGCTGCCCTTCCACATCT 1009
Db      1 UGCGUGCCCUCCACAUUC 19

RESULT 661
US-11-101-244-491199
; Sequence 491199, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491199
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491199

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy      769 CATCCGACACAGATTATATG 787
Db      1 CAUCCGACACAGATUUUAUG 19

RESULT 662
US-11-101-244-491200
; Sequence 491200, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10

; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491201
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491201

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy      550 GCCGCTGCTTCGCCAGTA 568
Db      1 GCCGCTGCTTCGCCAGTA 19

RESULT 663
US-11-101-244-491201
; Sequence 491201, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491201
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491201

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      753 GATCGAATGCGCAGAGCAT 771
Db      1 GAUCCGAUUGCCAGAGCAU 19

RESULT 664
US-11-101-244-491202
; Sequence 491202, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491202
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491202
```

;; PRIOR FILING DATE: 2002-11-14
;; NUMBER OF SEQ ID NOS: 1591911
;; SOFTWARE: Proprietary
;; SEQ ID NO 491202
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-11-101-244-491202

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 480 CACCTATGCTGCCAAC 498
Db 1 CACCUGCGUCCACAC 19

RESULT 665
US-11-101-244-491203
; Sequence 491203, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491203
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491203

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 479 TCACCTATGCTGCCAAC 497
Db 1 UCACCGUCCGUCACAA 19

RESULT 666
US-11-101-244-491204
; Sequence 491204, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14

;; NUMBER OF SEQ ID NOS: 1591911
;; SOFTWARE: Proprietary
;; SEQ ID NO 491204
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-11-101-244-491204

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 4.6e+02;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1384 TCACGACATGACAGAGA 1402
Db 1 UCCAGACGAGACAGAGA 19

RESULT 667
US-11-101-244-491205
; Sequence 491205, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491205
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491205

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1218 GAATCCACCCGGTATCTC 1236
Db 1 GAATCCACCCGGUATCUC 19

RESULT 668
US-11-101-244-491206
; Sequence 491206, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911

```

; SOFTWARE: Proprietary
; SEQ ID NO 491206
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491206

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      1119 CATCTACTGCTGCTCTCAAT 1137
Db      1 CAUCUACUGCCUCCUCAU 19

RESULT 669
US-11-101-244-491207
; Sequence 491207, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491207
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491207

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      504 GTACTACGCGCTGTCTTAC 522
Db      1 GUACUACGCGCCUUCUCA 19

RESULT 670
US-11-101-244-491208
; Sequence 491208, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary

```

```

; SEQ ID NO 491208
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491208

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 52.6%; Pred. No. 4.6e+02;
Matches 10; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY      1601 CAATCTCTCCCTATCTTGG 1619
Db      1 CAUUCUUCUCCUUAUCUUUG 19

RESULT 671
US-11-101-244-491209
; Sequence 491209, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491209
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491209

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      233 ACTCAGACCTCTCCCAAA 251
Db      1 ACUCAGACUUCUCCCAAA 19

RESULT 672
US-11-101-244-491210
; Sequence 491210, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491210

```



```
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491210
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1747 CGAGTGCTCATTTCAAGAT 1765
Db 1 CGAGGCTCATUTUCAGAU 19
```

```
RESULT 673
US-11-101-244-491211
; Sequence 491211, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491211
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491211
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1687 GACCAGCTTTCTCAAGA 1705
Db 1 GACCAGCTTUCUCAAGA 19
```

```
RESULT 674
US-11-101-244-491212
; Sequence 491212, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491212
; LENGTH: 19
```

```
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491212
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1642 AACCAATCAGTCACTT 1660
Db 1 AACCAAAUCCACUACCU 19
```

```
RESULT 675
US-11-101-244-491213
; Sequence 491213, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491213
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491213
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1519 TCAGAAACCCCTCACT 1537
Db 1 UCAGAAACACCCUCCACACU 19
```

```
RESULT 676
US-11-101-244-491214
; Sequence 491214, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491214
; LENGTH: 19
; TYPE: RNA
```

```
; ORGANISM: Homo sapiens
US-11-101-244-491214

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      840 GCGGATGCGCTATGCATAC 858
DB      1 GGUGAUGGCUAGCAUAC 19

RESULT 677
US-11-101-244-491215
; Sequence 491215, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491215
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491215

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      203 GCTTCGAATGGATTAAGT 221
DB      1 GCUTCAGAAUGGUAACGU 19

RESULT 678
US-11-101-244-491216
; Sequence 491216, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491216
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
```

```
US-11-101-244-491216

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      543 TCCCATCGCCGCTGTCTTC 561
DB      1 UCCCAUCCGCCGCUUCUUC 19

RESULT 679
US-11-101-244-491217
; Sequence 491217, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491217
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491217

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      492 CCACACGAATGTAATCTAC 510
DB      1 CCACACGAATGTAATCTAC 19

RESULT 680
US-11-101-244-491218
; Sequence 491218, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491218
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491218
```

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1274 AGACCACCATCTCCACAGT 1292
|||:|||||:|||||:
Db 1 AGACCACCAUUCUCCACAGU 19

RESULT 681
US-11-101-244-491219
; Sequence 491219, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491219
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491219

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 401 GGACAGTGACGAACACTATT 419
|||:|||||:|||||:
Db 1 GGACAGUGACGAACUUAUU 19

RESULT 682
US-11-101-244-491220
; Sequence 491220, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491220
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491220

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 247 CCAACATCTCCACTAACA 265
|||:|||||:|||||:
Db 1 CCAACAUUCUCCACUACA 19

RESULT 683
US-11-101-244-491221
; Sequence 491221, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491221
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491221

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 773 CGAACAGATTATGAGAA 791
|||:|||||:|||||:
Db 1 CGAACAGAUUUAUGAGAA 19

RESULT 684
US-11-101-244-491224
; Sequence 491224, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491224
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491224

Query Match 1.1%; Score 19; DB 1; Length 19;

Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 789 GAAAGTGACACATCGT 807
Db 1 GAAAGUGUACCAUCUGU 19

RESULT 685
US-11-101-244-491225
; Sequence 491225, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491225
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491225

Query Match
Best Local Similarity 57.9%; Pred. No. 4.6e+02;
Matches 11; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
QY 809 TGACTGTGCTGATCTACTT 827
Db 1 UGACUGUGCUGAUCUACU 19

RESULT 686
US-11-101-244-491226
; Sequence 491226, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491226
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491226

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;

Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1033 CCAGATCTCTACTGAAGA 1051
Db 1 CCAGAUUCUACCUCAAGA 19

RESULT 687
US-11-101-244-491227
; Sequence 491227, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491227
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491227

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 650 CCAAGTGTGCTGATCTGCT 668
Db 1 CCAAGUGGUCUACUUGUGU 19

RESULT 688
US-11-101-244-491229
; Sequence 491229, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491229
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491229

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Oy 461 TCATACAGTGTGACTT 479
Db 1 UCAAUACAGUGGUGAACU 19

RESULT 689
US-11-101-244-491231
; Sequence 491231, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEO ID NOS: 1591911
; SOFTWARE: Proprietary
; SEO ID NO 491231
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491231

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Oy 600 GTACATGCCATCATCAT 618
Db 1 GUAACUGGCGCAUCACU 19

RESULT 690
US-11-101-244-491232
; Sequence 491232, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEO ID NOS: 1591911
; SOFTWARE: Proprietary
; SEO ID NO 491232
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491232

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 398 TGAGACAGTGCAGACTA 416
Db 1 UGAGACAGUGGACGACUA 19

RESULT 691
US-11-101-244-491233
; Sequence 491233, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEO ID NOS: 1591911
; SOFTWARE: Proprietary
; SEO ID NO 491233
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491233

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Oy 787 GAGAAAGTACACACT 805
Db 1 GAGAAAGUGACACACU 19

RESULT 692
US-11-101-244-491234
; Sequence 491234, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEO ID NOS: 1591911
; SOFTWARE: Proprietary
; SEO ID NO 491234
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491234

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Oy 578 TGACGGCTGTGCCTTGA 596

Db 1 UGACGGCUGGCGCCUUUGA 19

RESULT 693
US-11-101-244-491236
; Sequence 491236, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491236
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491236

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 777 CAAGTTTATGGAAGTG 795
Db 1 CAAGAUUUAUGAAGGUG 19

RESULT 694
US-11-101-244-491237
; Sequence 491237, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491237
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491237

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 766 GAGCATCCGAACAAGATT 784
|||||:|||||:|||||:|

Db 1 GAGCAUCCGACACAGAUUU 19

RESULT 695
US-11-101-244-491238
; Sequence 491238, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491238
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491238

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 761 GGCACAGCATCCGACAA 779
Db 1 GGCACAGCAUCCGACAA 19

RESULT 696
US-11-101-244-491241
; Sequence 491241, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491241
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491241

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 576 CATGACGGCTGTGCGCTTT 594
Db 1 CAUGACGGCUGUGGCCUUU 19

```
RESULT 697
US-11-101-244-491244
; Sequence 491244, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491244
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491244

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 4.6e+02;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      395 GAATGAGCAGTGACGAA 413
Db      1 GAATGAGCAGTGACGAA 19

RESULT 698
US-11-101-244-491245
; Sequence 491245, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491245
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491245

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      375 GATCATCTTAGCCACAAA 393
Db      1 GAUCAUCUAGCCACAAA 19
```

```
RESULT 699
US-11-101-244-491248
; Sequence 491248, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491248
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491248

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      447 CTCGATGCTGCTGATCAAT 465
Db      1 CUCCAGUCUGCAUUCUAAU 19

RESULT 700
US-11-101-244-491251
; Sequence 491251, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491251
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491251

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1031 ACCGATCTCTTACTGAA 1049
Db      1 ACCCGAUCUCUACCTGAA 19
```

```
RESULT 701
US-11-101-244-491252
; Sequence 491252, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491252
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491252
```

```
Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      356 GCAACGTGTGATGATGTG 374
          |||||:|:|:|:|:|:|:|
Db      1 GCAACGUGUGAUGAUGUG 19
```

```
RESULT 702
US-11-101-244-491256
; Sequence 491256, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491256
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491256
```

```
Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      266 CCTGGAGACCCATCAGTT 284
          ||:|||||:|:|:|:|:|:|
Db      1 CCUGGAGACCCAAUACAGU 19
```

RESULT 703

```
US-11-101-244-491262
; Sequence 491262, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491262
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491262
```

```
Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 4.6e+02;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      764 CAGAGCATCCGACACAGAT 782
          |||||:|:|:|:|:|:|
Db      1 CAGAGCAUCCGACACAGAU 19
```

```
RESULT 704
US-11-101-244-491263
; Sequence 491263, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491263
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491263
```

```
Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      841 GTGATTGGCTATGCATACA 859
          |:|:|:|:|:|:|:|:|
Db      1 GUGAUUGGCUAGCAUACA 19
```

```
RESULT 705
US-11-101-244-491264
```



```
; Sequence 491264, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491264
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491264
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 737 GCAGAGTCGTGTCATGAT 755
Db 1 GCAGAGTCGUGGCAUAGAU 19
```

```
RESULT 706
US-11-101-244-491265
; Sequence 491265, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491265
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491265
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 245 CCCCAACATCTCCACTAA 263
Db 1 CCCCAACATCTCCACTAA 19
```

```
RESULT 707
US-11-101-244-491268
; Sequence 491268, Application US/11101244
```

```
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491268
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491268
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 941 GCAAGTCGTCAAAATGAT 959
Db 1 GCAAGTCGUGCAAAUAGAU 19
```

```
RESULT 708
US-11-101-244-491269
; Sequence 491269, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491269
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491269
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 261 TAACACCTCGGAACCAAT 279
Db 1 TAACACCTCGGAACCAAU 19
```

```
RESULT 709
US-11-101-244-491270
; Sequence 491270, Application US/11101244
; Publication No. US20050246794A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ PRIOR FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491270
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-491270

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 583 GCTGTGGCTTTGATAGGT 601
Db 1 GCGUGGCGCTTUGAGUGU 19

RESULT 710
US-11-101-244-491271
/ Sequence 491271, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ PRIOR FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491271
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-491271

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ PRIOR FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491272
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-491272

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 786 TGAGAAAGTGACCAATC 804
Db 1 UGAGAAAGUGUACCAACUC 19

RESULT 712
US-11-101-244-491273
/ Sequence 491273, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ PRIOR FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491273
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-491273

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 652 AAAGTGCACTGTGTCA 670
Db 1 AAAGUGUACUUGUUGCA 19

RESULT 713
US-11-101-244-491274
/ Sequence 491274, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
```

```

; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491274
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491274
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 354 GGGCACTGCTAGTANG 372
Db 1 GGGCACTGCTAGTANG 19
```

```

RESULT 714
US-11-101-244-491275
; Sequence 491275, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491275
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491275
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1026 CATCAACCCAGATCTTAC 1044
Db 1 CAUCAACCCAGATCTTAC 19

RESULT 715
US-11-101-244-491276
; Sequence 491276, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
```

```

; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491276
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491276
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 4.6e+02;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 806 GTGACCTGCTGATCTA 824
Db 1 GTGACCTGCTGATCTA 19
```

```

RESULT 716
US-11-101-244-491278
; Sequence 491278, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491278
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491278
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 763 CCAGAGCATCCGAACAGA 781
Db 1 CCAGAGCATCCGAACAGA 19

RESULT 717
US-11-101-244-491279
; Sequence 491279, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
```

```

; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491279
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491279

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      503 GGTACTACGCGCTGTTCTTA 521
Db      1 GGUACUACGCGCCUGUCUA 19

```

```

RESULT 718
US-11-101-244-491280
; Sequence 491280, Application US/11101244
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491280
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491280

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 4.6e+02;
Matches 11; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      332 TCATTGTGAGCTCTGT 350
Db      1 UCAUUGUGUGACUCUCU 19

```

```

RESULT 719
US-11-101-244-491281
; Sequence 491281, Application US/11101244
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin

```

```

; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491281
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491281

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      772 CCGAACCAAGATTATGAGA 790
Db      1 CCGAACCAAGAUUUAUGAGA 19

```

```

RESULT 720
US-11-101-244-491282
; Sequence 491282, Application US/11101244
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491282
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491282

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1036 GATCTCTACCTGAGAGACT 1054
Db      1 GAUUCUCACCGAAGAGAG 19

```

```

RESULT 721
US-11-101-244-491283
; Sequence 491283, Application US/11101244
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William

```

```

; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491283
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491283

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      991 TGCGTGCCTTCCACATCT 1009
Db      1 UGCGUGCCCUCCACACUCU 19

RESULT 722
US-11-101-244-491284
; Sequence 491284, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491284
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491284

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      769 CATCGAACAAGATTATG 787
Db      1 CAUCCGAACAAGAUUUAUG 19

RESULT 723
US-11-101-244-491285
; Sequence 491285, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
```

```

; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491285
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491285

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      753 GATCGAATGCCAGAGCAT 771
Db      1 GAUCCAUGGCCAGAGCAU 19

RESULT 724
US-11-101-244-491286
; Sequence 491286, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491286
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491286

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      550 GCCGCTGTCTTCCGCGACTA 568
Db      1 GCCGCGUCUCCGCCAGUA 19

RESULT 725
US-11-101-244-491287
; Sequence 491287, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
```

```
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491287
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491287

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      480 CACCTATGCTGTCCACAC 498
Db      1 CACCUAUGCUGUCCACAC 19

RESULT 726
US-11-101-244-491288
; Sequence 491288, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491288
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491288

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      479 TCACCTATGCTGTCCACA 497
Db      1 UCACCUAUGCUGUCCACAA 19

RESULT 727
US-11-101-244-491291
; Sequence 491291, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
```

```
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491291
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491291

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      1119 CATCTACTGCTGCTCAAT 1137
Db      1 CAUCUACUGCUGCUCUCAAU 19

RESULT 728
US-11-101-244-491292
; Sequence 491292, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491292
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491292

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      504 GTACTACGCGCTGTCTAC 522
Db      1 GUACTACGCGCUGUUCUAC 19

RESULT 729
US-11-101-244-491294
; Sequence 491294, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; CURRENT APPLICATION NUMBER: US/11/101,244
```

```
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491294
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491294

Query Match      1.1%: Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      233 ACTGAGACCTCTCCCAAA 251
Db      1 ACUCAGACCTCCTCCCAAA 19

RESULT 730
US-11-101-244-491296
; Sequence 491296, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491296
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491296

Query Match      1.1%: Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy      840 GGTGATTGGCTATGCATAC 858
Db      1 GGUGAUGGCUAUGCAUAC 19

RESULT 731
US-11-101-244-491297
; Sequence 491297, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
```

```
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491297
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491297

Query Match      1.1%: Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      492 CCACACGAATGCTACTAC 510
Db      1 CCACACGAATGCTACTAC 19

RESULT 732
US-11-101-244-491298
; Sequence 491298, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491298
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491298

Query Match      1.1%: Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy      203 GCTTCGAATGATTAAGT 221
Db      1 GCUCGAAATGGAUAAAGU 19

RESULT 733
US-11-127-877-153
; Sequence 153, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
```

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; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 153
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-153

Query Match
Best Local Similarity 100.0%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 528 GTTCACACACTTCTTCCC 546
Db 1 GTTCACACACTTCTTCCC 19

RESULT 734
US-11-127-877-154
; Sequence 154, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 154
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-154

Query Match
Best Local Similarity 100.0%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 799 CACATCTGTGACATGTGC 817
Db 1 CACATCTGTGACATGTGC 19

RESULT 735
US-11-127-877-155
; Sequence 155, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
```

```

; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 155
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-155

Query Match
Best Local Similarity 100.0%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1027 ATCAACCCAGATCTTACC 1045
Db 1 ATCAACCCAGATCTTACC 19

RESULT 736
US-11-127-877-156
; Sequence 156, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 156
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-156

Query Match
Best Local Similarity 100.0%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1137 TGACAGGTCCGCTGGGC 1155
Db 1 TGACAGGTCCGCTGGGC 19

RESULT 737
US-11-127-877-474
; Sequence 474, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 474
; LENGTH: 19
```



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; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-474

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      857 ACACCGTAGTGGGAATCAG 875
Db      1 ACACCGTAGTGGGAATCAG 19

RESULT 738
US-10-310-914A-51927
; Sequence 51927, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 51927
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-51927

Query Match      1.1%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 5.8e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1308 GAGGAGCCAGAGAGCGGCCCC 1329
Db      1 GAGGAGCCAGAGAGCGGCCCC 22

RESULT 739
US-10-310-914A-746504/c
; Sequence 746504, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 746504
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-746504

Query Match      1.1%; Score 18.8; DB 1; Length 23;
Best Local Similarity 90.9%; Pred. No. 6.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1299 GGCCGACGAGAGGAGCGGAG 1320
Db      23 GGCCGACGAGAGGAGCGGAG 2

RESULT 740
US-10-770-726-10079/c

; Sequence 10079, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyelech
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770.726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10079
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-10079

Query Match      1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.9e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1049 AGAAGTTATCCAGCAGTC 1068
Db      20 AGAAGTTATCCAGCAGTC 1

RESULT 741
US-10-770-726-10445/c
; Sequence 10445, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyelech
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770.726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10445
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-10445

Query Match      1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.9e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1049 AGAAGTTATCCAGCAGTC 1068
Db      20 AGAAGTTATCCAGCAGTC 1

RESULT 742
US-10-310-914A-1313224/c
; Sequence 1313224, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1313224
```

; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1313224

Query Match 1.0%; Score 18.4; DB 1; Length 23;
Best Local Similarity 95.0%; Pred. No. 6.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1265 GCCGCTGGAGACCAACATC 1284
DB 21 GCCGCTGGAGACCAAC 2

RESULT 743
US-10-310-914A-1313247/c
; Sequence 1313247, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1313247
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1313247

Query Match 1.0%; Score 18.4; DB 1; Length 23;
Best Local Similarity 95.0%; Pred. No. 6.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1265 GCCGCTGGAGACCAACATC 1284
DB 20 GCCGCTGGAGACCAAC 1

RESULT 744
US-09-930-503-39
; Sequence 39, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREOF
; FILE REFERENCE: 39245-173913
; CURRENT FILING DATE: 2001-08-16
; CURRENT APPLICATION NUMBER: US/09/930,503
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-39

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1038 TCTTACTGAGAGAGTT 1055

DB 1 TCTTACTGAGAGAGTT 18

RESULT 745
US-09-930-503-58/c
; Sequence 58, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREOF
; FILE REFERENCE: 39245-173913
; CURRENT FILING DATE: 2001-08-16
; CURRENT APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-58

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1038 TCTTACTGAGAGAGTT 1055
DB 18 TCTTACTGAGAGAGTT 1

RESULT 746
US-10-146-354A-32/c
; Sequence 32, Application US/10146354A
; Publication No. US20030054381A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Seymour, Albert B.
; APPLICANT: Nelson, Darcy L.
; APPLICANT: Webb, Suzin M.
; APPLICANT: Affourtit, Jason P.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS IN THE HUMAN NEUROKININ 1 RECEPTOR GENE AND
; TITLE OF INVENTION: USES IN DIAGNOSIS AND TREATMENT OF DISEASES
; FILE REFERENCE: PCI0461AGPR
; CURRENT FILING DATE: 2002-08-15
; CURRENT APPLICATION NUMBER: US/10/146,354A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/293,425
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; NAME/KEY: misc_feature
; LOCATION: (1)..(18)
; OTHER INFORMATION: artificial / primer
US-10-146-354A-32

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 58 CGCCAGTTCAGCTTCAA 75
Db 18 CGCCAGTTCAGCTTCAA 1

RESULT 747
US-10-005-956-1124/c

Sequence 1124, Application US/10005956
Publication No. US20030113726A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: D0053NP
CURRENT APPLICATION NUMBER: US/10/005,956
CURRENT FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: 60/251,015
PRIOR FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: 60/263,678
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 60/273,037
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 1579
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1124
LENGTH: 18
TYPE: DNA
ORGANISM: Homo sapiens
US-10-005-956-1124

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 581 CGGCTGTGCGCTTGAATA 598
Db 18 CGGCTGTGCGCTTGAATA 1

RESULT 748
US-10-005-956-1218

Sequence 1218, Application US/10005956
Publication No. US20030113726A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: D0053NP
CURRENT APPLICATION NUMBER: US/10/005,956
CURRENT FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: 60/251,015
PRIOR FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: 60/263,678
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 60/273,037
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 1579
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1218
LENGTH: 18
TYPE: DNA
ORGANISM: Homo sapiens
US-10-005-956-1218

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1301 CCCACGAGAGAGCCAG 1318
Db 1 CCCACGAGAGAGCCAG 18

RESULT 749
US-10-310-914A-386268/c

Sequence 386268, Application US/10310914A
Publication No. US2006003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 386268
LENGTH: 18
TYPE: RNA
ORGANISM: Human
US-10-310-914A-386268

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 98 CTTTCACCTCCTCTCT 115
Db 18 CTTTCACCTCCTCTCT 1

RESULT 750

Sequence 386291, Application US/10310914A
Publication No. US2006003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 386291
LENGTH: 18
TYPE: RNA
ORGANISM: Human
US-10-310-914A-386291

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 104 ACCCTCCTGTCTGCTTA 121
Db 18 ACCCTCCTGTCTGCTTA 1

RESULT 751

Sequence 386293, Application US/10310914A
Publication No. US2006003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 386293
LENGTH: 18
TYPE: RNA

```
; ORGANISM: Human
; US-10-310-914A-386293

Query Match      1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1639 CTCGAACCAATGACTGA 1656
DB      18 CTCGAACCAATGACTGA 1

RESULT 752
US-10-310-914A-1157285/c
; Sequence 1157285, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1157285
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
; US-10-310-914A-1157285

Query Match      1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1287 CACAGTGTGGGGGCCCA 1304
DB      18 CACAGTGTGGGGGCCCA 1

RESULT 753
US-10-310-914A-386292/c
; Sequence 386292, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 386292
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
; US-10-310-914A-386292

Query Match      1.0%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      116 GCTTAGAAGAGCCCTGA 133
DB      18 GCTTAGAAGAGCCCTGA 1

RESULT 754
US-11-083-784-491261
; Sequence 491261, Application US/11083784
```

```
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491261
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-083-784-491261

Query Match      1.0%; Score 18; DB 1; Length 19;
Best Local Similarity 77.8%; Pred. No. 5.6e+02;
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      197 CGCCTAGCTTGAATG 214
DB      2 CGCCTAGCTTGAATG 19

RESULT 755
US-11-101-244-491261
; Sequence 491261, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491261
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-491261

Query Match      1.0%; Score 18; DB 1; Length 19;
Best Local Similarity 77.8%; Pred. No. 5.6e+02;
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      197 CGCCTAGCTTGAATG 214
DB      2 CGCCTAGCTTGAATG 19

RESULT 756
US-10-310-914A-1305132/c
```

```
; Sequence 1305132, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuznet
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1305132
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1305132
```

```
Query Match 1.0%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1403 GCTTCAGCTTCTCCTCCA 1420
Db 21 GCTTCAGCTTCTCCTCCA 4
```

```
RESULT 757
US-10-005-956-1303
; Sequence 1303, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005.956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1303
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12)..(12)
; OTHER INFORMATION: wherein "n" equals a C3 phosphoramidite linker.
US-10-005-956-1303
```

```
Query Match 1.0%; Score 18; DB 1; Length 22;
Best Local Similarity 94.7%; Pred. No. 6.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1681 AGGTGGAGCAGCTTTTCC 1699
Db 1 AGGTGGAGCAGCAGCTTTTCC 19
```

```
RESULT 758
US-10-201-187-44/c
; Sequence 44, Application US/10201187
; Publication No. US20030104478A1
; GENERAL INFORMATION:
; APPLICANT: Witcamer, Valerie
; APPLICANT: Communi, David
; APPLICANT: Vandenbergaeerde, Ann
; APPLICANT: Detheux, Michel
```

```
; APPLICANT: Parmentier, Marc
; TITLE OF INVENTION: Natural Ligand of G Protein Coupled Receptor ChemR23 and Uses The
; FILE REFERENCE: 9409/2045
; CURRENT APPLICATION NUMBER: US/10/201.187
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US09/905,253
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic primer
; NAME/KEY: misc_feature
; LOCATION: (1)..(21)
; OTHER INFORMATION: Synthetic primer
US-10-201-187-44
```

```
Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 6.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 669 CATCTGGGTCCTGGCTCTCT 689
Db 21 CATCTGGGTCCTGGCTCTCTT 1
```

```
RESULT 759
US-10-603-566-38/c
; Sequence 38, Application US/10603566
; Publication No. US20040086966A1
; GENERAL INFORMATION:
; APPLICANT: Witcamer, Valerie
; APPLICANT: Communi, David
; APPLICANT: Vandenbergaeerde, Ann
; APPLICANT: Detheux, Michel
; APPLICANT: Parmentier, Marc
; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of Chemerin
; FILE REFERENCE: 9409/2212
; CURRENT APPLICATION NUMBER: US/10/603.566
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 09/905,253
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/201,187
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic primer
; NAME/KEY: misc_feature
; LOCATION: (1)..(21)
; OTHER INFORMATION: Synthetic primer
US-10-603-566-38
```

```
Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 6.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 669 CATCTGGGTCCTGGCTCTCT 689
Db 21 CATCTGGGTCCTGGCTCTCTT 1
```

```
RESULT 760
US-10-893-485-38/c
; Sequence 38, Application US/10893485
; Publication No. US20050155090A1
; GENERAL INFORMATION:
; APPLICANT: Wiltamer, Valerie
; APPLICANT: Communi, David
; APPLICANT: Vandenbogaerde, Ann
; APPLICANT: Detheux, Michel
; APPLICANT: Parmentier, Marc
; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of Chemerink
; FILE REFERENCE: 9409/2045C
; CURRENT APPLICATION NUMBER: US/10/893,485
; CURRENT FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US10/603,566
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 09/905,253
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/201,187
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic primer
; NAME/KEY: misc feature
; LOCATION: (1)..(21)
; OTHER INFORMATION: Synthetic primer
US-10-893-485-38

Query Match
Best Local Similarity 1.0%; Score 17.8; DB 1; Length 21;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 669 CATCTGGGTCCTGGCTCTCTCT 689
Db 21 CATCTGGGTCCTGGCTCTCTT 1

RESULT 761
US-10-310-914A-322519
; Sequence 322519, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 322519
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-322519

Query Match
Best Local Similarity 1.0%; Score 17.8; DB 1; Length 21;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 129 CTTGAGCCCGGCGCCAGCC 149
||:|||||
```

```
Db 1 CTTGAGCCCGGCGCCAGCC 21

RESULT 762
US-11-134-811-38/c
; Sequence 38, Application US/11134811
; Publication No. US20060024750A1
; GENERAL INFORMATION:
; APPLICANT: Wiltamer, Valerie
; APPLICANT: Communi, David
; APPLICANT: Vandenbogaerde, Ann
; APPLICANT: Detheux, Michel
; APPLICANT: Parmentier, Marc
; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of Chemerink
; FILE REFERENCE: 9409/2043
; CURRENT APPLICATION NUMBER: US/11/134,811
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 10/603,566
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 09/905,253
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/201,187
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: PCT/EP02/07647
; PRIOR FILING DATE: 2002-07-09
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic primer
; NAME/KEY: misc feature
; LOCATION: (1)..(21)
; OTHER INFORMATION: Synthetic primer
US-11-134-811-38

Query Match
Best Local Similarity 1.0%; Score 17.8; DB 1; Length 21;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 669 CATCTGGGTCCTGGCTCTCTCT 689
Db 21 CATCTGGGTCCTGGCTCTTCT 1

RESULT 763
US-10-310-914A-467163/c
; Sequence 467163, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 467163
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-467163

Query Match
Best Local Similarity 1.0%; Score 17.8; DB 1; Length 22;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 882 GGCCAGTGAATCCCCGGGGA 902
Db 21 GGCCAGGAGGTCCCCGGGGA 1

RESULT 764

US-10-310-914A-467164/c
; Sequence 467164, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 467164
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-467164

Query Match 1.0%; Score 17.8; DB 1; Length 22;
Best Local Similarity 90.5%; Pred. No. 7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 882 GGCCAGTGAATCCCCGGGGA 902
Db 21 GGCCAGGAGGTCCCCGGGGA 1

RESULT 765

US-10-310-914A-965080/c
; Sequence 965080, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 965080
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-965080

Query Match 1.0%; Score 17.8; DB 1; Length 22;
Best Local Similarity 90.5%; Pred. No. 7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 997 CCCTTCACATCTCTCTCTC 1017
Db 22 CCCTTCACATCTCTCTCTC 2

RESULT 766

US-10-310-914A-1184635
; Sequence 1184635, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1184635
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1184635

Query Match 1.0%; Score 17.8; DB 1; Length 22;
Best Local Similarity 61.9%; Pred. No. 7e+02;
Matches 13; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 532 CACACTCTTCCCATGCC 552
Db 1 CACACCTUCCUCCCAUCCCC 21

RESULT 767

US-10-005-956-82/c
; Sequence 82, Application US/10005956
; Publication No. US2003013726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005.956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 82
; LENGTH: 19
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-005-956-82

Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 6.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 663 CTGTCATCTGGGTCTG 681
Db 19 CTGTGATATGGGTCTG 1

RESULT 768

US-10-005-956-86/c
; Sequence 86, Application US/10005956
; Publication No. US2003013726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005.956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 86
; LENGTH: 19

```
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-005-956-86

Query Match      1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 6.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1529 CCTCAGCTGGAGCTTGA 1547
Db      19 CCTCAGCTAGGACTTGA 1

RESULT 769
US-10-005-956-144
; Sequence 144, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 144
; LENGTH: 19
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-005-956-144

Query Match      1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 6.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      534 CAACCTCTTCCAGCGCC 552
Db      1 CAACCTCTTCCAGCGCC 19

RESULT 770
US-10-005-956-148/C
; Sequence 148, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 148
; LENGTH: 19
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-005-956-148

Query Match      1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 6.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1626 TCATGCTGTGACTCAAA 1644
Db      19 TCATGCTGTGACTCAAA 1

RESULT 771
US-10-005-956-150/C
; Sequence 150, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 150
; LENGTH: 19
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-005-956-150

Query Match      1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 6.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1335 CACACCTCTGTCCTGGAC 1353
Db      19 CACACCTCATCCTGGAC 1
```

```
RESULT 772
US-10-310-914A-88048/C
; Sequence 88048, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kiyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 88048
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-88048
```

```
Query Match      1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 6.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      167 AGGGGGGTGTGTACAGAT 185
Db      19 AGGGGGGTGTGTACAGAT 1
```

```
RESULT 773
US-10-310-914A-1153363
; Sequence 1153363, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
```



```

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kruzac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087,0200,CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patent version 3.3
; SEQ ID NO: 1153363
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1153363

```

```

Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 6.2e+02;
Matches 13; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 675 GATCTGGCTCTCTGCTG 693
Db 1 GGUCCGCGCUCUCGCTG 19

```

```

RESULT 774
US-11-083-784-49660
; Sequence 49660, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 49660
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-49660

```

```

Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 6.2e+02;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1109 ACAUCCCATCATCTACTG 1127
Db 1 ACAUCCCAUCCAUCCUACUG 19

RESULT 775
US-11-083-784-103957
; Sequence 103957, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen

```

```

; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 103957
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-103957

```

```

Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 6.2e+02;
Matches 11; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 668 TCATCTGGCTCTGCTCT 686
Db 1 UCAUCUGGUCUCGUCU 19

```

```

RESULT 776
US-11-083-784-490753
; Sequence 490753, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 490753
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-490753

```

```

Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 6.2e+02;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1104 CATGTACACCCATCATC 1122
Db 1 CAUGUACAUCCCAUCCAUCC 19

```

```

RESULT 777
US-11-083-784-490758
; Sequence 490758, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela

```

```

; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13490US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 490758
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-490758

```

```

Query Match      1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 6.2e+02;
Matches 13; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1106 TGTAACACCCATCATCTTA 1124
      :|:|||||:|:|:|:|:|:|:|:|
DB      1 GUACAACCCCAUCUACUUA 19

```

```

RESULT 778
US-11-083-784-490759
; Sequence 490759, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13490US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 490759
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-490759

```

```

Query Match      1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 6.2e+02;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1107 GTRCAACCCCATCATCTTAC 1125
      |:|||||:|:|:|:|:|:|:|:|
DB      1 GUACAACCCCAUCUACUUA 19

```

```

RESULT 779
US-11-083-784-490763
; Sequence 490763, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13490US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 490763
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-490763

```

```

Query Match      1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 6.2e+02;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1109 ACAACCCCATCATCTCTAG 1127
      |||||:|:|:|:|:|:|:|:|
DB      1 ACAACCCCAUCUACUUA 19

```

```

RESULT 780
US-11-083-784-491328
; Sequence 491328, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13490US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491328
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491328

```

```

Query Match      1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 6.2e+02;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      562 GCCAGTATCTACTCATGCA 580
      |||||:|:|:|:|:|:|:|:|
DB      1 GCCAGCAUCUACUCCAUCA 19

```

```

RESULT 781
US-11-083-784-491368

```

```
; Sequence 491368, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491368
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491368
```

```
Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 6.2e+02;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1104 CATGTACACCCCATCTATC 1122
Db 1 GACGACAUCCCAUCAC 19
```

```
RESULT 782
US-11-083-784-491376
; Sequence 491376, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491376
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491376
```

```
Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 6.2e+02;
Matches 13; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1106 TGTACACCCCATCTATCTA 1124
Db 1 UGACAAUCCCAUCACU 19
```

```
RESULT 783
US-11-083-784-491384
; Sequence 491384, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491384
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491384
```

```
Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 6.2e+02;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1107 GTACACCCCATCTATCTAC 1125
Db 1 GUACAAUCCCAUCACU 19
```

```
RESULT 784
US-11-083-784-491392
; Sequence 491392, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491392
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491392
```

```
Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 6.2e+02;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1109 ACAACCCCATCTATCTACTG 1127
```

Db 1 ACAUCCCAUACAUCUACUG 19

RESULT 785
US-11-083-784-854916

; Sequence 854916, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 854916
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-854916

Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 6.2e+02;
Matches 12; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 106 CCTCTGTCGTCTTGAA 124
Db 1 CCUCCUGUCGUUAGAA 19

RESULT 786

US-11-083-784-877764/C
; Sequence 877764, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 877764
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-877764

Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 6.2e+02;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1402 AGCTTCAGCTTCTCTCCA 1420
Db 19 AGCTTCAGCATCTCTCCA 1

RESULT 787
US-11-083-784-946470/C

; Sequence 946470, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 946470
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-946470

Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 6.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1722 TTCTGGAAGTGACTTGAC 1740
Db 19 TTCTGGAAGTGACTTGAC 1

RESULT 788

US-11-083-784-1141173
; Sequence 1141173, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1141173
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1141173

Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 6.2e+02;
Matches 13; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
479 TCACCTAAGCTGTCCACA 497
:||||:||||:||||:
Db 1 UCACCUAUGCUGUCCAGAA 19

RESULT 789
US-11-083-784-1245667/c
; Sequence 1245667, Application US/11083784
; Publication No. US20050246794AI
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1245667
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1245667

Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 6.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
652 AAAGTGTCTCTGTCTCA 670
|||||
Db 19 AAAGTGTCTCTGTCTCA 1

RESULT 790
US-11-101-244-49660
; Sequence 49660, Application US/1101244
; Publication No. US20050246794AI
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 49660
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-49660

US-11-101-244-49660
Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 6.2e+02;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
1109 ACAACCCCATCCTACTG 1127
|||||
Db 1 ACAUCCCAUCCUACUG 19

RESULT 791
US-11-101-244-103957
; Sequence 103957, Application US/1101244
; Publication No. US20050246794AI
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 103957
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-103957

Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 6.2e+02;
Matches 11; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
668 TCATCTGGGTCGCGCT 686
:|:|:|:|:|:|:|:|:|:
Db 1 UCAUCGGGUCUCGUCU 19

RESULT 792
US-11-101-244-490753
; Sequence 490753, Application US/1101244
; Publication No. US20050246794AI
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 490753
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-490753

Best Local Similarity 73.7%; Pred. No. 6.2e+02;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 562 GCCAGTACTTACTCCATCA 580
Db 1 GCCAGCAUCUACUCCAUCA 19

RESULT 797

US-11-101-244-491368
; Sequence 491368, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491368
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491368

Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 6.2e+02;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1104 CATGTACACCCCATCATC 1122
Db 1 CAUGACAUCUCCAUCAUC 19

RESULT 798
US-11-101-244-491376
; Sequence 491376, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491376
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491376

Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 6.2e+02;

Matches 13; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1106 TGTCACCCCATCATCTA 1124
Db 1 UGUACAUCUCCAUCAUCA 19

RESULT 799

US-11-101-244-491384
; Sequence 491384, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491384
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491384

Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 6.2e+02;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1107 GTACACCCCATCATCTAC 1125
Db 1 GUACAUCUCCAUCAUCA 19

RESULT 800
US-11-101-244-491392
; Sequence 491392, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491392
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491392

Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 6.2e+02;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

QY      1109 ACAACCCCATCTACTG 1127
          ||||| ||||: ||: ||: |
Db      1 ACAUCCCAUCUACUG 19

```

```

RESULT: 80
US-11-101-244-854916
; Sequence: 854916, Application: US/11101244
; Publication No.: US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ. ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ. ID NO: 854916
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-854916

```

Query Match	1.0%;	Score 17.4;	DB 1;	Length 19;
Best Local Similarity	63.2%;	Pred. No. 6.2e+02;		
Matches 12;	Conservative 6;	Mismatches 1;	Indels 0;	Gaps 0;

Qy	106	CCTCCTGTCCTTAGAA	124
		: : : : : :	
Db	1	CCUCCUGUCGCUAAGAA	19

```

RESULT 802
US-11-101-244-877764/c
; Sequence 877764, Application US/11101244
; Publication NO. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khoroova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIORITY FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 159111
; SOFTWARE: Proprietary
; SEQ ID NO 877764
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-877764

```

Query Match	1.0%;	Score 17.4;	DB 1;	Length 19;
Best Local Similarity	94.7%;	Pred. No. 6.2e+02;		
Matches 18;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

```

QY      1402 AGCTTCAGCTTCTCTCCA 1420
          |||||
Db      19 AGCTTCAGCATCTCTCCA 1

```

```

RESULT 803
US-11-101-244-946470/C
; Sequence 946470, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 946470
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-946470

```

Query Match	1.0%;	Score 17.4;	DB 1;	Length 19;
Best Local Similarity	94.7%;	Pred. No. 6.2e+02;		
Matches 18;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

QY		1722	TTCTGGAAGTGCATTGGC	1740
Db		19	TTCTGGAAGTGACCTTGGC	1

```

RESULT 804
US-11-101-244-1141173
/ Sequence 1141173, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 1141173
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-1141173

```

Query Match	1.0%	Score 17.4;	DB 1;	Length 19;
Best Local Similarity	68.4%;	Pred. No. 6.2e+02;		
Matches 13;	Conservative 5;	Mismatches 1;	Indels 0;	Gaps 0.

479 TCACCTATGCTGTCCACAA 497

Db 1 UCACCUAUGCUGCCAGAA 19

RESULT 805
US-11-101-244-1245667/c
; Sequence 1245667, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1245667
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1245667

Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 6.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 652 AAAGTGCATCTGTGTCA 670
Db 19 AAAGTGCATCTGTGTCA 1

RESULT 806
US-10-310-914A-515099
; Sequence 515099, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 515099
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-515099

Query Match 1.0%; Score 17.4; DB 1; Length 21;
Best Local Similarity 57.9%; Pred. No. 7.1e+02;
Matches 11; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Qy 663 CTGTGTCATCTGGCTCTG 681
Db 3 CUGUGUCUCUCUGGUCUG 21

RESULT 807
US-10-310-914A-1308283/c
; Sequence 1308283, Application US/10310914A
; Publication No. US20060003322A1

; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1308283
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1308283

Query Match 1.0%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 7.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 365 TAGTGATGTGATCATCTT 383
Db 19 TAGTGATGTGATCATCTT 1

RESULT 808
US-10-310-914A-138766/c
; Sequence 138766, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 138766
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-138766

Query Match 1.0%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 986 TCTGCTGCTGCCCTTC 1002
Db 17 TCTGCTGCTGCCCTTC 1

RESULT 809
US-10-310-914A-822037/c
; Sequence 822037, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 822037
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-822037

```
Query Match      1.0%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels
```

QY	525	CAAGTTCACAACTTCT	541
Db	18	CAAGTTCACAACTTCT	2

RESULT 810

```

US-11-083784-128453
; Sequence 128453, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 128453
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-128453

```

Query Match	1.0%;	Score 17;	DB 1;	Length 19;
Best Local Similarity	82.4%;	Pred. No. 6.7e+02;		
Matches 14;	Conservative 3;	Mismatches 0;	Indels 0;	Gaps 0;

```

QY      922 GAGCAAGTCTCTGCCAA 938
          |||||:|:|||||
Db      1  GAGCAAGUCUCUGCCAA 17

```

RESULT 811

```

US-11-083-784-128543
Sequence 128543, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 1349905
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 128543
LENGTH: 19

```

```

; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-128543

```

Query Match	1.0%;	Score 17;	DB 1;	Length 19;
Best Local Similarity	82.4%;	Pred. No. 6.7e+02;		
Matches	14;	Conservative	3;	Mismatches 0;
				Indels 0;
				Gaps 0;

QY 922 GAGCAAGTCTCTGCCAA 938
|||||:|:|:|
Db 1 GAGCAAGTCTCTGCCAA 17

```

RESULT 812
US-11-083-784-1265096
1 Sequence 1265096, Application US/11083784
2 Publication No. US20050245475A1
3 GENERAL INFORMATION:
4 APPLICANT: Dharmacon, Inc.
5 APPLICANT: Khvorova, Anastasia
6 APPLICANT: Reynolds, Angela
7 APPLICANT: Leake, Devin
8 APPLICANT: Marshall, William
9 APPLICANT: Scaringe, Stephen
10 TITLE OF INVENTION: Functional and Hyperfunctional siRNA
11 FILE REFERENCE: 1349905
12 CURRENT APPLICATION NUMBER: US/11/083,784
13 CURRENT FILING DATE: 2005-03-18
14 PRIOR APPLICATION NUMBER: US/10/714,333
15 PRIOR FILING DATE: 2003-11-14
16 PRIOR APPLICATION NUMBER: 60/502,050
17 PRIOR FILING DATE: 2003-09-10
18 PRIOR APPLICATION NUMBER: 60/426,137
19 PRIOR FILING DATE: 2002-11-14
20 NUMBER OF SEQ ID NOS: 151911
21 SOFTWARE: Proprietary
22 SEQ ID NO: 1265096
23 LENGTH: 19
24 TYPE: RNA
25 ORGANISM: Homo sapiens
US-11-083-784-1265096

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Query Match	1.0%;	Score 17;	DB 1;	Length 19;
Best Local Similarity	82.4%;	Pred. No. 6.7e+02;		
Matches 14;	Conservative	3;	Mismatches 0;	Indels 0;
			Gaps	0;

QY 1533 ACAC~~TGG~~AGCTTGCAAA 1549
|||:||||:|||||
Db 3 ACACUGGAGC~~UUG~~CAAA 19

RESULT 813

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US-11-101-244-128453
/ Sequence 128453, Application US/11101244
/ Publication No. US20050246794A1
/
GENERAL INFORMATION:
/
APPLICANT: Dharmacon, Inc.
/
APPLICANT: Khvorovta, Anastasia
/
APPLICANT: Keynolds, Angela
/
APPLICANT: Leake, Devin
/
APPLICANT: Marshall, William
/
APPLICANT: Scaringe, Stephen
/
TITLE OF INVENTION: Functional and Hyperfunctional sRNA
/
FILE REFERENCE: 13499US
/
CURRENT APPLICATION NUMBER: US/11/101,244
/
CURRENT FILING DATE: 2005-04-07
/
PRIOR APPLICATION NUMBER: 60/502,050
/
PRIOR FILING DATE: 2003-09-10
/
PRIOR APPLICATION NUMBER: 60/426,137
/
PRIOR FILING DATE: 2002-11-14
/
NUMBER OF SEQ ID NOS: 1591911
/
SOFTWARE: Proprietary
/
SEQ ID NO 128453

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; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-128453

Query Match
Best Local Similarity 82.4%; Pred. No. 6.7e+02;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 922 GAGCAAGCTCTGCGCAA 938
Db 1 GAGCAAGCTCTGCGCAA 17

RESULT 814
US-11-101-244-128543
; Sequence 128543, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacom, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 128543
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-128543

Query Match
Best Local Similarity 82.4%; Pred. No. 6.7e+02;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 922 GAGCAAGCTCTGCGCAA 938
Db 1 GAGCAAGCTCTGCGCAA 17

RESULT 815
US-11-101-244-1265096
; Sequence 1265096, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacom, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1265096
; LENGTH: 19
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; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1265096

Query Match
Best Local Similarity 82.4%; Pred. No. 6.7e+02;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1533 ACACGGGAGCTTGCAAA 1549
Db 3 ACACGGGAGCTTGCAAA 19

RESULT 816
US-10-310-914A-160462/c
; Sequence 160462, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiner, Krutaz
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 160462
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-160462

Query Match
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1326 CCCCAGGCCACACCTT 1342
Db 17 CCCCAGGCCACACCTT 1

RESULT 817
US-10-023-066A-25/c
; Sequence 25, Application US/10023066A
; Publication No. US20030056242A1
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND
; COMPANY
; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
; INCREASING THE LYSINE AND
; THREONINE CONTENT OF THE SEEDS OF
; PLANTS
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS
; AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD VERSION 2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/023,066A
; FILING DATE: 29-Apr-2002
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BARBARA C. SIEGELL
```

REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4931
TELEFAX: 302-773-0164
TELEX: 835420
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..21
OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
82"
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-10-023-066A-25

Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1404 CTTGAGCTTCTCTCCA 1420
Db 19 CTTGAGCTTCTCTCCA 3

RESULT 818
US-10-023-066A-41/C
Sequence 41, Application US/10023066A
Publication No. US20030056242A1
GENERAL INFORMATION:
APPLICANT: E. I. DU PONT DE NEMOURS AND
COMPANY
TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
INCREASING THE LYSINE AND
THREONINE CONTENT OF THE SEEDS OF
PLANTS
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS
AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,066A
FILING DATE: 29-Apr-2002
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4931
TELEFAX: 302-773-0164
TELEX: 835420
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
type: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..21
OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
86"
SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-10-023-066A-41

Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1404 CTTGAGCTTCTCTCCA 1420
Db 19 CTTGAGCTTCTCTCCA 3

RESULT 819
US-10-023-066A-43/C
Sequence 43, Application US/10023066A
Publication No. US20030056242A1
GENERAL INFORMATION:
APPLICANT: E. I. DU PONT DE NEMOURS AND
COMPANY
TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
INCREASING THE LYSINE AND
THREONINE CONTENT OF THE SEEDS OF
PLANTS
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS
AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,066A
FILING DATE: 29-Apr-2002
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4931
TELEFAX: 302-773-0164
TELEX: 835420
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..21
OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
88"

SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-10-023-066A-43

Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1404 CTTGAGCTTCTCTCCA 1420
Db 19 CTTGAGCTTCTCTCCA 3

RESULT 820

US-10-804-678-25/c
Sequence 25, Application US/10804678
Publication No. US2005005330A1
GENERAL INFORMATION:
APPLICANT: EPELBAUM, SABINE URSULA
FALCO, SAVERIO CARL
MCDEVITT, RAYMOND ERVIN, III
TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
INCREASING THE LYSINE CONTENT OF
THE SEEDS OF PLANTS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT OFFICE 97
SOFTWARE: MICROSOFT WINDOWS 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/804,678
FILING DATE: 19-Mar-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/049,304
FILING DATE: 27-Mar-1998
APPLICATION NUMBER: 08/824,627
FILING DATE: MARCH 27, 1997
ATTORNEY/AGENT INFORMATION:
NAME: CHRISTENBURY, LYNNE M.
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB-1037-F
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-5481
TELEFAX: 302-892-7949
TELEX: 835420
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..21
OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
82"
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-10-804-678-25

Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1404 CTTGAGCTTCTCTCCA 1420
Db 19 CTTGAGCTTCTCTCCA 3

RESULT 821

US-10-804-678-41/c
Sequence 41, Application US/10804678
Publication No. US2005005330A1
GENERAL INFORMATION:
APPLICANT: EPELBAUM, SABINE URSULA
FALCO, SAVERIO CARL
MCDEVITT, RAYMOND ERVIN, III
TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
INCREASING THE LYSINE CONTENT OF
THE SEEDS OF PLANTS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT OFFICE 97
SOFTWARE: MICROSOFT WINDOWS 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/804,678
FILING DATE: 19-Mar-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/049,304
FILING DATE: 27-Mar-1998
APPLICATION NUMBER: 08/824,627
FILING DATE: MARCH 27, 1997
ATTORNEY/AGENT INFORMATION:
NAME: CHRISTENBURY, LYNNE M.
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB-1037-F
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-5481
TELEFAX: 302-892-7949
TELEX: 835420
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..21
OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
86"
SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-10-804-678-41

Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1404 CTTGAGCTTCTCTCCA 1420
Db 19 CTTGAGCTTCTCTCCA 3

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RESULT 822
US-10-804-678-43/c
; Sequence 43, Application US/10804678
; Publication No. US2005005330A1
; GENERAL INFORMATION:
; APPLICANT: EPELBAUM, SABINE URSULA
; FALCO, SAVERIO CARL
; MCDEVITT, RAYMOND ERYIN, III
; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
; INCREASING THE LYSINE CONTENT OF
; THE SEEDS OF PLANTS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT OFFICE 97
; SOFTWARE: MICROSOFT WINDOWS 95
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/804,678
; FILING DATE: 19-Mar-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,304
; FILING DATE: 27-Mar-1998
; APPLICATION NUMBER: 08/824,627
; FILING DATE: MARCH 27, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: CHRISTENDURY, LYNN M.
; REGISTRATION NUMBER: 30,971
; REFERENCE/DOCKET NUMBER: BB-1037-F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-5481
; TELEFAX: 302-892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..21
; OTHER INFORMATION: /product= "synthetic
; oligonucleotide"
; /standard_name= "SM
; 88"
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-10-804-678-43
;
Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1404 CTTGACCTTCTCTCTCA 1420
DB 19 CTTGACCTTCTCTCTCA 3
;
RESULT 823
US-10-376-566-63/c
; Sequence 63, Application US/10376566
; Publication No. US2003015814A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie

```

```

; APPLICANT: Mark P. Roach
; APPLICANT: Erich Koller
; TITLE OF INVENTION: ANTISENSE MODULATION OF ESTROGEN RECEPTOR BETA EXPRESSION
; FILE REFERENCE: RTS-0347
; CURRENT APPLICATION NUMBER: US/10/376,566
; CURRENT FILING DATE: 2003-02-27
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 96
; SEQ ID NO 63
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-10-376-566-63
;
Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 7.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 434 CTTGCGGAGGCGCTTCATG 453
DB 20 CTTGACCGAGCGCTTCATG 1
;
RESULT 824
US-10-310-914A-279471/c
; Sequence 279471, Application US/10310914A
; Publication No. US2006000332A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 279471
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
; US-10-310-914A-279471
;
Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 7.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1715 ATTGCATTTCTGGAAGTGAC 1734
DB 20 ATTGCATTTCTGGAATGAC 1
;
RESULT 825
US-10-310-914A-460312
; Sequence 460312, Application US/10310914A
; Publication No. US2006000332A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 460312
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human

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US-10-310-914A-460312

Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 7.5e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 130 CTGAGCCCCAGCGCCAGCC 149
|:|||||:|||||
Db 1 CUUAGCCCCAGCGCCAGCC 20

RESULT 826

US-10-310-914A-1145210
; Sequence 1145210, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1145210
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1145210

Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 70.0%; Pred. No. 7.5e+02;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 978 CTTGCCATCTGCTGCTGC 997
|:|||||:|||||
Db 1 CUGGCCACCTGCGCGCC 20

RESULT 827

US-10-770-726-10314/C
; Sequence 10314, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770.726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10314
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNA1
US-10-770-726-10314

Query Match 1.0%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 7.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1049 AGAAGTTATCCACAGGTC 1068
|:|||||:|||||
Db 21 AAAAGTTATCAAGCAGGTC 2

RESULT 828

US-10-310-914A-43024/C
; Sequence 43024, Application US/10310914A

; Publication No. US20060003322A1

; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 43024
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-43024

Query Match 1.0%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 7.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 134 GCCCAGCGCCAGCCAG 153
|:|||||:|||||
Db 21 GCCCAGCGCCAGCCAG 2

RESULT 829

US-10-310-914A-151367
; Sequence 151367, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 151367
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-151367

Query Match 1.0%; Score 16.8; DB 1; Length 21;
Best Local Similarity 65.0%; Pred. No. 7.9e+02;
Matches 13; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 980 TCGCATCTGCTGCTGCC 999
|:|||||:|||||
Db 2 UCCCCUCUGCGUGCC 21

RESULT 830

US-10-310-914A-201071/C
; Sequence 201071, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 201071
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human

US-10-310-914A-201071

Query Match 1.0%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 7.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1295 TGGGGGCCCGAGGAG 1314

DB 21 TGGGGGCCCGAGGAG 2

RESULT 831

US-10-310-914A-412673/C
; Sequence 412673, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 412673
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-412673

Query Match 1.0%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 7.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1604 TTCTTCCTATCTTGGCAC 1623

DB 21 TTCTTCCTATCTTGGCAC 2

RESULT 832

US-10-310-914A-444744/C
; Sequence 444744, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 444744
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-444744

Query Match 1.0%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 7.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1562 GGGTTAGGAAACATTCCA 1561

DB 21 GGGTTAGGAAACATTCCA 2

RESULT 833

US-10-310-914A-800870
; Sequence 800870, Application US/10310914A
; Publication No. US20060003322A1

; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 800870
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-800870

Query Match 1.0%; Score 16.8; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. No. 7.9e+02;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 640 GCCACAGCCACCAAGTGT 659

DB 1 GCCACAGCCACCAAGTGT 20

RESULT 834

US-10-310-914A-843549
; Sequence 843549, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 843549
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-843549

Query Match 1.0%; Score 16.8; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. No. 7.9e+02;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 715 TCACACACGAGACCATGCC 734

DB 2 TCACACACGAGACCATGCC 21

RESULT 835

US-10-138-674-2971/C
; Sequence 2971, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2971
; LENGTH: 18


```

; TYPE: RNA
; ORGANISM: Mus musculus
; US-10-138-674-2971

Query Match
Best Local Similarity 94.4%; Score 16.4; DB 1; Length 18;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 624 CCAGCCCCGGCTGTCAGC 641
DB 18 CCAGCCCGCGCTGTCAGC 1

RESULT 836
; Sequence 2971, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MHHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2971
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Mus musculus
; US-10-287-949A-2971

Query Match
Best Local Similarity 94.4%; Score 16.4; DB 1; Length 18;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 624 CCAGCCCCGGCTGTCAGC 641
DB 18 CCAGCCCGCGCTGTCAGC 1

RESULT 837
; US-10-951-303-2971/c
; Sequence 2971, Application US/10951303
; Publication No. US20050227937A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MHHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/10/951,303
; PRIOR APPLICATION NUMBER: US/09/685,664
; PRIOR FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2971
; LENGTH: 18
; TYPE: RNA
```

```

; ORGANISM: Mus musculus
; US-10-951-303-2971

Query Match
Best Local Similarity 94.4%; Score 16.4; DB 1; Length 18;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 624 CCAGCCCCGGCTGTCAGC 641
DB 18 CCAGCCCGCGCTGTCAGC 1

RESULT 838
; US-10-310-914A-336642/c
; Sequence 336642, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 336642
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
; US-10-310-914A-336642

Query Match
Best Local Similarity 94.4%; Score 16.4; DB 1; Length 18;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1551 AGGTCAGTATGGGTAG 1568
DB 18 AGGTCATATAGGTAG 1

RESULT 839
; US-10-310-914A-999588
; Sequence 999588, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 999588
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
; US-10-310-914A-999588

Query Match
Best Local Similarity 83.3%; Score 16.4; DB 1; Length 18;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1453 GGTGACAGCCCCCACTGCC 1470
DB 1 GGUGACAGCCCCCUCUGCC 18

RESULT 840
; US-10-310-914A-1071407
; Sequence 1071407, Application US/10310914A
```

```
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1071407
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1071407

Query Match          0.9%; Score 16.4; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 7e+02;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1448 TGGCAGGTGACGCCCCCA 1465
Db      1 UGCAGAGGGGAGCCCCCA 18

RESULT 841
US-10-310-914A-1378476
; Sequence 1378476, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1378476
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1378476

Query Match          0.9%; Score 16.4; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 7e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1233 TCTCCAGACCCAGGCGAG 1250
Db      1 UCUGCAGACCCAGGCGAG 18

RESULT 842
US-10-310-914A-687663
; Sequence 687663, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 687663
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human

US-10-310-914A-687663
Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 77.8%; Pred. No. 7.5e+02;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      890 AGATCCCGGGGACTCTCT 907
Db      2 AGCTCCCGGGGACTCTCCU 19

RESULT 843
US-10-310-914A-1378477
; Sequence 1378477, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1378477
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1378477

Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1233 TCTCCAGACCCAGGCGAG 1250
Db      1 UCUGCAGACCCAGGCGAG 18

RESULT 844
US-10-310-914A-1384285/C
; Sequence 1384285, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1384285
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1384285

Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1006 ATCTTCTCTCTCTGCCC 1023
Db      19 ACCTTCTCTCTCTGCCC 2

RESULT 845
US-11-083-784-49684
; Sequence 49684, Application US/11083784
; Publication No. US20050245475A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 49684
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-49684
```

```

Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 7.5e+02;
Matches 12; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1114 CCCACATCTACTCTGTCG 1131
Db      1   CCCAUCACUACUCGUCUC 18
```

```

RESULT 846
US-11-083-784-209546/C
; Sequence 209546, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 209546
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-209546
```

```

Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1001 TCCACATCTTCTCTCC 1018
Db      18 TCCACCTCTTCTCTCC 1
```

RESULT 847

```

US-11-083-784-405179/C
; Sequence 405179, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 405179
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-405179
```

```

Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1405 TTCAGCTTCTCTCCATT 1422
Db      19 TTCAGCTTCTCTCCATT 2
```

```

RESULT 848
US-11-083-784-427206
; Sequence 427206, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 427206
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-427206
```

```

Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 7.5e+02;
Matches 12; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1550 AAGGTCAGTATGGTTA 1567
Db      2   AAGGTCACUUAUGGUA 19
```

```
RESULT 849
US-11-083-784-491396
; Sequence 491396, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Reynolds, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491396
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491396

Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 77.8%; Pred. No. 7.5e+02;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1095 GAGCTCCACCACTGTCACAA 1112
Db      1 GAGCTCCACCAUGUCAA 18

RESULT 850
US-11-083-784-521114
; Sequence 521114, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 521114
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-521114

Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 72.2%; Pred. No. 7.5e+02;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1048 AAGAACTTATCCACGAG 1065
Db      2 AAGAAGUUUAUCCAGAG 19

RESULT 851
US-11-083-784-531574
; Sequence 531574, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 531574
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-531574

Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1274 AGACCACTCTCCACGAG 1291
Db      1 AGACUACCAUCCACGAG 18

RESULT 852
US-11-083-784-531575
; Sequence 531575, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 531575
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-531575

Query Match          0.9%; Score 16.4; DB 1; Length 19;
```

Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1274 AGACCAACCATCTCCACAG 1291
Db 1 AGACUACCAUCUCCACAG 18

RESULT 853

US-11-083-784-531674
; Sequence 531674, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 531674
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-531674

Query Match
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1274 AGACCAACCATCTCCACAG 1291
Db 1 AGACUACCAUCUCCACAG 18

RESULT 854

US-11-083-784-531675
; Sequence 531675, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 531675
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens

US-11-083-784-531675

Query Match
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1274 AGACCAACCATCTCCACAG 1291
Db 1 AGACUACCAUCUCCACAG 18

RESULT 855

US-11-083-784-531774
; Sequence 531774, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 531774
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-531774

Query Match
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1274 AGACCAACCATCTCCACAG 1291
Db 1 AGACUACCAUCUCCACAG 18

RESULT 856

US-11-083-784-531775
; Sequence 531775, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 531775

```

; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-531775

```

```

Query Match
Best Local Similarity 83.3%; Score 16.4; DB 1; Length 19;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1274 AGACCAACATCTCCACAG 1291
Db 1 AGACUACCAUCCACACAG 18

```

```

RESULT 857
US-11-083-784-531872
; Sequence 531872, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Reynolds, Angela
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 531872
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-531872

```

```

Query Match
Best Local Similarity 83.3%; Score 16.4; DB 1; Length 19;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1274 AGACCAACATCTCCACAG 1291
Db 1 AGACUACCAUCCACACAG 18

```

```

RESULT 858
US-11-083-784-531873
; Sequence 531873, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14

```

```

; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 531873
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-531873

```

```

Query Match
Best Local Similarity 83.3%; Score 16.4; DB 1; Length 19;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1274 AGACCAACATCTCCACAG 1291
Db 1 AGACUACCAUCCACACAG 18

```

```

RESULT 859
US-11-083-784-531972
; Sequence 531972, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 531972
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-531972

```

```

Query Match
Best Local Similarity 83.3%; Score 16.4; DB 1; Length 19;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1274 AGACCAACATCTCCACAG 1291
Db 1 AGACUACCAUCCACACAG 18

```

```

RESULT 860
US-11-083-784-531973
; Sequence 531973, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050

```

PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 531973
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-531973

Query Match 0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1274 AGACCACCATCTCCACAG 1291
DB 1 AGACUACCAUCUCCACAG 18

RESULT 861
US-11-083-784-532071
Sequence 532071, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
PRIOR FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 532071
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-532071

Query Match 0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1274 AGACCACCATCTCCACAG 1291
DB 1 AGACUACCAUCUCCACAG 18

RESULT 862
US-11-083-784-532072
Sequence 532072, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18

PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 532072
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-532072

Query Match 0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1274 AGACCACCATCTCCACAG 1291
DB 1 AGACUACCAUCUCCACAG 18

RESULT 863
US-11-083-784-578805/C
Sequence 578805, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
PRIOR FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 578805
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-578805

Query Match 0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1720 ATTTCGAAGTGAAGCTT 1737
DB 19 ATTTCGAAGTGAAGCTT 2

RESULT 864
US-11-083-784-723652
Sequence 723652, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA

```

FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO: 723652
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-723652

```

```

Query Match      0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      392 AAAGATGAGGACAGTGA 409
DB      2 AAAGAUAGAAACAGUGA 19

```

```

RESULT 865
US-11-083-784-723752
Sequence 723752, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO: 723752
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-723752

```

```

Query Match      0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      392 AAAGATGAGGACAGTGA 409
DB      2 AAAGAUAGAAACAGUGA 19

```

```

RESULT 866
US-11-083-784-911949
Sequence 911949, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin

```

```

APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO: 911949
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-911949

```

```

Query Match      0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 72.2%; Pred. No. 7.5e+02;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1643 AACCAATCAGTCACTT 1660
DB      2 AACCAAUACACUGAAAU 19

```

```

RESULT 867
US-11-083-784-928479/c
Sequence 928479, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO: 928479
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-928479

```

```

Query Match      0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1007 TCTTCTCTCTGCGCCT 1024
DB      19 TCTTCTCTCTCTGCGCCT 2

```

```

RESULT 868
US-11-083-784-1141172
Sequence 1141172, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.

```



```

: APPLICANT: Khvorova, Anastasia
: APPLICANT: Reynolds, Angela
: APPLICANT: Leake, Devin
: APPLICANT: Marshall, William
: APPLICANT: Scaringe, Stephen
: TITLE OF INVENTION: Functional and Hyperfunctional siRNA
: FILE REFERENCE: 13499US
: CURRENT APPLICATION NUMBER: US/11/083,784
: CURRENT FILING DATE: 2005-03-18
: PRIOR APPLICATION NUMBER: US/10/714,333
: PRIOR FILING DATE: 2003-11-14
: PRIOR APPLICATION NUMBER: 60/502,050
: PRIOR FILING DATE: 2003-09-10
: PRIOR APPLICATION NUMBER: 60/426,137
: PRIOR FILING DATE: 2002-11-14
: NUMBER OF SEQ ID NOS: 1591911
: SOFTWARE: Proprietary
: SEQ ID NO 1141172
: LENGTH: 19
: TYPE: RNA
: ORGANISM: Homo sapiens
US-11-083-784-1141172

```

```

Query Match      0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 72.2%; Pred. No. 7.5e+02;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      480 CACCTATGCTGTCCACAA 497
Db      1 CACCUAUCGUCGUCGACGAA 18

```

```

RESULT 869
US-11-083-784-1259943/c
: Sequence 1259943, Application US/11083784
: Publication No. US20050245475A1
: GENERAL INFORMATION:
: APPLICANT: Dharmoon, Inc.
: APPLICANT: Khvorova, Anastasia
: APPLICANT: Reynolds, Angela
: APPLICANT: Leake, Devin
: APPLICANT: Marshall, William
: APPLICANT: Scaringe, Stephen
: TITLE OF INVENTION: Functional and Hyperfunctional siRNA
: FILE REFERENCE: 13499US
: CURRENT APPLICATION NUMBER: US/11/083,784
: CURRENT FILING DATE: 2005-03-18
: PRIOR APPLICATION NUMBER: US/10/714,333
: PRIOR FILING DATE: 2003-11-14
: PRIOR APPLICATION NUMBER: 60/502,050
: PRIOR FILING DATE: 2003-09-10
: PRIOR APPLICATION NUMBER: 60/426,137
: PRIOR FILING DATE: 2002-11-14
: NUMBER OF SEQ ID NOS: 1591911
: SOFTWARE: Proprietary
: SEQ ID NO 1259943
: LENGTH: 19
: TYPE: RNA
: ORGANISM: Homo sapiens
US-11-083-784-1259943

```

```

Query Match      0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      650 CCAAGTGTGTCATCTGTG 667
Db      19 CCAAGTGTGACATCTGTG 2

```

```

RESULT 870
US-11-083-784-1473036/c
: Sequence 1473036, Application US/11083784

```

```

: Publication No. US20050245475A1
: GENERAL INFORMATION:
: APPLICANT: Dharmoon, Inc.
: APPLICANT: Khvorova, Anastasia
: APPLICANT: Reynolds, Angela
: APPLICANT: Leake, Devin
: APPLICANT: Marshall, William
: APPLICANT: Scaringe, Stephen
: TITLE OF INVENTION: Functional and Hyperfunctional siRNA
: FILE REFERENCE: 13499US
: CURRENT APPLICATION NUMBER: US/11/083,784
: CURRENT FILING DATE: 2005-03-18
: PRIOR APPLICATION NUMBER: US/10/714,333
: PRIOR FILING DATE: 2003-11-14
: PRIOR APPLICATION NUMBER: 60/502,050
: PRIOR FILING DATE: 2003-09-10
: PRIOR APPLICATION NUMBER: 60/426,137
: PRIOR FILING DATE: 2002-11-14
: NUMBER OF SEQ ID NOS: 1591911
: SOFTWARE: Proprietary
: SEQ ID NO 1473036
: LENGTH: 19
: TYPE: RNA
: ORGANISM: Homo sapiens
US-11-083-784-1473036

```

```

Query Match      0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1417 TCCATGTGCTCTCCTG 1434
Db      19 TCCATGTGCTCTCCTG 2

```

```

RESULT 871
US-11-083-784-1484938
: Sequence 1484938, Application US/11083784
: Publication No. US20050245475A1
: GENERAL INFORMATION:
: APPLICANT: Dharmoon, Inc.
: APPLICANT: Khvorova, Anastasia
: APPLICANT: Reynolds, Angela
: APPLICANT: Leake, Devin
: APPLICANT: Marshall, William
: APPLICANT: Scaringe, Stephen
: TITLE OF INVENTION: Functional and Hyperfunctional siRNA
: FILE REFERENCE: 13499US
: CURRENT APPLICATION NUMBER: US/11/083,784
: CURRENT FILING DATE: 2005-03-18
: PRIOR APPLICATION NUMBER: US/10/714,333
: PRIOR FILING DATE: 2003-11-14
: PRIOR APPLICATION NUMBER: 60/502,050
: PRIOR FILING DATE: 2003-09-10
: PRIOR APPLICATION NUMBER: 60/426,137
: PRIOR FILING DATE: 2002-11-14
: NUMBER OF SEQ ID NOS: 1591911
: SOFTWARE: Proprietary
: SEQ ID NO 1484938
: LENGTH: 19
: TYPE: RNA
: ORGANISM: Homo sapiens
US-11-083-784-1484938

```

```

Query Match      0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 61.1%; Pred. No. 7.5e+02;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      657 GGTGATGTGTGTCATCTG 674
Db      1 GGCGAUCGUCGUCGACGUC 18

```

RESULT 872
US-11-101-244-49684
; Sequence 49684, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 49684
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-49684

Query Match 0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 7.5e+02;
Matches 12; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1114 CCCATCATCTACTGCTGC 1131
DB 1 CCCAUCACUCCUACUCGUC 18

RESULT 873
US-11-101-244-209546/C
; Sequence 209546, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 209546
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-209546

Query Match 0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1001 TCCACATCTTCTCTCC 1018
DB 18 TCCACCTCTCTCTCTCC 1

RESULT 874

US-11-101-244-405179/C
; Sequence 405179, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 405179
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-405179

Query Match 0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1405 TTCAGCTTCTCTCTCCAT 1422
DB 19 TTCAGCTTCTCTCTCCAT 2

RESULT 875
US-11-101-244-427206
; Sequence 427206, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 427206
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-427206

Query Match 0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 7.5e+02;
Matches 12; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1550 AAGGCTCAGTATGGGTTA 1567
DB 2 AAGGCTCAGTATGGGTTA 19

RESULT 876
US-11-101-244-491396

```
; Sequence 491396, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491396
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491396

Query Match
Best Local Similarity 0.9%; Score 16.4; DB 1; Length 19;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1095 GAGCTCCACCATGTACAA 1112
Db 1 GAGCTCAACCAUGUACAA 18

RESULT 877
US-11-101-244-521114
; Sequence 521114, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 521114
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-521114

Query Match
Best Local Similarity 0.9%; Score 16.4; DB 1; Length 19;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 531574
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-531574

Query Match
Best Local Similarity 0.9%; Score 16.4; DB 1; Length 19;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1274 AGACCACCATCTCCACAG 1291
Db 1 AGACUACCAUCUCCACAG 18

RESULT 879
US-11-101-244-531575
; Sequence 531575, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 531575
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-531575

Query Match
Best Local Similarity 0.9%; Score 16.4; DB 1; Length 19;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1274 AGACCACCATCTCCACAG 1291
Db 1 AGACUACCAUCUCCACAG 18

RESULT 880
US-11-101-244-531674
; Sequence 531674, Application US/11101244
; Publication No. US20050246794A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ PRIOR FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 531674
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-531674

Query Match      0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1274 AGACCACCATCTCCACAG 1291
Db      1 AGACUACCAUCCACACAG 18

RESULT 881
US-11-101-244-531675
/ Sequence 531675, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ PRIOR FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 531675
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-531675

Query Match      0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ PRIOR FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 531774
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-531774

Query Match      0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1274 AGACCACCATCTCCACAG 1291
Db      1 AGACUACCAUCCACACAG 18

RESULT 883
US-11-101-244-531775
/ Sequence 531775, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ PRIOR FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 531775
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-531775

Query Match      0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1274 AGACCACCATCTCCACAG 1291
Db      1 AGACUACCAUCCACACAG 18

RESULT 884
US-11-101-244-531872
/ Sequence 531872, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
```

```

; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 531872
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-531872

Query Match
Best Local Similarity 83.3%; Score 16.4; DB 1; Length 19;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1274 AGACCAACCATCTCCACAG 1291
Db 1 AGACUACCAUCUCCACAG 18
```

```

RESULT 885
US-11-101-244-531873
; Sequence 531873, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 531873
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-531873
```

```

Query Match
Best Local Similarity 83.3%; Score 16.4; DB 1; Length 19;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1274 AGACCAACCATCTCCACAG 1291
Db 1 AGACUACCAUCUCCACAG 18

RESULT 886
US-11-101-244-531972
; Sequence 531972, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
```

```

; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 531972
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-531972

Query Match
Best Local Similarity 83.3%; Score 16.4; DB 1; Length 19;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1274 AGACCAACCATCTCCACAG 1291
Db 1 AGACUACCAUCUCCACAG 18
```

```

RESULT 887
US-11-101-244-531973
; Sequence 531973, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 531973
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-531973
```

```

Query Match
Best Local Similarity 83.3%; Score 16.4; DB 1; Length 19;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1274 AGACCAACCATCTCCACAG 1291
Db 1 AGACUACCAUCUCCACAG 18

RESULT 888
US-11-101-244-532071
; Sequence 532071, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
```

```
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ PRIOR FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 532071
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-532071
```

```
Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1274 AGACCACCATCTCCACAG 1291
Db      1 AGACUACCAUCUCCACAG 18
```

```
RESULT 889
US-11-101-244-532072
/ Sequence 532072, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 532072
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-532072
```

```
Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1274 AGACCACCATCTCCACAG 1291
Db      1 AGACUACCAUCUCCACAG 18
```

```
RESULT 890
US-11-101-244-578805/c
/ Sequence 578805, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
```

```
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ PRIOR FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 578805
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-578805
```

```
Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1720 ATTTCTGGAAGTACTTT 1737
Db      19 ATTTCTGGAAGTACTT 2
```

```
RESULT 891
US-11-101-244-723652
/ Sequence 723652, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 723652
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-723652
```

```
Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      392 AAAGATGAGGACAGTGA 409
Db      2 AAAGATGAGGACAGTGA 19
```

```
RESULT 892
US-11-101-244-723752
/ Sequence 723752, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
```

```

; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 723752
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-723752
```

```

Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      392 AAGAGATGAGCAGCTGA 409
Db      2 AAGAAUGAGAACAGUGA 19
```

```

RESULT 893
US-11-101-244-911949
; Sequence 911949, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 911949
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-911949
```

```

Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 72.2%; Pred. No. 7.5e+02;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```

Qy      1643 AACCAATCACTGAAGCTT 1660
Db      2 AACCAAAUCACUGAAAUU 19
```

```

RESULT 894
US-11-101-244-928479/c
; Sequence 928479, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
```

```

; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 928479
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-928479
```

```

Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1007 TCTTCTCTCTCTGCGCCT 1024
Db      19 TCTTCTCTCTCTGCGCCT 2
```

```

RESULT 895
US-11-101-244-1141172
; Sequence 1141172, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1141172
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1141172
```

```

Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 72.2%; Pred. No. 7.5e+02;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```

Qy      480 CACCTATGCTGTCACAA 497
Db      1 CACCUAUGCTUGCCAGAA 18
```

```

RESULT 896
US-11-101-244-1259943/c
; Sequence 1259943, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
```

```
FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1259943
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1259943

Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      650 CCAAGTGTCTCTCTG 667
Db      19 CCAAGTGTCTCTCTG 2

RESULT 897
US-11-101-244-1473036/c
; Sequence 1473036, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1473036
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1473036

Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1417 TCCATGTGCTTCTCTAG 1434
Db      19 TCCATGTGCTTCTCTG 2

RESULT 898
US-11-101-244-1484938
; Sequence 1484938, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
```

```
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1484938
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1484938

Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 61.1%; Pred. No. 7.5e+02;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY      657 GGTCTGTGTGTCATCTG 674
Db      1 GGGCAUCUGUGUCACUCG 18

RESULT 899
US-09-967-669-87/c
; Sequence 87, Application US/09967669
; Publication No. US2003092650A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Frier
; TITLE OF INVENTION: ANTISENSE MODULATION OF SPHINGOSINE-1-PHOSPHATE LYASE EXPRESSION
; FILE REFERENCE: RTS-0259
; CURRENT APPLICATION NUMBER: US/09/967,669
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 87
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-967-669-87

Query Match          0.9%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      963 TGTGTGTGTGACCTT 980
Db      18 TGTGTGTGTGACCTT 1

RESULT 900
US-10-996-951-3
; Sequence 3, Application US/10996951
; Publication No. US20050255493A1
; GENERAL INFORMATION:
; APPLICANT: Macaulay, Valentine Moya
; APPLICANT: Schell, Muhammad
; TITLE OF INVENTION: MOLECULAR TARGETING OF THE IGF-1 RECEPTOR
; FILE REFERENCE: 351044-0011
; CURRENT APPLICATION NUMBER: US/10/996,951
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: PCT/GB03/02306
; PRIOR FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 0212303.2
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial
```



```
FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-10-996-951-3
Query Match
Best Local Similarity 0.9%; Score 16.4; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1409 GCCTTCCTCCCAATGTC 1426
DB 3 GCCTTCCTCCCAATGTC 20

RESULT 901
US-10-310-914A-157159
; Sequence 157159, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kivuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; NUMBER OF SEQ ID NOS: 2002-12-06
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 157159
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
; US-10-310-914A-157159

Query Match
Best Local Similarity 0.9%; Score 16.4; DB 1; Length 20;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 125 GGACCTGAGCCCGCAGGC 142
DB 3 GGACCTGAGCCCGCAGGC 20

RESULT 902
US-10-310-914A-428826
; Sequence 428826, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kivuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 428826
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
; US-10-310-914A-428826

Query Match
Best Local Similarity 0.9%; Score 16.4; DB 1; Length 20;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1231 TATTCGAGACCCGAGGC 1248
DB 3 UATCUCGAGACCCGAGGC 20

RESULT 903
US-10-310-914A-677516
; Sequence 677516, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kivuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 677516
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
; US-10-310-914A-677516

Query Match
Best Local Similarity 0.9%; Score 16.4; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1305 CGAGGAGAGCCGAGGA 1322
DB 3 CAAGGAGAGCCGAGGA 20

RESULT 904
US-10-310-914A-1236794/C
; Sequence 1236794, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kivuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1236794
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
; US-10-310-914A-1236794

Query Match
Best Local Similarity 0.9%; Score 16.4; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1690 CAGCTTTCTCTCAAGAC 1707
DB 19 CAGCTTTCTCTCAAGAC 2

RESULT 905
US-09-780-164-770
; Sequence 770, Application US/09780164
; Publication No. US20030092646A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blact, Larry
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
; FILE REFERENCE: 400/010
; CURRENT APPLICATION NUMBER: US/09/780,164
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 60/185,516
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 770
```

; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-164-770

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 7.1e+02;
Matches 10; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 801 CATCTGTCGACGTCG 816
DB 2 CAUCUGUGACUGUG 17

RESULT 906
US-11-083-784-523603/C

; Sequence 523603, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 523603
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-523603

Query Match 0.9%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1003 CACATCTTCTCTCTCC 1018
DB 16 CACATCTTCTCTCTCC 1

RESULT 907
US-11-083-784-1146200/C

; Sequence 1146200, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14

; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1146200
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1146200

Query Match 0.9%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 999 CTTCACATCTTCTTC 1014
DB 17 CTTCACATCTTCTTC 2

RESULT 908
US-11-101-244-523603/C

; Sequence 523603, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 523603
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-523603

Query Match 0.9%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1003 CACATCTTCTCTCTCC 1018
DB 16 CACATCTTCTCTCTCC 1

RESULT 909
US-11-101-244-1146200/C

; Sequence 1146200, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary
SEQ ID NO 1146200
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-1146200

Query Match 0.9%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 999 CTTCCACATCTTCTTC 1014
|||
Db 17 CTTCCACATCTTCTTC 2

RESULT 910
US-10-370-860A-10/C
Sequence 10, Application US/10370860A
Publication No. US20030219791A1
GENERAL INFORMATION:
APPLICANT: NOVO NORDISK A/S
APPLICANT: Wahl, Philip
APPLICANT: No. US20030219791A1by, Peder Lisby
APPLICANT: Grondahl, Christian
TITLE OF INVENTION: A transducer of Maa Signalling
FILE REFERENCE: 6475.200-US
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/231,670
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: PA 2002 00277
PRIOR FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 09/934,948
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: PCT/DK01/00550
PRIOR FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: PA 2000 01259
PRIOR FILING DATE: 2000-08-25
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-10-370-860A-10

Query Match 0.9%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 680 TGGCTCTCCGCTGCG 695
|||
Db 16 TGGCTCTCTGCTGCG 1

RESULT 911
US-10-370-860A-12
Sequence 12, Application US/10370860A
Publication No. US20030219791A1
GENERAL INFORMATION:
APPLICANT: NOVO NORDISK A/S
APPLICANT: Wahl, Philip
APPLICANT: No. US20030219791A1by, Peder Lisby
APPLICANT: Grondahl, Christian
TITLE OF INVENTION: A transducer of Maa Signalling
FILE REFERENCE: 6475.200-US
CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/231,670
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: PA 2002 00277
PRIOR FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 09/934,948
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: PCT/DK01/00550
PRIOR FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: PA 2000 01259
PRIOR FILING DATE: 2000-08-25
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-10-370-860A-12

Query Match 0.9%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 680 TGGCTCTCCGCTGCG 695
|||
Db 5 TGGCTCTCTGCTGCG 20

RESULT 912
US-10-310-914A-157270
Sequence 157270, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiller, Kiyazut
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 157270
LENGTH: 20
TYPE: RNA
ORGANISM: Human
US-10-310-914A-157270

Query Match 0.9%; Score 16; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 8.6e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 125 GGACCTGAGCCCGCAG 140
|||
Db 4 GGACCTGAGCCCGCAG 19

RESULT 913
US-10-310-914A-454995
Sequence 454995, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiller, Kiyazut
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 454995

```

; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-454995

Query Match      0.9%; Score 16; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 8.6e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1449 GCGAGTGCAGCCCC 1464
      |||||:|||||
DB      2   GGCAGGUGCAGCCCC 17

RESULT 914
US-10-206-693-14/c
; Sequence 14, Application US/10206693
; Publication No. US20050261212A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA interference using Short Interfering RNA
; FILE REFERENCE: 900/034 (MBHB02-732)
; CURRENT FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 674
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense r
US-10-206-693-14

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1001 TCACATCTTCTCTCTCT 1019
      |||||:|||||
DB      19 TCCTCCTCTTCTCTCTCT 1

RESULT 915
US-10-206-693-240
; Sequence 240, Application US/10206693
; Publication No. US20050261212A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA interference Mediated Inhibition of Nogo and Nogo Receptor G
; FILE REFERENCE: 900/034 (MBHB02-732)
; CURRENT APPLICATION NUMBER: US/10/206,693
; CURRENT FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 674
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 240
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-206-693-240

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 47.4%; Pred. No. 8.4e+02;
Matches 9; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

QY      1001 TCACATCTTCTCTCTCT 1019
      |||||:|||||

```

```

Db          1 UCCUCCUCUUCUCCUCCU 19

RESULT 916
US-10-310-914A-151357
; Sequence 151357, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiller, Kvuaz
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310.914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 151357
LENGTH: 19
TYPE: RNA
ORGANISM: Human
US-10-310-914A-151357

Query March                                0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity                      68.4%; Pred. No. 8.4e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      981 CGCCATCTGCTGCGTCCCC 999
       |||::|||::|||
Db      1 CCCCUCUGCUGCGUGGCC 19

RESULT 917
US-10-310-914A-232218/c
; Sequence 232218, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiller, Kvuaz
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310.914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 232218
LENGTH: 19
TYPE: RNA
ORGANISM: Human
US-10-310-914A-232218

Query Match                               0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity                     89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      672 CTGGGTCTGCTGCTCTTG 690
       ||||||
Db     19 CCGGGTCTGCTCTCTTG 1

RESULT 918
US-10-310-914A-360899
; Sequence 360899, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiller, Kvuaz
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310.914A
CURRENT FILING DATE: 2002-12-06

```

NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 360899
LENGTH: 19
TYPE: RNA
ORGANISM: Human
US-10-310-914A-360899

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Oy 676 GTCTGCTCTCTCCGCTGCG 694
Db 1 GCCCUGGCTCUCGCGCGG 19

RESULT 919

US-10-310-914A-432064
Sequence 432064, Application US/10310914A
Publication No. US2006003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 432064
LENGTH: 19
TYPE: RNA
ORGANISM: Human
US-10-310-914A-432064

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 8.4e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 92 AAAAGCCTTCACCCCTCC 110
Db 1 AAAAGCCTTCACCCCTCC 19

RESULT 920
US-10-310-914A-542218
Sequence 542218, Application US/10310914A
Publication No. US2006003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 542218
LENGTH: 19
TYPE: RNA
ORGANISM: Human
US-10-310-914A-542218

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 52.6%; Pred. No. 8.4e+02;
Matches 10; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Oy 821 TCTACTCTCTCCCTGCTGCT 839
Db 1 UCUGCUCUCCTCCCTGCTGCT 19

RESULT 921
US-10-310-914A-846052/C
Sequence 846052, Application US/10310914A
Publication No. US2006003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 846052
LENGTH: 19
TYPE: RNA
ORGANISM: Human
US-10-310-914A-846052

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1306 GAGGAGGAGCCAGAGGACG 1324
Db 19 GAGGAGGAGCCAGAGGACG 1

RESULT 922
US-10-310-914A-855297
Sequence 855297, Application US/10310914A
Publication No. US2006003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 855297
LENGTH: 19
TYPE: RNA
ORGANISM: Human
US-10-310-914A-855297

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 8.4e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 1284 CTCGACGCTGCTGGGCGCC 1302
Db 1 CTCGACGCTGCTGGGCGCC 19

RESULT 923
US-10-310-914A-1016265/C
Sequence 1016265, Application US/10310914A
Publication No. US2006003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402


```

; SEQ ID NO 1138736
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-914A-1138736

Query Match
Best Local Similarity 89.5%; Score 15.8; DB 1; Length 19;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1383 CTCGAGCATGACAGAG 1401
Db 19 CTCGAGCATGACAGAG 1

RESULT 929
US-10-310-914A-1153367
; Sequence 1153367, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087,0200,CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1153367
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1153367

Query Match
Best Local Similarity 63.2%; Score 15.8; DB 1; Length 19;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 673 TGGGTCTGCTCTCTCTG 691
Db 1 UAGGUCGCGGCGCUCGCG 19

RESULT 930
US-11-014-373-235/c
; Sequence 235, Application US/11014373
; Publication No. US20050196781A1
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; APPLICANT: Robin, Howard
; TITLE OF INVENTION: RNA INTERFERENCE MEDIATED INHIBITION OF STAT3 GENE EXPRESSION
; FILE REFERENCE: 400/241 MBH04-1067
; CURRENT APPLICATION NUMBER: US/11/014,373
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: PCT/US 04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
```

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; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 678
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 235
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Target Sequence/siNA sense region
US-11-014-373-235

Query Match
Best Local Similarity 89.5%; Score 15.8; DB 1; Length 19;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 AGCCAGCGGCGGCGGCGG 26
Db 19 AGCCAGCGGCGGCGGCGG 1

RESULT 931
US-11-014-373-512
; Sequence 512, Application US/11014373
; Publication No. US20050196781A1
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; APPLICANT: Robin, Howard
; TITLE OF INVENTION: RNA INTERFERENCE MEDIATED INHIBITION OF STAT3 GENE EXPRESSION
; FILE REFERENCE: 400/241 MBH04-1067
; CURRENT APPLICATION NUMBER: US/11/014,373
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: PCT/US 04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 678
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 512
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Target Sequence/siNA sense region
US-11-014-373-512

Query Match
Best Local Similarity 89.5%; Score 15.8; DB 1; Length 19;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 AGCCAGCGGCGGCGGCGG 26
Db 1 AGCCAGCGGCGGCGGCGG 19
```

```
RESULT 932
US-11-083-784-2836
; Sequence 2836, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Reynolds, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 2836
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-2836
```

```
Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 8.4e+02;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      103 CACCTCTGCTGTCTTGA 121
Db      1 CACCCUCCUUCGCAUUA 19
```

```
RESULT 933
US-11-083-784-49632
; Sequence 49632, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 49632
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-49632
```

```
Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 8.4e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1104 CATGTACAACCCCATCATC 1122
Db      1 CAUCCACAUCGCCAUCUAUC 19
```

```
RESULT 934
US-11-083-784-49652
; Sequence 49652, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 49652
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-49652
```

```
Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1106 TGTACACCCCATCATCTA 1124
Db      1 UCUNCAUCCCAUCUAUCA 19
```

```
RESULT 935
US-11-083-784-96612
; Sequence 96612, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 96612
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-96612
```

```
Query Match      0.9%; Score 15.8; DB 1; Length 19;
```


Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 447 CTCGATGGCTGCATTCAT 465
|||:||||:||||:
Db 1 CGCCAGGCGUCGUCUUGAU 19

RESULT 936

US-11-083-784-104234/c

; Sequence 104234, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 104234
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-083-784-104234

Query Match

Best Local Similarity 89.5%; Score 15.8; DB 1; Length 19;
Pred. No. 8.4e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1000 TTCACATCTTCTCTCC 1018
|||||:|||||:|||||:
Db 19 TTCACATCTTCTCTCC 1

RESULT 937

US-11-083-784-116911

; Sequence 116911, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 116911
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens

US-11-083-784-116911

Query Match

Best Local Similarity 63.2%; Score 15.8; DB 1; Length 19;
Pred. No. 8.4e+02;

QY 506 ACTACGGGCTGTCTACTG 524
|||:||||:||||:||||:
Db 1 ACUACGGGCGUCUCUACUG 19

RESULT 938

US-11-083-784-116984

; Sequence 116984, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 116984
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-083-784-116984

Query Match

Best Local Similarity 63.2%; Score 15.8; DB 1; Length 19;
Pred. No. 8.4e+02;

QY 506 ACTACGGGCTGTCTACTG 524
|||:||||:||||:||||:
Db 1 ACUACGGGCGUCUCUACUG 19

RESULT 939

US-11-083-784-117020

; Sequence 117020, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 117020

```
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-117020
```

```
Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      506 ACTACGGCCTGTCTACTG 524
      ||:|||||:|:|:|:|:|
Db      1 ACUACGGCGCUCUCUACUG 19
```

```
RESULT 940
US-11-083-784-117049
; Sequence 117049, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 117049
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-117049
```

```
Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      506 ACTACGGCCTGTCTACTG 524
      ||:|||||:|:|:|:|:|
Db      1 ACUACGGCGCUCUCUACUG 19
```

```
RESULT 941
US-11-083-784-117107
; Sequence 117107, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
```

```
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 117107
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-117107
```

```
Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      506 ACTACGGCCTGTCTACTG 524
      ||:|||||:|:|:~|:|
Db      1 ACUACGGCGCUCUCUACUG 19
```

```
RESULT 942
US-11-083-784-117181
; Sequence 117181, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 117181
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-117181
```

```
Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      506 ACTACGGCCTGTCTACTG 524
      ||:|||||:|:~|:|:|
Db      1 ACUACGGCGCUCUCUACUG 19
```

```
RESULT 943
US-11-083-784-117219
; Sequence 117219, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
```

```
;; PRIOR FILING DATE: 2003-09-10
;; PRIOR APPLICATION NUMBER: 60/426,137
;; PRIOR FILING DATE: 2002-11-14
;; NUMBER OF SEQ ID NOS: 1591911
;; SOFTWARE: Proprietary
;; SEQ ID NO 117219
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-11-083-784-117219
```

```
Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      506 ACTACGGCCTGTTCTACTG 524
Db      1 ACUACGGGCGUCUCUCUACUG 19
```

```
RESULT 944
US-11-083-784-117250
; Sequence 117250, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 117250
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-117250
```

```
Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      506 ACTACGGCCTGTTCTACTG 524
Db      1 ACUACGGGCGUCUCUCUACUG 19
```

```
RESULT 945
US-11-083-784-155785
; Sequence 155785, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
```

```
;; PRIOR APPLICATION NUMBER: US/10/714,333
;; PRIOR FILING DATE: 2003-11-14
;; PRIOR APPLICATION NUMBER: 60/502,050
;; PRIOR FILING DATE: 2003-09-10
;; PRIOR APPLICATION NUMBER: 60/426,137
;; PRIOR FILING DATE: 2002-11-14
;; NUMBER OF SEQ ID NOS: 1591911
;; SOFTWARE: Proprietary
;; SEQ ID NO 155785
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-11-083-784-155785
```

```
Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 8.4e+02;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      650 CCAAGTGTCTATCTGTCT 668
Db      1 CCAAGGUGUCUCUCUGUGU 19
```

```
RESULT 946
US-11-083-784-190805
; Sequence 190805, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 190805
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-190805
```

```
Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 52.6%; Pred. No. 8.4e+02;
Matches 10; Conservative 7; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1002 CCACATCTTCTCTCTCTG 1020
Db      1 CCACAUUCUCUCUCUCUCUG 19
```

```
RESULT 947
US-11-083-784-190884
; Sequence 190884, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
```

```

; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 190884
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-190884

```

```

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 52.6%; Pred. No. 8.4e+02;
Matches 10; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      1002 CCACATCTTCTTCCTCG 1020
Db      1 CCACATCTTCTTCCTCG 19

```

```

RESULT 948
US-11-083-784-198455
; Sequence 198455, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 198455
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-198455

```

```

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      506 ACTACGGCCTGTCTACTG 524
Db      1 ACUACGGCGCUGUCUACUG 19

```

```

RESULT 949
US-11-083-784-198486
; Sequence 198486, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin

```

```

; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 198486
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-198486

```

```

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      506 ACTACGGCCTGTCTACTG 524
Db      1 ACUACGGCGCUGUCUACUG 19

```

```

RESULT 950
US-11-083-784-198511
; Sequence 198511, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 198511
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-198511

```

```

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      506 ACTACGGCCTGTCTACTG 524
Db      1 ACUACGGCGCUGUCUACUG 19

```

```

RESULT 951
US-11-083-784-198533
; Sequence 198533, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.

```

```

; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 198533
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-198533
```

```

Query Match
Best Local Similarity 63.2%; Score 15.8; DB 1; Length 19;
Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
```

```

QY 506 ACTACGGCCTGTCTACTG 524
Db 1 ACUACGGCGCUCUCUACUG 19

RESULT 952
US-11-083-784-198551
; Sequence 198551, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 198551
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-198551
```

```

Query Match
Best Local Similarity 63.2%; Score 15.8; DB 1; Length 19;
Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
```

```

; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 198589
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-198589
```

```

Query Match
Best Local Similarity 63.2%; Score 15.8; DB 1; Length 19;
Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
```

```

QY 506 ACTACGGCCTGTCTACTG 524
Db 1 ACUACGGCGCUCUCUACUG 19

RESULT 954
US-11-083-784-198623
; Sequence 198623, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 198623
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-198623
```

```

Query Match
Best Local Similarity 63.2%; Score 15.8; DB 1; Length 19;
Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
```

```

QY 506 ACTACGGCCTGTCTACTG 524
Db 1 ACUACGGCGCUCUCUACUG 19
```

RESULT 955
US-11-083-784-198673
; Sequence 198673, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 198673
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-198673

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 506 ACTACGGCGCTGTCTACTG 524
||:|||||:|:|:|:|
Db 1 ACUACGGCGCTGCTGCTGCTG 19

RESULT 956
US-11-083-784-198715
; Sequence 198715, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 198715
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-198715

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 506 ACTACGGCGCTGTCTACTG 524
||:|||||:|:|:|:|

Db 1 ACUACGGCGCTGCTGCTGCTG 19

RESULT 957
US-11-083-784-207465
; Sequence 207465, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 207465
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-207465

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 8.4e+02;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 986 TCTGCTGGCTGCTGCTGCTGCA 1004
||:|||||:|:|:|:|
Db 1 UCUCCTGCTGCTGCTGCTGCTGCA 19

RESULT 958
US-11-083-784-222212
; Sequence 222212, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 222212
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-222212

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 8.4e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 398 TGAGGACAGTGACGACTA 416
:|||||:|||||
Db 1 UGAGGACAGUCCACCACTA 19

```

RESULT 959
US-11-083-784-225150
; Sequence 725150, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 225150
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-225150

```

Query Match	0.9%	Score 15.8;	DB 1;	Length 19;
Best Local Similarity	73.7%	Pred. No. 8.4e+02;		
Matches 14; Conservative	3;	Mismatches 2;	Indels 0;	Gaps 0;

QY 75 AAAGAGTGTGCCCATAA 93
|||:|:|:|:
Db 1 AAGAGAGUCUGACCAUAA 19

```

RESULT 960
US-11-083-784-256569/c
; Sequence 256569, Application US/11083784
; Publication No. US20050245475A1
GENERAL INFORMATION:
; APPLICANT: Dharmacoin, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperf
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 256569
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-256569

```

	Query Match	Similarity	Score	DB 1	Length
Best Local	17	Conservative	89.5%	Pred. No. 8.4e+02	Indels 0; Gaps 0;
Matches	17	Conservative	0;	Mismatches 2;	Indels 0; Gaps 0;
Qy	984	CATCTGCTGAGCTGCCCTTC	1002		
Db	19	CATCTGCTGACTGCACCTTC	1		

```

CY      984  CATCGTGGGTGGCCCTTC 1002
      ||||| ||||| ||||| |||||
Db      19  CATCTGCTGACTGCACCTTC 1

RESULT 961
US-11-083-784-256617/c
; Sequence 256617, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khavrova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional sRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 256617
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-256617

```

Query Match	0.9%	Score 15.8	DB 1	Length 19
Best Local Similarly	89.5%	Pred. No. 8.4e+02		
Matches 17; Conservative	0	Mismatches 2	Indels 0	Gaps 0

```

Oy      985 ATCTGCTGCTGCCCTTC 1003
          |||||
Db      19 ATCTGCTGACTGCACCTTC 1

```

```

/ RESULT 962 US-11-083-784-259212/C
/ Sequence 259212, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Pharmaco, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ CURRENT FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/771,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 259212
/
/ TYPE: RNA
/ LENGTH: 19
/

```

; ORGANISM: Homo sapiens
US-11-083-784-259212

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1000 TTCACATCTTCTCTCC 1018

Db 19 TTCCTCATCTTCTCTCC 1

RESULT 963

US-11-083-784-275438/c
; Sequence 275438, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 275438
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-275438

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 526 AAGTTCACACTTCTTTC 544

Db 19 AACTTCACACATCTTTC 1

RESULT 964

US-11-083-784-398635
; Sequence 398635, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary

; SEQ ID NO 398635

; LENGTH: 19

; TYPE: RNA

; ORGANISM: Homo sapiens

US-11-083-784-398635

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1620 CCACCTCATGCTGTGTGA 1638

Db 1 CCACCCUAAUCCUGUGA 19

RESULT 965

US-11-083-784-411203/c
; Sequence 411203, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 411203
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-411203

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1000 TTCACATCTTCTCTCC 1018

Db 19 TTCCTCATCTTCTCTCC 1

RESULT 966

US-11-083-784-425415/c
; Sequence 425415, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137

;; PRIOR FILING DATE: 2002-11-14
;; NUMBER OF SEQ ID NOS: 1591911
;; SOFTWARE: Proprietary
;; SEQ ID NO 425415
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-11-083-784-425415

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1000 TTCACATCTTCTCTCC 1018
Db 19 TTCCTCATCTTCTCTCC 1

RESULT 967
US-11-083-784-482386
; Sequence 482386, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Reynolds, Angela
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 482386
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-482386

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 8.4e+02;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 986 TCTGCTGCTGCTCTTCA 1004
Db 1 UCUCUGGCUUCCUUCUA 19

RESULT 968
US-11-083-784-482438
; Sequence 482438, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14

;; PRIOR APPLICATION NUMBER: 60/502,050
;; PRIOR FILING DATE: 2003-09-10
;; PRIOR APPLICATION NUMBER: 60/426,137
;; PRIOR FILING DATE: 2002-11-14
;; NUMBER OF SEQ ID NOS: 1591911
;; SOFTWARE: Proprietary
;; SEQ ID NO 482438
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-11-083-784-482438

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 8.4e+02;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 986 TCTGCTGCTGCTCTTCA 1004
Db 1 UCUCUGGCUUCCUUCUA 19

RESULT 969
US-11-083-784-490736
; Sequence 490736, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 490736
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-490736

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 8.4e+02;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 447 CTCGATGCTGATTCAT 465
Db 1 CUGCAUGGCUUCCUUCUA 19

RESULT 970
US-11-083-784-490744
; Sequence 490744, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784

```

; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 490744
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-490744
```

```

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 8.4e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      562 GCCACTATCTACTCCATCA 580
      |||:||||:||||:|
Db      1  GUCAGCAUCUACUCCAUC 19
```

```

RESULT 971
US-11-083-784-490754
; Sequence 490754, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 490754
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-490754
```

```

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 8.4e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      1097 GCTCCACCAGTACACCC 1115
      ||:||||:||||:|
Db      1  GCUCAACCAUGUACAUC 19
```

```

RESULT 972
US-11-083-784-491301
; Sequence 491301, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
```

```

; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491301
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491301
```

```

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 8.4e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      1090 GCCATGAGCTCCACCATGT 1108
      |||:||||:||||:|
Db      1  GCAUAGCCUACAUC 19
```

```

RESULT 973
US-11-083-784-491346
; Sequence 491346, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491346
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491346
```

```

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 8.4e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      1097 GCTCCACCAGTACACCC 1115
      ||:||||:||||:|
Db      1  GCUCAACCAUGUACAUC 19
```

```

RESULT 974
US-11-083-784-491367
; Sequence 491367, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
```

```

; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491367
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491367

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 8.4e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 941 GCAGGCTGCTCAAAATGAT 959
Db 1 GAAAGCTGUCGCAAAUGAU 19

RESULT 975
US-11-083-784-491377
; Sequence 491377, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491377
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491377

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 986 TCTGCTGCTGCGCTTCA 1004
Db 1 UCUCGCGCTGCGCTCAUCA 19

RESULT 976
US-11-083-784-504820
; Sequence 504820, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 504820
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-504820

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 8.4e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1089 GGCATGAGCTCCACATG 1107
Db 1 GGCACUACGCTCCACAU 19

RESULT 977
US-11-083-784-520347/C
; Sequence 520347, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 520347
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-520347

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 571 TACTCATGACGCGTGG 589
Db 1 TTCTCAATGACGCGTGG 1

RESULT 978
US-11-083-784-521051
```

```
; Sequence 521051, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 521051
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-521051
```

```
Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1046 TGAAGAGTTATCCAGCA 1064
      : |||||:::|||
Db      1 UCAGAAGUUAUCCAGAA 19
```

```
RESULT 979
US-11-083-784-537233/c
; Sequence 537233, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 537233
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-537233
```

```
Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      652 AAAGTGCATCTGTGTC 670
      |||||:::|||
Db      19 AAAGGTATCTGTATCA 1
```

```
RESULT 980
US-11-083-784-548572
; Sequence 548572, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 548572
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-548572
```

```
Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 8.4e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      774 GAACAAGTTATGAGAA 792
      |||||:::|||
Db      1 GCACAACAUUAUGAGAA 19
```

```
RESULT 981
US-11-083-784-647566
; Sequence 647566, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 647566
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-647566
```

```
Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 8.4e+02;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1713 GCATTCATTCTGGAAT 1731
```

Db 1 GCAAUUCAUUUCUGAAGU 19

RESULT 982

US-11-083-784-647654
; Sequence 647654, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 647654
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-647654

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 8.4e+02;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1713 GCATTCATTCTTCGAACT 1731

Db 1 GCAAUUCAUUUCUGAAGU 19

RESULT 983

US-11-083-784-651197/c
; Sequence 651197, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 651197
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-651197

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 801 CATCTGTGACTGTGCTG 819

Db 19 CATCTGGGTGCTGTGCTG 1

RESULT 984

US-11-083-784-692671/c
; Sequence 692671, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 692671
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-692671

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 526 AAGTCCACAACCTCTTC 544

Db 19 AATTCACCACTCTTTC 1

RESULT 985

US-11-083-784-809922/c
; Sequence 809922, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 809922
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-809922

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 652 AAAGTGTCTATCTGTGCA 670
DB 19 AATGTGTCTATCTGTGCA 1

RESULT 986
US-11-083-784-835805
Sequence 835805, Application US/11083784

Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 835805
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-835805

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 8.4e+02;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 576 CATGACGCTGTGCTTT 594
DB 1 CAUGAUGAUGGCGCCUU 19

RESULT 987
US-11-083-784-895312/c
Sequence 895312, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 895312
LENGTH: 19

TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-895312

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1000 TTCACATCTTCTCTCC 1018
DB 19 TTCACATCTTCTCTCC 1

RESULT 988
US-11-083-784-946407/c
Sequence 946407, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 946407
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-946407

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1720 ATTCTGGAAGTACTTG 1738
DB 19 AATCTGGAAGTACTTG 1

RESULT 989
US-11-083-784-951796/c
Sequence 951796, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911

```
; SOFTWARE: Proprietary
; SEQ ID NO 951796
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-951796
```

```
Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      568 ATCTACCTCCATGACGCTG 566
Db      19 ATATCTCTCATGACGCTCTG 1
```

RESULT 990

```
US-11-083-784-973051
; Sequence 973051, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
```

```
; PRIOR APPLICATION NUMBER: US/10/714,333
```

```
; PRIOR FILING DATE: 2003-11-14
```

```
; PRIOR APPLICATION NUMBER: 60/502,050
```

```
; PRIOR FILING DATE: 2003-09-10
```

```
; PRIOR APPLICATION NUMBER: 60/426,137
```

```
; PRIOR FILING DATE: 2002-11-14
```

```
; NUMBER OF SEQ ID NOS: 1591911
```

```
; SOFTWARE: Proprietary
```

```
; SEQ ID NO 973051
```

```
; LENGTH: 19
```

```
; TYPE: RNA
```

```
; ORGANISM: Homo sapiens
```

```
US-11-083-784-973051
```

```
Query Match      0.9%; Score 15.8; DB 1; Length 19;
```

```
Best Local Similarity 73.7%; Pred. No. 8.4e+02;
```

```
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

OY 247 CCAACATCTCCACTACAC 265

Db 1 CCAACAUCUCACACUACA 19

```
RESULT 991
US-11-083-784-978358/c
; Sequence 978358, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
```

```
; PRIOR APPLICATION NUMBER: 60/426,137
```

```
; PRIOR FILING DATE: 2002-11-14
```

```
; NUMBER OF SEQ ID NOS: 1591911
```

```
; SOFTWARE: Proprietary
```

```
; SEQ ID NO 978358
```

```
; LENGTH: 19
```

```
; TYPE: RNA
```

```
; ORGANISM: Homo sapiens
```

```
US-11-083-784-978358
```

```
Query Match      0.9%; Score 15.8; DB 1; Length 19;
```

```
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
```

```
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

OY 1080 CATGTGCTGTGCTATGAGC 1098

Db 19 CATATGCTGTGCTATGAGC 1

RESULT 992

```
US-11-083-784-1073668/c
```

```
; Sequence 1073668, Application US/11083784
```

```
; Publication No. US20050245475A1
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Dharmacon, Inc.
```

```
; APPLICANT: Khvorova, Anastasia
```

```
; APPLICANT: Reynolds, Angela
```

```
; APPLICANT: Leake, Devin
```

```
; APPLICANT: Marshall, William
```

```
; APPLICANT: Scaringe, Stephen
```

```
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
```

```
; FILE REFERENCE: 13499US
```

```
; CURRENT APPLICATION NUMBER: US/11/083,784
```

```
; CURRENT FILING DATE: 2005-03-18
```

```
; PRIOR APPLICATION NUMBER: US/10/714,333
```

```
; PRIOR FILING DATE: 2003-11-14
```

```
; PRIOR APPLICATION NUMBER: 60/426,137
```

```
; PRIOR FILING DATE: 2002-11-14
```

```
; SOFTWARE: Proprietary
```

```
; SEQ ID NO 1073668
```

```
; LENGTH: 19
```

```
; TYPE: RNA
```

```
; ORGANISM: Homo sapiens
```

```
US-11-083-784-1073668
```

```
Query Match      0.9%; Score 15.8; DB 1; Length 19;
```

```
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
```

```
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

OY 1003 CACATCTTCTCTCTCTGC 1021

Db 19 CACTTCTTCTCTCTCTGC 1

RESULT 993

```
US-11-083-784-1077487/c
```

```
; Sequence 1077487, Application US/11083784
```

```
; Publication No. US20050245475A1
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Dharmacon, Inc.
```

```
; APPLICANT: Khvorova, Anastasia
```

```
; APPLICANT: Reynolds, Angela
```

```
; APPLICANT: Leake, Devin
```

```
; APPLICANT: Marshall, William
```

```
; APPLICANT: Scaringe, Stephen
```

```
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
```

```
; FILE REFERENCE: 13499US
```

```
; CURRENT APPLICATION NUMBER: US/11/083,784
```

```
; CURRENT FILING DATE: 2005-03-18
```

```
; PRIOR APPLICATION NUMBER: US/10/714,333
```

```
; PRIOR FILING DATE: 2003-11-14
```

```
; PRIOR APPLICATION NUMBER: 60/426,137
```

```
; PRIOR FILING DATE: 2002-11-14
```

```
; SOFTWARE: Proprietary
```

```
; SEQ ID NO 1073668
```

```
; LENGTH: 19
```

```
; TYPE: RNA
```

```
; ORGANISM: Homo sapiens
```

```
US-11-083-784-1073668
```

; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1077487
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1077487

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1572 AAACATTCATCTTGAGT 1590
|||
Db 19 AATCATTCATCATTTGAGT 1

RESULT 994
US-11-083-784-1112807/c
; Sequence 1112807, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1112807
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1112807

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 208 GAATGATTAAGTCTCTCC 226
|||
Db 19 GAATGATTAAGTCTCTCC 1

RESULT 995
US-11-083-784-1112871/c
; Sequence 1112871, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US

; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1112871
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1112871

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 208 GAATGATTAAGTCTCTCC 226
|||
Db 19 GAATGATTAAGTCTCTCC 1

RESULT 996
US-11-083-784-1115683/c
; Sequence 1115683, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1115683
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1115683

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1408 AGCTTCTCTCAATGTGC 1426
|||
Db 19 AGCTTCTCTCAATGTGC 1

RESULT 997
US-11-083-784-1115733/c
; Sequence 1115733, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William


```

; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 115733
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-115733
```

```

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1408 AGCTTCCTCCATGTC 1426
Db      19 AGCTTCACCCCAATGTC 1
```

```

RESULT 998
US-11-083-784-1141062/c
; Sequence 1141062, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1141062
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1141062
```

```

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1000 TTCACATCTTCTCTCC 1018
Db      19 TTCACATCTGCATCTCC 1
```

```

RESULT 999
US-11-083-784-1145497/c
; Sequence 1145497, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
```

```

; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1145497
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1145497
```

```

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1000 TTCACATCTTCTCTCC 1018
Db      19 TTCACATATCTTCTCC 1
```

```

RESULT 1000
US-11-083-784-1159730/c
; Sequence 1159730, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1159730
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1159730
```

```

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1000 TTCACATCTTCTCTCC 1018
Db      19 TTCCTATCTCTTCTCC 1
```

```

RESULT 1001
US-11-083-784-1257590/c
; Sequence 1257590, Application US/11083784
; Publication No. US20050245475A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1257590
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1257590

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1000 TTCACATCTTCTTCCTCC 1018
DB      19  TTCCTCTTCTTCTCTCC 1

RESULT 1002
US-11-083-784-1323231
; Sequence 1323231, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1323231
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1323231

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      1356 GACCTCAACTGCTCTTCA 1374
DB      1  GACCTGACCTGCTCTTCA 19

RESULT 1003

```

```

US-11-083-784-1350821/c
; Sequence 1350821, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1350821
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1350821

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      652 AAAGTGATCTGTGCTGA 670
DB      19  AATGTGATCTGTGCTGA 1

RESULT 1004
US-11-083-784-1351424/c
; Sequence 1351424, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1351424
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1351424

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      391 AAAAGATGAGGACAGTGA 409
DB      19  AAAATATGAGGACAGTGA 1

```

```
RESULT 1005
US-11-083-784-1370891/c
; Sequence 1370891, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1370891
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1370891
```

```
Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Oy 49 TATTCGAGCGCCAGTCA 67
19 TATTCGAGAGCCTGTCA 1
```

```
RESULT 1006
US-11-083-784-1388942
; Sequence 1388942, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1388942
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1388942
```

```
Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 8.4e+02;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
```

```
Oy 1116 CATCATCTACTGCTGCTC 1134
1 CAUCACUCACUCGCUCAUC 19
```

```
RESULT 1007
US-11-083-784-1513262/c
; Sequence 1513262, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1513262
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1513262
```

```
Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Oy 1000 TTCACATCTTCTTCTCTCC 1018
19 TTCGACCTCTTCTCTCTCC 1
```

```
RESULT 1008
US-11-083-784-1513264/c
; Sequence 1513264, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1513264
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1513264
```

```
Query Match 0.9%; Score 15.8; DB 1; Length 19;
```


Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 8.4e+02;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Qy 1104 CATGTACAACCCCATCATC 1122
Db 1 CAUCUACAUCCAUCCAUCAUC 19

RESULT 1013
US-11-101-244-49652
; Sequence 49652, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 49652
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-49652

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
Qy 1106 TGTACAACCCCATCATCTA 1124
Db 1 UCUCACAUCCAUCCAUCAUCA 19

RESULT 1014
US-11-101-244-96612
; Sequence 96612, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 96612
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-96612

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
Qy 447 CTCGATGAGCTGATTCAT 465
Db 1 CGCCAUUGCUCGUAUGAU 19

RESULT 1015
US-11-101-244-104234/C
; Sequence 104234, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 104234
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-104234

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1000 TTCCACATCTTCTCTCC 1018
Db 19 TTCACCTTCTCTTCTCC 1

RESULT 1016
US-11-101-244-116911
; Sequence 116911, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 116911
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-116911

Query Match 0.9%; Score 15.8; DB 1; Length 19;

Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 506 ACTACGGCCTGTTCTACTG 524
||:|||||:|:|:|:|:
Db 1 ACUACGGCGCUCUCUACUG 19

RESULT 1017

US-11-101-244-116984
; Sequence 116984, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 116984
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-116984

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 506 ACTACGGCCTGTTCTACTG 524
||:|||||:|:|:|:|:
Db 1 ACUACGGCGCUCUCUACUG 19

RESULT 1018

US-11-101-244-117020
; Sequence 117020, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 117020
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-117020

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;

Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 506 ACTACGGCCTGTTCTACTG 524
||:|||||:|:|:|:|:
Db 1 ACUACGGCGCUCUCUACUG 19

RESULT 1019

US-11-101-244-117049
; Sequence 117049, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 117049
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-117049

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 506 ACTACGGCCTGTTCTACTG 524
||:|||||:|:~|:|:|:|:
Db 1 ACUACGGCGCUCUCUACUG 19

RESULT 1020

US-11-101-244-117107
; Sequence 117107, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 117107
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-117107

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Oy 506 ACTACGGCGCTGTCTACTCG 524
Db 1 ACUACGGCGCGUCUCUCACUG 19

RESULT 1021

US-11-101-244-117181
; Sequence 117181, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 117181
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-117181

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Oy 506 ACTACGGCGCTGTCTACTCG 524
Db 1 ACUACGGCGCGUCUCUCACUG 19

RESULT 1022

US-11-101-244-117219
; Sequence 117219, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 117219
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-117219

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Oy 506 ACTACGGCGCTGTCTACTCG 524
Db 1 ACUACGGCGCGUCUCUCACUG 19

RESULT 1023

US-11-101-244-117250
; Sequence 117250, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 117250
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-117250

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Oy 506 ACTACGGCGCTGTCTACTCG 524
Db 1 ACUACGGCGCGUCUCUCACUG 19

RESULT 1024

US-11-101-244-155785
; Sequence 155785, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 155785
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-155785

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 8.4e+02;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Db 1 CCAAGUGUCUCUCUGU 19

```

RESULT 1025
US-11-101-244-190805
; Sequence 190805, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 190805
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-190805

```

Query Match 0.9%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 52.6%; Pred. No. 8.4e+02;
 Matches 10; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1002 CCACATCTTCTTCCCTCG 1020
 Db 1 CCACATCTTCTTCCCTCG 19

```

RESULT 1026
US-11-101-244-190884
; Sequence 190884, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 190884
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-190884

```

Query Match 0.9%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 52.6%; Pred. No. 8.4e+02;
 Matches 10; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1002 CCACATCTTCTTCCCTCG 1020
 Db 1 CCACATCTTCTTCCCTCG 19

Db 1 CCAAGUGUCUCUCUGU 19

```

RESULT 1027
US-11-101-244-198455
; Sequence 198455, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 198455
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-198455

```

Query Match 0.9%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 63.2%; Pred. No. 8.4e+02;
 Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 506 ACTACGGCCTGTCTTACTG 524
 Db 1 ACUACGGCCTGTCTTACTG 19

```

RESULT 1028
US-11-101-244-198486
; Sequence 198486, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 198486
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-198486

```

Query Match 0.9%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 63.2%; Pred. No. 8.4e+02;
 Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 506 ACTACGGCCTGTCTTACTG 524
 Db 1 ACUACGGCCTGTCTTACTG 19


```

RESULT 1029
US-11-101-244-198511
; Sequence 198511, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 198511
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-198511

```

```

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      506 ACTACGGCGCTGTTCTACTG 524
DB      1 ACUACGGCGCUCUCUACUCG 19

```

```

RESULT 1030
US-11-101-244-198533
; Sequence 198533, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 198533
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-198533

```

```

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      506 ACTACGGCGCTGTTCTACTG 524
DB      1 ACUACGGCGCUCUCUACUCG 19

```

```

RESULT 1031
US-11-101-244-198551
; Sequence 198551, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 198551
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-198551

```

```

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      506 ACTACGGCGCTGTTCTACTG 524
DB      1 ACUACGGCGCUCUCUACUCG 19

```

```

RESULT 1032
US-11-101-244-198589
; Sequence 198589, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 198589
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-198589

```

```

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      506 ACTACGGCGCTGTTCTACTG 524
DB      1 ACUACGGCGCUCUCUACUCG 19

```

```

RESULT 1033
US-11-101-244-198623
; Sequence 198623, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 198623
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-198623

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      506 ACTACGGCCTGTTCTACTG 524
Db      1 ACUACGGGCGUCGUCUACUG 19

RESULT 1034
US-11-101-244-198673
; Sequence 198673, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 198673
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-198673

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      506 ACTACGGCCTGTTCTACTG 524
Db      1 ACUACGGGCGUCGUCUACUG 19

RESULT 1035

```

```

US-11-101-244-198715
; Sequence 198715, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 198715
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-198715

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      506 ACTACGGCCTGTTCTACTG 524
Db      1 ACUACGGGCGUCGUCUACUG 19

RESULT 1036
US-11-101-244-207465
; Sequence 207465, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 207465
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-207465

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 8.4e+02;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY      986 TCTGCTGGCTGCGCTTCCA 1004
Db      1 UCUCGCGGCGUCGUCUCAA 19

RESULT 1037
US-11-101-244-222212

```

```
; Sequence 222212, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 222212
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-222212
```

```
Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 8.4e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 398 TGAGGACAGTGACGACTA 416
Db 1 UGAGGACAGUCACCAUA 19
```

```
RESULT 1038
US-11-101-244-225150
; Sequence 225150, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 225150
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-225150
```

```
Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 8.4e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 75 AAAAGAGTCTGCCCATAA 93
Db 1 AAGGAGGUGGACCAUA 19
```

```
RESULT 1039
US-11-101-244-256569/c
; Sequence 256569, Application US/11101244
```

```
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 256569
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-256569
```

```
Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 984 CATCTGCTGGCTGCCCTTC 1002
Db 19 CATCTGCTGACTGCATTC 1
```

```
RESULT 1040
US-11-101-244-256617/c
; Sequence 256617, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 256617
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-256617
```

```
Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 985 ATCTGCTGCTGCCCTTC 1003
Db 19 ATCTGCTGACTGCATTC 1
```

```
RESULT 1041
US-11-101-244-259212/c
; Sequence 259212, Application US/11101244
; Publication No. US20050246794A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 259212
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-259212

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1000 TTCACATCTTCTCTCTCC 1018
Db      19  TTCTCATCTTCTTCTCATCC 1

RESULT 1042
US-11-101-244-275438/c
/ Sequence 275438, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 275438
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-275438

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      526 AAGTTCACACTTCTTTC 544
Db      19  AACTTCACACATCTTTC 1

RESULT 1043
US-11-101-244-398635
/ Sequence 398635, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
```

```
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 398635
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-398635

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Oy      1620 CCACCCATCAGCTGTGGA 1638
Db      1  CCACCCUAAUCCUGUGGA 19

RESULT 1044
US-11-101-244-411203/c
/ Sequence 411203, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 411203
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-411203

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1000 TTCACATCTTCTCTCTCC 1018
Db      19  TTCTCATCTTCTTCTCATCC 1

RESULT 1045
US-11-101-244-425415/c
/ Sequence 425415, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
```

```

; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 425415
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-425415

Query Match
Best Local Similarity 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1000 TTCACATCTTCTCTCC 1018
DB 19 TTCCTCATCTTCTCTCC 1
```

```

RESULT 1046
US-11-101-244-482386
; Sequence 482386, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 482386
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-482386

Query Match
Best Local Similarity 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 8.4e+02;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 986 TCTGCTGGCTGCCCTTCCA 1004
DB 1 UCUGCUGGCUCCUCCUUA 19
```

```

RESULT 1047
US-11-101-244-482438
; Sequence 482438, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
```

```

; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 482438
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-482438

Query Match
Best Local Similarity 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 8.4e+02;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 986 TCTGCTGGCTGCCCTTCCA 1004
DB 1 UCUGCUGGCUCCUCCUUA 19
```

```

RESULT 1048
US-11-101-244-490736
; Sequence 490736, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Angela
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 490736
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-490736
```

```

Query Match
Best Local Similarity 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 8.4e+02;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 447 CTCATGGCTGCATTCAT 465
DB 1 CUGAUGGCUCCUCCUUAU 19
```

```

RESULT 1049
US-11-101-244-490744
; Sequence 490744, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
```

```
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ PRIOR FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 490744
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-490744

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 8.4e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      562 GCCAGTATCTACTCCATGA 580
Db      1 GUCAGCAUCUACUCCAUCA 19

RESULT 1050
US-11-101-244-490754
/ Sequence 490754, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmoon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 490754
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-490754

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 8.4e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1097 GCTCCACCATGTACACCC 1115
Db      1 GCUCUACCAUUGACAUC 19

RESULT 1051
US-11-101-244-491301
/ Sequence 491301, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmoon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
```

```
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ PRIOR FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491301
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-491301

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 8.4e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      1090 GCCATGAGCTCCACCATGT 1108
Db      1 GCAUGAGCUCACCAUCGU 19

RESULT 1052
US-11-101-244-491346
/ Sequence 491346, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmoon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491346
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-491346

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 8.4e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1097 GCTCCACCATGTACACCC 1115
Db      1 GCUCACCAUGUACAUC 19

RESULT 1053
US-11-101-244-491367
/ Sequence 491367, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmoon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
```

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; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491367
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-491367

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 8.4e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      941 GCAAGTGTGTCAAATGAT 959
Db      1 GAAAGGUGUCAAAUAUGAU 19

RESULT 1054
US-11-101-244-491377
; Sequence 491377, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491377
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-491377

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      986 TCTGCTGCTGCGCTTCCA 1004
Db      1 UCUCGUGGUGCCCUAUA 19

RESULT 1055
US-11-101-244-504820
; Sequence 504820, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
```

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; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 504820
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-504820

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 8.4e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1089 GGCCATGAGCTCCACCATG 1107
Db      1 GGCCAUCAAGCUCCAACAU 19

RESULT 1056
US-11-101-244-520347/c
; Sequence 520347, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 520347
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-520347

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      571 TACTCATGACGCGCTGTG 589
Db      19 TTCTCATGACGCGCTGTG 1

RESULT 1057
US-11-101-244-521051
; Sequence 521051, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
```

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; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 521051
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-521051

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
```

Qy 1046 TGAAGAAATTATCCAGCA 1064
: |||||:::|||||
Db 1 UCAAGAGUUAUCCAGAA 19

```
RESULT 1058
US-11-101-244-537233/c
; Sequence 537233, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 537233
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-537233

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 652 AAAGTCATCTGTGTCA 670
|||||:::|||||
Db 19 AAAGTCATCTGTATCA 1

```
RESULT 1059
US-11-101-244-548572
; Sequence 548572, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
```

```
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 548572
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-548572

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 8.4e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

Qy 774 GAACAAGTTTATGAGAA 792
|||||:::|||||
Db 1 GCAACACAUUUGAGAA 19

```
RESULT 1060
US-11-101-244-647566
; Sequence 647566, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 647566
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-647566

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 8.4e+02;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
```

Qy 1713 GCATTCATTTCGAACT 1731
|||:::|||||
Db 1 GCAUUCAUUUCUGAAGU 19

```
RESULT 1061
US-11-101-244-647654
; Sequence 647654, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
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; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 647654
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-647654

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 8.4e+02;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY      1713 GCATTCATTCTGTGAAGT 1731
Db      1 GCAUUCUAUUCUGAAGU 19

RESULT 1062
US-11-101-244-651197/c
; Sequence 651197, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 651197
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-651197

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      801 CATCTGTGTGACTGTGCTG 819
Db      19 CATCTGGGTGCTGTCTG 1

RESULT 1063
US-11-101-244-692671/c
; Sequence 692671, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
```

```

; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 692671
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-692671

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      526 AAGTTCACACACTTCTTC 544
Db      19 AATTCCACCACTTCTTC 1

RESULT 1064
US-11-101-244-809922/c
; Sequence 809922, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 809922
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-809922

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      652 AAAGTGTGATCTGTGTCA 670
Db      19 AATGTGTCACTGTGTCA 1

RESULT 1065
US-11-101-244-835805
; Sequence 835805, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
```

; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 835805
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-101-244-835805

Query Match 0.9%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 57.9%; Pred. No. 8.4e+02;
 Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 576 CATGACGGCTGTGACCTT 594
 Db 1 CAUGAUGAUGGCGCCUUU 19

RESULT 1066
 US-11-101-244-895312/C
 ; Sequence 895312, Application US/11101244
 ; Publication No. US20050246794A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmacon, Inc.
 ; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 13499US
 ; CURRENT FILING DATE: 2005-04-07
 ; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 895312
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-101-244-895312

Query Match 0.9%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 8.4e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1000 TTCACATCTTCTCTCC 1018
 Db 19 TTCAGTCTTCTCTCC 1

RESULT 1067
 US-11-101-244-946407/C
 ; Sequence 946407, Application US/11101244
 ; Publication No. US20050246794A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmacon, Inc.
 ; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 13499US
 ; CURRENT FILING DATE: 2005-04-07
 ; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-09-10

; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 946407
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-101-244-946407

Query Match 0.9%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 8.4e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1720 ATTTCTGGAAGTACCTTG 1738
 Db 19 AATTCTGGAAGTACCTTG 1

RESULT 1068
 US-11-101-244-951796/C
 ; Sequence 951796, Application US/11101244
 ; Publication No. US20050246794A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmacon, Inc.
 ; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 13499US
 ; CURRENT FILING DATE: 2005-04-07
 ; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 951796
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-101-244-951796

Query Match 0.9%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 8.4e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 568 ATCTACTCATGACGCTG 586
 Db 19 ATATCTCATGACGCTG 1

RESULT 1069
 US-11-101-244-973051
 ; Sequence 973051, Application US/11101244
 ; Publication No. US20050246794A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmacon, Inc.
 ; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 13499US
 ; CURRENT FILING DATE: 2005-04-07
 ; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/426,137

PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 973051
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-973051

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 8.4e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 247 CCAACATCTCCACTACCA 265
Db 1 CCAACACUCCACACUACA 19

RESULT 1070
US-11-101-244-978358/c
Sequence 978358, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 978358
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-978358

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1080 CATGTGCTGGCCATGAGC 1098
Db 19 CATGTGCTGGCTCATGAGC 1

RESULT 1071
US-11-101-244-1073668/c
Sequence 1073668, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14

NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1073668
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-1073668

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1003 CACATCTTCTCCCTCC 1021
Db 19 CACTTCTTCTCTCTCC 1

RESULT 1072
US-11-101-244-1077487/c
Sequence 1077487, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1077487
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-1077487

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1572 AAACATTCATCCTTGAGT 1590
Db 19 AATCATTCATCATTGAGT 1

RESULT 1073
US-11-101-244-1112807/c
Sequence 1112807, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911

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; SOFTWARE: Proprietary
; SEQ ID NO 1112807
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1112807

Query Match
Best Local Similarity 89.5%; Score 15.8; DB 1; Length 19;
Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 208 GAATGATTAACGTCCTCC 226
Db 19 GAAGTGATTAACGTCCTCC 1

RESULT 1074
US-11-101-244-1112871/c
; Sequence 1112871, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1112871
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1112871

Query Match
Best Local Similarity 0.9%; Score 15.8; DB 1; Length 19;
Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 208 GAATGATTAACGTCCTCC 226
Db 19 GAAGTGATTAACGTCCTCC 1

RESULT 1075
US-11-101-244-1115683/c
; Sequence 1115683, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
```

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; SEQ ID NO 1115683
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1115683

Query Match
Best Local Similarity 89.5%; Score 15.8; DB 1; Length 19;
Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1408 AGCTTCTCCTCCATGTGC 1426
Db 19 AGCTTCAACCAATGTGC 1

RESULT 1076
US-11-101-244-1115733/c
; Sequence 1115733, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1115733
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1115733

Query Match
Best Local Similarity 0.9%; Score 15.8; DB 1; Length 19;
Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1408 AGCTTCTCCTCCATGTGC 1426
Db 19 AGCTTCAACCAATGTGC 1

RESULT 1077
US-11-101-244-1141062/c
; Sequence 1141062, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1141062
```

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; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1141062

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1000 TTCACATCTTCTCTCTCC 1018
Db      19   TTCACATCTCTGCTCTCC 1

RESULT 1078
US-11-101-244-1145497/c
; Sequence 1145497, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1145497
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1145497

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1000 TTCACATCTTCTCTCTCC 1018
Db      19   TTCACATATCTCTCTCC 1

RESULT 1079
US-11-101-244-1159730/c
; Sequence 1159730, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1159730
; LENGTH: 19
; TYPE: RNA
```

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; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1159730

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1000 TTCACATCTTCTCTCTCC 1018
Db      19   TTCCTCATCTCTCTCTCC 1

RESULT 1080
US-11-101-244-1257590/c
; Sequence 1257590, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1257590
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1257590

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1000 TTCACATCTTCTCTCTCC 1018
Db      19   TTCCTCTTCTCTCTCTCC 1

RESULT 1081
US-11-101-244-1323231
; Sequence 1323231, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1323231
; LENGTH: 19
; TYPE: RNA
```

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; ORGANISM: Homo sapiens
US-11-101-244-1323231

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      1356 GACCTCCAACTGCTCTCA 1374
DB      1 GACCTGCACCTGCCTCUCA 19

RESULT 1082
US-11-101-244-1350821/c
; Sequence 1350821, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1350821
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1350821

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      652 AAAGTGTCATCTGTCTCA 670
DB      19 AATGTGTCATCTGGGTCA 1

RESULT 1083
US-11-101-244-1351424/c
; Sequence 1351424, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1351424
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
```

```
US-11-101-244-1351424

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      391 AAAAGATGAGCAGCTCA 409
DB      19 AAAATATGAGGCGCAGTCA 1

RESULT 1084
US-11-101-244-1370891/c
; Sequence 1370891, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1370891
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1370891

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      49 TATTTGAGGCCAGTTCA 67
DB      19 TATTTGAGAGCCTGTCA 1

RESULT 1085
US-11-101-244-1388942
; Sequence 1388942, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1388942
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1388942
```

Query Match 0.9%: Score 15.8; DB 1; Length 19;
Best Local Similarity 57.9%: Pred. No. 8.4e+02;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1116 CATCATCTACTGCTGCTCC 1134
||:||||:|:|:|:
DB 1 CAUCAUCUACUGCUACUAC 19

RESULT 1086
US-11-101-244-1513262/C
; Sequence 1513262, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1513262
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1513262

Query Match 0.9%: Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%: Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1000 TTCACATCTTCTCTCTCC 1018
|||||
DB 19 TTGACCTCTTCTCTCTCC 1

RESULT 1087
US-11-101-244-1513264/C
; Sequence 1513264, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1513264
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1513264

Query Match 0.9%: Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%: Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1000 TTCACATCTTCTCTCTCC 1018
|||||
DB 19 TTGACCTCTTCTCTCTCC 1

RESULT 1088
US-11-101-244-1564341/C
; Sequence 1564341, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1564341
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1564341

Query Match 0.9%: Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%: Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1655 GAACCTTGCTGAGCCTGTA 1673
|||||
DB 19 GAACCTTGACAGCCTTTA 1

RESULT 1089
US-11-101-244-1582659/C
; Sequence 1582659, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1582659
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1582659

Query Match 0.9%: Score 15.8; DB 1; Length 19;

```
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1402 AGCTCAGCTTCCTCCCA 1420
DB 19 ATCTTCAGCATCTCTCCA 1

RESULT 1090
US-11-069-611-255/c
; Sequence 255, Application US/11069611
; Publication No. US20060058255A1
; GENERAL INFORMATION:
; APPLICANT: Chen, et al.
; TITLE OF INVENTION: RNAi Based Therapeutics for Allergic Rhinitis and Asthma
; FILE REFERENCE: 0492611-0614
; CURRENT APPLICATION NUMBER: US/11/069,611
; CURRENT FILING DATE: 2005-03-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 255
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Mouse sequence
US-11-069-611-255

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 948 GGTCAAAATGATGATGTC 966
DB 19 GGTGAAATGATGATGTC 1

RESULT 1091
US-09-780-533A-1841
; Sequence 1841, Application US/09780533A
; Publication No. US2003006011A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blact, Larry
; APPLICANT: McSwigen, Jim
; APPLICANT: Chowirita, Bharat
; APPLICANT: Haebertl, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1841
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-1841

Query Match 0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.9e+02;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 619 CCCCTCAGCCCGGCT 635
DB 1 CCCGCCAGCCCGGCT 17

RESULT 1092
US-09-848-754A-3109/c
; Sequence 3109, Application US/09848754A

; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MBH00-958-1 (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3109
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-3109

Query Match 0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1693 CTTTCTCAGAGGCC 1709
DB 17 CTTTCTCAGAGGCC 1

RESULT 1093
US-10-138-674-2435/c
; Sequence 2435, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2435
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-138-674-2435

Query Match 0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 716 CAACCAAGAGACCATG 732
DB 17 CAACCAAGAGACCATG 1

RESULT 1094
US-10-287-949A-2435/c
; Sequence 2435, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
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SOFTWARE: Patentin version 3.0
SEQ ID NO 2435
LENGTH: 17
TYPE: RNA
ORGANISM: Mus musculus
US-10-287-949A-2435

Query Match 0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 716 CAACACAGAGACCATG 732
DB 17 CAACACAGAGACCATG 1

RESULT 1095
US-10-712-672-1375
Sequence 1375, Application US/10712672
Publication No. US20040102413A1
GENERAL INFORMATION:
APPLICANT: Ribozyne Pharmaceuticals, Inc.
APPLICANT: Chowrira, Bharat
APPLICANT: McSwigen, Jim
APPLICANT: Stinchcomb, Dan
TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
FILE REFERENCE: MHB00-882-C (400/019)
CURRENT APPLICATION NUMBER: US/10/712,672
CURRENT FILING DATE: 2003-11-13
PRIOR APPLICATION NUMBER: US/09/653,225
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/197,769
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/150,713
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 5586
SOFTWARE: Patentin version 3.0
SEQ ID NO 1375
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-10-712-672-1375

Query Match 0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 7.9e+02;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1686 GGACGAGCTTTCTCA 1702
DB 1 GGCGCAGCUUCCUCA 17

RESULT 1096
US-10-951-303-2435/c
Sequence 2435, Application US/10951303
Publication No. US20050227937A1
GENERAL INFORMATION:
APPLICANT: Ribozyne Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwigen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Becabedo, Jaime
TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
FILE REFERENCE: MHB00-876-K (400/021)
CURRENT APPLICATION NUMBER: US/10/951,303
CURRENT FILING DATE: 2004-09-27
PRIOR APPLICATION NUMBER: US/09/685,664
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08

PRIOR APPLICATION NUMBER: US 09/371,772
PRIOR FILING DATE: 1999-08-10
NUMBER OF SEQ ID NOS: 8231
SOFTWARE: Patentin version 3.0
SEQ ID NO 2435
LENGTH: 17
TYPE: RNA
ORGANISM: Mus musculus
US-10-951-303-2435

Query Match 0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 716 CAACACAGAGACCATG 732
DB 17 CAACACAGAGACCATG 1

RESULT 1097
US-09-850-948-19/c
Sequence 19, Application US/09850948
Publication No. US20030059770A1
GENERAL INFORMATION:
APPLICANT: Yang, Jianxin
APPLICANT: An, Songzhu
APPLICANT: Tularik Inc.
TITLE OF INVENTION: Polypeptides and Nucleic Acids Associated with Cancer
FILE REFERENCE: 018781-008300US
CURRENT APPLICATION NUMBER: US/09/850,948
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:quantitative
US-09-850-948-19

Query Match 0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 8.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 986 TCTGCTGCTGCCCTTC 1002
DB 18 TCTGCTGCTGCCCTTC 2

RESULT 1098
US-10-273-575-19/c
Sequence 19, Application US/10273575
Publication No. US20030108931A1
GENERAL INFORMATION:
APPLICANT: Yang, Jianxin
APPLICANT: An, Songzhu
APPLICANT: Tularik Inc.
TITLE OF INVENTION: Polypeptides and Nucleic Acids Associated with Cancer
FILE REFERENCE: 018781-008300US
CURRENT APPLICATION NUMBER: US/10/273,575
CURRENT FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: US/09/850,948
PRIOR FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:quantitative

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; OTHER INFORMATION: RT-PCR primer OGRI reverse
; US-10-273-575-19

Query Match          0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 8.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      986 TCTGCTGCTGCTCCCTTC 1002
      18 TCTGCTGCTGCTGCTCCCTTC 2

RESULT 1099
US-10-680-402-70
; Sequence 70; Application US/10680402
; Publication No. US20040147732A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRLMY9, EXPRESSED
; FILE REFERENCE: D0045A CIP
; CURRENT APPLICATION NUMBER: US/10/680,402
; PRIOR FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: U.S. 09/964,923
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: U.S. 60/235,709
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: U.S. 60/261,775
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: U.S. 60/309,625
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 70
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-680-402-70

Query Match          0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 8.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      309 CCTTTGGGCGAGCTGCCT 325
      2 CCTTTGGGCGAGCTGCCT 18

Db

RESULT 1100
US-10-310-914A-230274/C
; Sequence 230274; Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazut
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 230274
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
; US-10-310-914A-230274

Query Match          0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 8.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      619 CCCCTCCAGCCCGGCT 635

; OTHER INFORMATION: RT-PCR primer OGRI reverse
; US-10-273-575-19

Query Match          0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 8.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      619 CCCCTCCAGCCCGGCT 635
```

```
Db      18 CCCCTTCAGCCCCGGCT 2

RESULT 1101
US-10-310-914A-677466
; Sequence 677466; Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazut
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 677466
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
; US-10-310-914A-677466

Query Match          0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 8.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1305 CGAGGAGGAGCCGAGG 1321
      2 CAAGGAGGAGCCGAGG 18

Db

RESULT 1102
US-10-310-914A-677474
; Sequence 677474; Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazut
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 677474
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
; US-10-310-914A-677474

Query Match          0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 8.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1308 CGAGGAGCCGAGGAGC 1324
      1 CGAGGAGCCGAGGAGG 17

Db

RESULT 1103
US-10-310-914A-800869
; Sequence 800869; Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazut
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
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CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 800869
LENGTH: 18
TYPE: RNA
ORGANISM: Human
US-10-310-914A-800869

Query Match 0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 8.5e+02;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 640 GCCACGCCACCAAGT 656
Db 1 GCCACACCAACCAAGU 17

RESULT 1104
US-10-310-914A-888641/c
Sequence 888641, Application US/10310914A
Publication No. US2006003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shlier, Kuvzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310.914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 888641
LENGTH: 18
TYPE: RNA
ORGANISM: Human
US-10-310-914A-888641

Query Match 0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 8.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1304 ACGAGAGAGGCCAGAG 1320
Db 18 AGGAGAGAGGCCAGAG 2

RESULT 1105
US-10-310-914A-892826/c
Sequence 892826, Application US/10310914A
Publication No. US2006003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shlier, Kuvzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310.914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 892826
LENGTH: 18
TYPE: RNA
ORGANISM: Human
US-10-310-914A-892826

Query Match 0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 8.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 828 CCTCCCTGCTGCTGA 844
|||||

Db 18 CCTCCCTGCTGCTGA 2

RESULT 1106
US-10-310-914A-1042518
Sequence 1042518, Application US/10310914A
Publication No. US2006003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shlier, Kuvzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310.914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1042518
LENGTH: 18
TYPE: RNA
ORGANISM: Human
US-10-310-914A-1042518

Query Match 0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 70.6%; Pred. No. 8.5e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 519 CTACTGCAGTTCACA 535
Db 1 CUACUGCAAGUCCAAA 17

RESULT 1107
US-10-310-914A-1145229
Sequence 1145229, Application US/10310914A
Publication No. US2006003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shlier, Kuvzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310.914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1145229
LENGTH: 18
TYPE: RNA
ORGANISM: Human
US-10-310-914A-1145229

Query Match 0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 76.5%; Pred. No. 8.5e+02;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 981 GCCCATCTGCTGCTGC 997
Db 2 CGCCACCTGCTGCTGC 18

RESULT 1108
US-10-310-914A-1350814/c
Sequence 1350814, Application US/10310914A
Publication No. US2006003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shlier, Kuvzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310.914A
CURRENT FILING DATE: 2002-12-06

```

; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1350814
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1350814

Query Match          0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 8.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1346 CCCTGACCTGACCTCC 1362
Db      17  CCCTGCCCTGACCTCC 1

RESULT 1109
US-10-665-951-1515
; Sequence 1515, Application US/10665951
; Publication No. US20040138163A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwigen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Pavco, Pamela
; TITLE OF INVENTION: RNA interference Mediated Inhibition of Vascular Endothelial
; TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/131 (MHB02-742-F)
; CURRENT APPLICATION NUMBER: US/10/665,951
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US 10/664,668
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: PCT/US 03/05022
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/399,348
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US 60/393,796
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 10/287,949
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/306,747
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: PCT/US 02/17674
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2455
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1515
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense
US-10-665-951-1515

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      139 AGGCGCCAGCCACGAGA 155
Db      2  AGGCGCCAGCCACGAGA 18

RESULT 1110
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US-10-665-951-1762/c
; Sequence 1762, Application US/10665951
; Publication No. US20040138163A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwigen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Pavco, Pamela
; TITLE OF INVENTION: RNA interference Mediated Inhibition of Vascular Endothelial
; TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/141 (MHB02-742-F)
; CURRENT APPLICATION NUMBER: US/10/665,951
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US 10/664,668
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: PCT/US 03/05022
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/399,348
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US 60/393,796
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 10/287,949
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/306,747
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: PCT/US 02/17674
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2455
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1762
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-665-951-1762

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      139 AGGCGCCAGCCACGAGA 155
Db      18 AGGCGCCAGCCACGAGA 2

RESULT 1111
US-10-758-155-1515
; Sequence 1515, Application US/10758155
; Publication No. US20050075304A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwigen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Pavco, Pamela
; TITLE OF INVENTION: RNA interference Mediated Inhibition of Vascular Endothelial
; TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/141 (MHB02-742-N)
; CURRENT APPLICATION NUMBER: US/10/758,155
; PRIOR FILING DATE: 2004-01-12
; PRIOR APPLICATION NUMBER: US 10/665,951
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US 10/664,668
; PRIOR FILING DATE: 2003-09-18
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;; PRIOR APPLICATION NUMBER: PCT/US 03/05022
;; PRIOR FILING DATE: 2003-02-20
;; PRIOR APPLICATION NUMBER: US 60/399,348
;; PRIOR FILING DATE: 2002-07-29
;; PRIOR APPLICATION NUMBER: US 60/393,796
;; PRIOR FILING DATE: 2002-07-03
;; PRIOR APPLICATION NUMBER: US 10/287,949
;; PRIOR FILING DATE: 2002-11-04
;; PRIOR APPLICATION NUMBER: US 10/306,747
;; PRIOR FILING DATE: 2002-11-27
;; PRIOR APPLICATION NUMBER: PCT/US 02/17674
;; PRIOR FILING DATE: 2002-05-29
;; PRIOR APPLICATION NUMBER: US 60/358,580
;; PRIOR FILING DATE: 2002-02-20
;; PRIOR APPLICATION NUMBER: US 60/363,124
;; PRIOR FILING DATE: 2002-03-11
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 2751
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 1515
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense r
US-10-758-155-1515
```

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Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY      139 AGGGCCAGCCACAGGA 155
Db      2  AGGGCCAGCCACCGGA 18
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RESULT 1112
US-10-758-155-1762/c
;; Sequence 1762, Application US/10758155
;; Publication No. US20050075304A1
;; GENERAL INFORMATION:
;; APPLICANT: Sirna Therapeutics, Inc.
;; APPLICANT: McSwiggen, James
;; APPLICANT: Beigelman, Leonid
;; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
;; TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
;; FILE REFERENCE: 400/141 (MBH02742-N)
;; CURRENT APPLICATION NUMBER: US/10/758,155
;; CURRENT FILING DATE: 2004-01-12
;; PRIOR APPLICATION NUMBER: US 10/665,951
;; PRIOR FILING DATE: 2003-09-18
;; PRIOR APPLICATION NUMBER: US 10/664,668
;; PRIOR FILING DATE: 2003-09-18
;; PRIOR APPLICATION NUMBER: PCT/US 03/05022
;; PRIOR FILING DATE: 2003-02-20
;; PRIOR APPLICATION NUMBER: US 60/399,348
;; PRIOR FILING DATE: 2002-07-29
;; PRIOR APPLICATION NUMBER: US 60/393,796
;; PRIOR FILING DATE: 2002-07-03
;; PRIOR APPLICATION NUMBER: US 10/287,949
;; PRIOR FILING DATE: 2002-11-04
;; PRIOR APPLICATION NUMBER: US 10/306,747
;; PRIOR FILING DATE: 2002-11-27
;; PRIOR APPLICATION NUMBER: PCT/US 02/17674
;; PRIOR FILING DATE: 2002-05-29
;; PRIOR APPLICATION NUMBER: US 60/358,580
;; PRIOR FILING DATE: 2002-02-20
;; PRIOR APPLICATION NUMBER: US 60/363,124
;; PRIOR FILING DATE: 2002-03-11
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 2751
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;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 1762
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-758-155-1762
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```
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY      139 AGGGCCAGCCACAGGA 155
Db      18 AGGGCCAGCCACCGGA 2
```

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RESULT 1113
US-10-831-620-1515
;; Sequence 1515, Application US/10831620
;; Publication No. US20050148530A1
;; GENERAL INFORMATION:
;; APPLICANT: Sirna Therapeutics, Inc.
;; APPLICANT: McSwiggen, James
;; APPLICANT: Beigelman, Leonid
;; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
;; TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
;; FILE REFERENCE: 400/152 (MBH02-742-O)
;; CURRENT APPLICATION NUMBER: US/10/831,620
;; CURRENT FILING DATE: 2004-04-23
;; PRIOR APPLICATION NUMBER: US 10/764,957
;; PRIOR FILING DATE: 2004-01-26
;; PRIOR APPLICATION NUMBER: US 10/757,803
;; PRIOR FILING DATE: 2004-01-14
;; PRIOR APPLICATION NUMBER: US 10/758,155
;; PRIOR FILING DATE: 2004-01-12
;; PRIOR APPLICATION NUMBER: US 10/720,448
;; PRIOR FILING DATE: 2003-11-24
;; PRIOR APPLICATION NUMBER: US 10/712,633
;; PRIOR FILING DATE: 2003-11-13
;; PRIOR APPLICATION NUMBER: US 10/693,059
;; PRIOR FILING DATE: 2003-10-23
;; PRIOR APPLICATION NUMBER: US 10/670,011
;; PRIOR FILING DATE: 2003-09-23
;; PRIOR APPLICATION NUMBER: US 10/665,951
;; PRIOR FILING DATE: 2003-09-18
;; PRIOR APPLICATION NUMBER: US 10/664,668
;; PRIOR FILING DATE: 2003-09-18
;; PRIOR APPLICATION NUMBER: US 10/665,255
;; PRIOR FILING DATE: 2003-09-16
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 2751
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 1515
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense r
```

```
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
OY      139 AGGGCCAGCCACAGGA 155
Db      2  AGGGCCAGCCACCGGA 18
```

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RESULT 1114
US-10-831-620-1762/C
; Sequence 1762, Application US/10831620
; Publication No. US20050148530A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Payco, Pamela
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
; TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/152 (MBHB02-742-C)
; CURRENT APPLICATION NUMBER: US/10/831,620
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/764,957
; PRIOR FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/758,155
; PRIOR FILING DATE: 2004-01-12
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/712,633
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/670,011
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/665,951
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US 10/664,668
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US 10/665,255
; PRIOR FILING DATE: 2003-09-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2751
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1762
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-831-620-1762
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      139 AGCGCCGACGACGAGA 155
DB      18 AGCGCCGACGACGCGA 2

RESULT 1115
US-10-923-330-216
; Sequence 216, Application US/10923330
; Publication No. US20050153916A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)
; FILE REFERENCE: 400/209 (MBHB02-708-C)
; CURRENT APPLICATION NUMBER: US/10/923,330
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US03/04088
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: PCT/US04/16390
```

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; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-11-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 768
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 216
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense r
US-10-923-330-216
```

```
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 9e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      463 AATACAGTGTGAACCT 479
DB      3 AAGCAGUGUGAACU 19
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RESULT 1116
US-10-923-330-439/C
; Sequence 439, Application US/10923330
; Publication No. US20050153916A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)
; FILE REFERENCE: 400/209 (MBHB02-708-C)
; CURRENT APPLICATION NUMBER: US/10/923,330
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US03/04088
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-11-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 768
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 439
; LENGTH: 19
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; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-923-330-439

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      463 AATACAGTGTGAACCTT 479
Db      17 AAGACAGTGTGAACCTT 1

RESULT 1117
US-10-844-076-1515
; Sequence 1515, Application US/10844076
; Publication No. US20050171039A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwigen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Pavco, Pamela
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
; TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: 400/159 (MBH02-742-R)
; CURRENT FILING DATE: 2004-05-11
; PRIOR APPLICATION NUMBER: US/10/844,076
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/831,620
; PRIOR FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US 10/764,957
; PRIOR FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/758,155
; PRIOR FILING DATE: 2004-01-12
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/712,633
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/670,011
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/665,951
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US 10/664,668
; PRIOR FILING DATE: 2003-09-18
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2755
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1515
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense r
US-10-844-076-1515

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      139 AGGCGCCAGCCACGGA 155
Db      2 AGGCGCCAGCCACGGA 18

RESULT 1118
US-10-844-076-1762/C
; Sequence 1762, Application US/10844076
; Publication No. US20050171039A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwigen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Pavco, Pamela
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
; TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: 400/159 (MBH02-742-R)
; CURRENT FILING DATE: 2004-05-11
; PRIOR APPLICATION NUMBER: US/10/844,076
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/831,620
; PRIOR FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US 10/764,957
; PRIOR FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/758,155
; PRIOR FILING DATE: 2004-01-12
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/712,633
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/670,011
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/665,951
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US 10/664,668
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2755
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1762
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-844-076-1762

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      139 AGGCGCCAGCCACGGA 155
Db      18 AGGCGCCAGCCACGGA 2

RESULT 1119
US-10-923-182-62
; Sequence 62, Application US/10923182
; Publication No. US2005017666A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwigen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Pavco, Pamela
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
; TITLE OF INVENTION: Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/227 (MBH04-423-A)
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/10/923,182
; PRIOR FILING DATE: 2004-05-11
; PRIOR APPLICATION NUMBER: US 60/570,086
; PRIOR FILING DATE: 2004-05-11
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: PCT/US04/13456
; PRIOR FILING DATE: 2004-04-30
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; PRIOR APPLICATION NUMBER: US 10/780,447
; PRIOR FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: US 60/292,217
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/362,016
; PRIOR FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US 60/363,883
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/311,865
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: US 10/727,780
; PRIOR FILING DATE: 2003-12-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 810
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 62
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense
US-10-923-182-62
Query Match
Best Local Similarity 70.6%; Pred. No. 9e+02; DB 1; Length 19;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1110 CAACCCCATCATCTACT 1126
DB 3 CAACCCCATCATCTACT 19

RESULT 1120
US-10-923-182-149/C
; Sequence 149, Application US/10923182
; Publication No. US20050176666A1
; GENERAL INFORMATION:
; APPLICANT: Sigma Therapeutics, Inc.
; APPLICANT: James, McSwiggen
; APPLICANT: Ivan, Roberts
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of GPR4 and AA1 Gene
; FILE REFERENCE: 400/227 (MEHB04-423-A)
; CURRENT APPLICATION NUMBER: US/10/923,182
; PRIOR FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US 60/570,086
; PRIOR FILING DATE: 2004-05-11
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: PCT/US04/13456
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US 10/780,447
; PRIOR FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: US 60/292,217
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/362,016
; PRIOR FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US 60/363,883
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/311,865
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: US 10/727,780
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 810
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 149
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:

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; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-923-182-149
Query Match
Best Local Similarity 94.1%; Pred. No. 9e+02; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1110 CAACCCCATCATCTACT 1126
DB 17 CAACCCCATCATCTACT 1

RESULT 1121
US-10-962-898-1515
; Sequence 1515, Application US/10962898
; Publication No. US20050222066A1
; GENERAL INFORMATION:
; APPLICANT: Sigma Therapeutics, Inc.
; APPLICANT: Richards, Ivan
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Vascular Endothelial
; TITLE OF INVENTION: Growth Factor And Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: 400/236 (MEHB02-742-0)
; CURRENT APPLICATION NUMBER: US/10/962,898
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: US 10/944,644
; PRIOR FILING DATE: 2004-09-16
; PRIOR APPLICATION NUMBER: US 10/844,076
; PRIOR FILING DATE: 2004-05-11
; PRIOR APPLICATION NUMBER: US 10/831,620
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/764,957
; PRIOR FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US 10/670,011
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/665,255
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/664,767
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: PCT/US03/05022
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/393,796
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/399,348
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1515
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense
US-10-962-898-1515
Query Match
Best Local Similarity 94.1%; Pred. No. 9e+02; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 139 AGGCGCCAGCCACCGGA 155
DB 2 AGGCGCCAGCCACCGGA 18

RESULT 1122
US-10-962-898-1762/C
; Sequence 1762, Application US/10962898
; Publication No. US20050222066A1
; GENERAL INFORMATION:
; APPLICANT: Sigma Therapeutics, Inc.
; APPLICANT: Richards, Ivan

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; APPLICANT: McSwigen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Vascular Endothelial
; TITLE OF INVENTION: Growth Factor And Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: 400/236 (MBHB02-742-U)
; CURRENT FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: US 10/944,644
; PRIOR FILING DATE: 2004-09-16
; PRIOR APPLICATION NUMBER: US 10/844,076
; PRIOR FILING DATE: 2004-05-11
; PRIOR APPLICATION NUMBER: US 10/831,620
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/764,957
; PRIOR FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US 10/664,767
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: PCT/US03/05022
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/393,796
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/399,348
; PRIOR FILING DATE: 2002-07-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1762
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-962-898-1762

Query Match      0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      139 AGGCGCCAGCCACGAGA 155
Db      18 AGGCGCCAGCCACCGCA 2

RESULT 1123
US-10-944-611-1515
; Sequence 1515, Application US/10944611
; Publication No. US20050233998A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Jadhav, Vasant
; APPLICANT: Kosken, Karl
; APPLICANT: Zinnen, Shawn
; APPLICANT: Vaish, Narendra
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Vascular Endothelial
; TITLE OF INVENTION: Growth Factor And Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: 400/235 (MBHB02-742-S)
; CURRENT APPLICATION NUMBER: US/10/944,611
; CURRENT FILING DATE: 2004-09-16
; PRIOR APPLICATION NUMBER: US 10/844,076
; PRIOR FILING DATE: 2004-05-11
; PRIOR APPLICATION NUMBER: US 10/831,620
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/764,957
; PRIOR FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US 10/670,011
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/665,255
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; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/664,767
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: PCT/US03/05022
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/393,796
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/399,348
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1515
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense r
US-10-944-611-1515

Query Match      0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      139 AGGCGCCAGCCACGAGA 155
Db      2 AGGCGCCAGCCACCGCA 18

RESULT 1124
US-10-944-611-1762/c
; Sequence 1762, Application US/10944611
; Publication No. US20050233998A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Jadhav, Vasant
; APPLICANT: Kosken, Karl
; APPLICANT: Zinnen, Shawn
; APPLICANT: Vaish, Narendra
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Vascular Endothelial
; TITLE OF INVENTION: Growth Factor And Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: 400/235 (MBHB02-742-S)
; CURRENT APPLICATION NUMBER: US/10/944,611
; CURRENT FILING DATE: 2004-09-16
; PRIOR APPLICATION NUMBER: US 10/844,076
; PRIOR FILING DATE: 2004-05-11
; PRIOR APPLICATION NUMBER: US 10/831,620
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/764,957
; PRIOR FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US 10/670,011
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/665,255
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/664,767
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: PCT/US03/05022
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/393,796
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/399,348
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1762
; LENGTH: 19
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; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-944-611-1762

Query Match      0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1;

QY      139 AGGCGCCAGCCACGGA 155
DB      18 AGGCGCCAGCCACGGA 2

RESULT 1125
US-10-206-693-35
; Sequence 35, Application US/10206693
; Publication No. US20050261212A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: RNA interference Mediated Inhibition of Nogo and Nogo Receptor Ge
; FILE REFERENCE: 900/034 (MBHB02-732)
; CURRENT FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 674
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
US-10-206-693-35

Query Match      0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 15; Conservative 1; Mismatches 1;

QY      619 CCCCTCCAGCCCGGCT 635
DB      1 CCCCGCCAGCCCGGCU 17

RESULT 1126
US-10-206-693-261/C
; Sequence 261, Application US/10206693
; Publication No. US20050261212A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: RNA interference Mediated Inhibition of Nogo and Nogo Receptor Ge
; FILE REFERENCE: 900/034 (MBHB02-732)
; CURRENT FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 674
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 261
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-206-693-261

Query Match      0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1;

QY      619 CCCCTCCAGCCCGGCT 635

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DB      19 CCCCCCAGCCCGGCT 3

RESULT 1127
US-10-310-914A-288078/C
; Sequence 288078, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 288078
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-288078

Query Match      0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1;

QY      653 AAGTGTGATCTGTGTC 669
DB      17 ACGTGTGATCTGTGTC 1

RESULT 1128
US-10-310-914A-394088/C
; Sequence 394088, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 394088
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-394088

Query Match      0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1;

QY      1686 GGACCAGCTTTCTCA 1702
DB      17 GGCGCAGCTTTCTCA 1

RESULT 1129
US-10-310-914A-410563/C
; Sequence 410563, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 410563
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-410563

```

CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 410563
LENGTH: 19
TYPE: RNA
ORGANISM: Human
US-10-310-914A-410563

Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 919 CACGACGACTCTCTGC 935
DB 17 CACGACGACTCTCTGC 1

RESULT 1130

US-10-310-914A-477720
Sequence 477720, Application US/10310914A
Publication No. US2006003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiller, Kuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310.914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 477720
LENGTH: 19
TYPE: RNA
ORGANISM: Human
US-10-310-914A-477720

Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 76.5%; Pred. No. 9e+02;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1437 CACGAGGCTTTGGCAG 1453
DB 3 CACGAGGACUUGGCAG 19

RESULT 1131

US-10-310-914A-522254
Sequence 522254, Application US/10310914A
Publication No. US2006003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiller, Kuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310.914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 522254
LENGTH: 19
TYPE: RNA
ORGANISM: Human
US-10-310-914A-522254

Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 9e+02;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1403 GCTTACGCTTCTCTCC 1419
||:|||||:|:|

DB 3 GCUGACGCTTCTCTCC 19

RESULT 1132

US-10-310-914A-522262
Sequence 522262, Application US/10310914A
Publication No. US2006003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiller, Kuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310.914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 522262
LENGTH: 19
TYPE: RNA
ORGANISM: Human
US-10-310-914A-522262

Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 9e+02;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1403 GCTTACGCTTCTCTCC 1419
DB 1 GCUGACGCTTCTCTCC 17

RESULT 1133

US-10-310-914A-629950/C
Sequence 629950, Application US/10310914A
Publication No. US2006003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiller, Kuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310.914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 629950
LENGTH: 19
TYPE: RNA
ORGANISM: Human
US-10-310-914A-629950

Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 62 AGTTACGCTTTCAAAA 78
DB 19 AGTTACGCTTTCAATTA 3

RESULT 1134

US-10-310-914A-742052
Sequence 742052, Application US/10310914A
Publication No. US2006003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiller, Kuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310.914A
CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 742052
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Human
 US-10-310-914A-742052

Query Match 0.9%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 1;

QY 1296 GGGGGCCACGAGGAGG 1312
 |||||
 Db 3 GGGGGCCACGAGGAGG 19

RESULT 1135
 US-10-310-914A-860138/c
 ; Sequence 860138, Application US/10310914A
 ; Publication No. US20060003322A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentwich, Isaac
 ; APPLICANT: Shiller, Kyuzat
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 ; FILE REFERENCE: 06087.0200.CPUS01
 ; CURRENT APPLICATION NUMBER: US/10/310,914A
 ; CURRENT FILING DATE: 2002-12-06
 ; NUMBER OF SEQ ID NOS: 1388402
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 860138
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Human
 US-10-310-914A-860138

Query Match 0.9%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 1;

QY 664 TGTGTCATCTGGGTCT 680
 |||||
 Db 18 TGTGTCATCTGGGTCT 2

RESULT 1136
 US-10-310-914A-1181389
 ; Sequence 1181389, Application US/10310914A
 ; Publication No. US20060003322A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentwich, Isaac
 ; APPLICANT: Shiller, Kyuzat
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 ; FILE REFERENCE: 06087.0200.CPUS01
 ; CURRENT APPLICATION NUMBER: US/10/310,914A
 ; CURRENT FILING DATE: 2002-12-06
 ; NUMBER OF SEQ ID NOS: 1388402
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 1181389
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Human
 US-10-310-914A-1181389

Query Match 0.9%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 76.5%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
 Matches 13; Conservative 3; Mismatches 1;

QY 894 CCCCCGAGCTCTCTG 910
 |||||
 Db 1 CCCCCGAGCTCTCTG 17

RESULT 1137
 US-10-310-914A-1280868/c
 ; Sequence 1280868, Application US/10310914A
 ; Publication No. US20060003322A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentwich, Isaac
 ; APPLICANT: Shiller, Kyuzat
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 ; FILE REFERENCE: 06087.0200.CPUS01
 ; CURRENT APPLICATION NUMBER: US/10/310,914A
 ; CURRENT FILING DATE: 2002-12-06
 ; NUMBER OF SEQ ID NOS: 1388402
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 1280868
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Human
 US-10-310-914A-1280868

Query Match 0.9%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 1;

QY 963 TGTGTCATCTGGGTCT 979
 |||||
 Db 17 TGTGTCATCTGGGTCT 1

RESULT 1138
 US-10-310-914A-1309499
 ; Sequence 1309499, Application US/10310914A
 ; Publication No. US20060003322A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentwich, Isaac
 ; APPLICANT: Shiller, Kyuzat
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 ; FILE REFERENCE: 06087.0200.CPUS01
 ; CURRENT APPLICATION NUMBER: US/10/310,914A
 ; CURRENT FILING DATE: 2002-12-06
 ; NUMBER OF SEQ ID NOS: 1388402
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 1309499
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Human
 US-10-310-914A-1309499

Query Match 0.9%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 58.8%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
 Matches 10; Conservative 6; Mismatches 1;

QY 418 TTTCTGCTGAACCTGCG 434
 ::|||
 Db 3 UUDCTGCTGAACCTGCG 19

RESULT 1139
 US-10-310-914A-1319661
 ; Sequence 1319661, Application US/10310914A
 ; Publication No. US20060003322A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentwich, Isaac
 ; APPLICANT: Shiller, Kyuzat
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 ; FILE REFERENCE: 06087.0200.CPUS01
 ; CURRENT APPLICATION NUMBER: US/10/310,914A
 ; CURRENT FILING DATE: 2002-12-06
 ; NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 1319661

LENGTH: 19

TYPE: RNA

ORGANISM: Human

US-10-310-914A-1319661

Query Match 0.9%; Score 15.4; DB 1; Length 19;

Best Local Similarity 64.7%; Pred. No. 9e+02; 1;

Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1403 GCTCAGCTTCTCTCC 1419

Db 1 GCUCAGCUCACCUCC 17

RESULT 1140

US-10-310-914A-1375299/c

Sequence 1375299, Application US/10310914A

Publication No. US2006003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Shiller, Kuznet

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310.914A

PRIOR FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 1375299

LENGTH: 19

TYPE: RNA

ORGANISM: Human

US-10-310-914A-1375299

Query Match 0.9%; Score 15.4; DB 1; Length 19;

Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 619 CCCCTCCAGCCCCGCT 635

Db 17 CCCACACGCCCCGCT 1

RESULT 1141

US-11-083-784-2195

Sequence 2195, Application US/11083784

Publication No. US20050245475A1

GENERAL INFORMATION:

APPLICANT: Dharmoon, Inc.

APPLICANT: Khvorova, Anastasia

APPLICANT: Reynolds, Angela

APPLICANT: Leake, Devin

APPLICANT: Marshall, William

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/083.784

PRIOR FILING DATE: 2005-03-18

PRIOR APPLICATION NUMBER: US/10/714.333

PRIOR FILING DATE: 2003-11-14

PRIOR APPLICATION NUMBER: 60/502,050

PRIOR FILING DATE: 2003-09-10

PRIOR APPLICATION NUMBER: 60/426,137

PRIOR FILING DATE: 2002-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO 2195

LENGTH: 19

TYPE: RNA

ORGANISM: Homo sapiens

US-11-083-784-2195

Query Match 0.9%; Score 15.4; DB 1; Length 19;

Best Local Similarity 70.6%; Pred. No. 9e+02; 1;

Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 463 AATCAGTGTGTAAGT 479

Db 3 AAGCAGUGGUGAACU 19

RESULT 1142

US-11-083-784-19634/c

Sequence 19634, Application US/11083784

Publication No. US20050245475A1

GENERAL INFORMATION:

APPLICANT: Dharmoon, Inc.

APPLICANT: Khvorova, Anastasia

APPLICANT: Reynolds, Angela

APPLICANT: Leake, Devin

APPLICANT: Marshall, William

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/083.784

PRIOR FILING DATE: 2005-03-18

PRIOR APPLICATION NUMBER: US/10/714.333

PRIOR FILING DATE: 2003-11-14

PRIOR APPLICATION NUMBER: 60/502,050

PRIOR FILING DATE: 2003-09-10

PRIOR APPLICATION NUMBER: 60/426,137

PRIOR FILING DATE: 2002-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO 19634

LENGTH: 19

TYPE: RNA

ORGANISM: Homo sapiens

US-11-083-784-19634

Query Match 0.9%; Score 15.4; DB 1; Length 19;

Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1404 CTTGAGCTTCTCTCCA 1420

Db 17 CTTGAGCTTCTCTCCA 1

RESULT 1143

US-11-083-784-51038/c

Sequence 51038, Application US/11083784

Publication No. US20050245475A1

GENERAL INFORMATION:

APPLICANT: Dharmoon, Inc.

APPLICANT: Khvorova, Anastasia

APPLICANT: Reynolds, Angela

APPLICANT: Leake, Devin

APPLICANT: Marshall, William

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/083.784

PRIOR FILING DATE: 2005-03-18

PRIOR APPLICATION NUMBER: US/10/714.333

PRIOR FILING DATE: 2003-11-14

PRIOR APPLICATION NUMBER: 60/502,050

PRIOR FILING DATE: 2003-09-10

PRIOR APPLICATION NUMBER: 60/426,137

PRIOR FILING DATE: 2002-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO 51038

LENGTH: 19

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/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-51038

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 19;
Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1005 CATCTTCTCTCTCTGC 1021
Db 17 CATCTTCTCTCTCTGC 1

RESULT 1144
US-11-083-784-61485/c
/ Sequence 61485, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT FILING DATE: 2005-03-18
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 61485
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-61485

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 19;
Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1530 CTCACACTGGGACTTGC 1546
Db 17 CTCACACTGGGACTTGC 1

RESULT 1145
US-11-083-784-66269/c
/ Sequence 66269, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT FILING DATE: 2005-03-18
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
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/ SOFTWARE: Proprietary
/ SEQ ID NO 66269
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-66269

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 19;
Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1067 TCTACCTGGCCATCATG 1083
Db 19 TCTACCTGGCCATCATG 3

RESULT 1146
US-11-083-784-66270/c
/ Sequence 66270, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT FILING DATE: 2005-03-18
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 66270
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-66270

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 19;
Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1067 TCTACCTGGCCATCATG 1083
Db 17 TCTACCTGGCCATCATG 1

RESULT 1147
US-11-083-784-119668/c
/ Sequence 119668, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT FILING DATE: 2005-03-18
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
```

;; PRIOR APPLICATION NUMBER: 60/426,137
;; PRIOR FILING DATE: 2002-11-14
;; NUMBER OF SEQ ID NOS: 1591911
;; SOFTWARE: Proprietary
;; SEQ ID NO 119668
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-11-083-784-119668

Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1;

QY 1358 CCTCAACTGCTCTTCA 1374
DB 18 CCTCAACTGCTCTTCA 2

RESULT 1148
US-11-083-784-132395/c
; Sequence 132395, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 132395
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-132395

Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1;

QY 1005 CATCTCTCTCTCTGC 1021
DB 17 CATCTCTCTCTCTGC 1

RESULT 1149
US-11-083-784-143402/c
; Sequence 143402, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333

;; PRIOR FILING DATE: 2003-11-14
;; PRIOR APPLICATION NUMBER: 60/502,050
;; PRIOR FILING DATE: 2003-09-10
;; PRIOR APPLICATION NUMBER: 60/426,137
;; PRIOR FILING DATE: 2002-11-14
;; NUMBER OF SEQ ID NOS: 1591911
;; SOFTWARE: Proprietary
;; SEQ ID NO 143402
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-11-083-784-143402

Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1;

QY 1446 TTGGCAGTGTCAGCCC 1462
DB 17 TTGGCAGTGTCAGCCC 1

RESULT 1150
US-11-083-784-202084
; Sequence 202084, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 202084
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-202084

Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 12; Conservative 4; Mismatches 1;

QY 1033 CCAGATCTTACTCGAA 1049
DB 1 CCAGATCTTACTCGAA 17

RESULT 1151
US-11-083-784-202116
; Sequence 202116, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US


```

; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 232235
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-232235
```

```

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY      1024 TACATCAACCCGATCT 1040
      |||||
Db       17  TACATCAACCCCAATCT 1
```

```

RESULT 1156
US-11-083-784-237477/c
; Sequence 237477, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 237477
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-237477
```

```

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY      1404 CTTGAGCTTCTCTCCA 1420
      |||||
Db       17  CTTGAGCTTCTCTCCA 1
```

```

RESULT 1157
US-11-083-784-262644
; Sequence 262644, Application US/11083784
; Publication No. US20050245475A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 262644
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-262644
```

```

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 76.5%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```

QY      313 TGGGAGCTGCTTACAC 329
      :|||
Db       2  UGGAGAGCTGCTTACAC 18
```

```

RESULT 1158
US-11-083-784-304519
; Sequence 304519, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 304519
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-304519
```

```

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```

QY      993 GCGGCCCTTCCACATCT 1009
      ||:||||:|||||
Db       3  GCGGCCCTTCCACATCT 19
```

```

RESULT 1159
```

```
US-11-083-784-360639
; Sequence 360639, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 360639
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-360639
```

```
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 76.5%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 13; Conservative 3; Mismatches 1;
```

```
QY      1350 GGACCTGACCTCCACT 1366
      |||||:|||||:
DB      1  GCACCTGGCTCCACU 17
```

```
RESULT 1160
US-11-083-784-368528
; Sequence 368528, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR APPLICATION NUMBER: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 368528
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-368528
```

```
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 12; Conservative 4; Mismatches 1;
```

```
QY      1742 GCATGCCAGTCTCAT 1758
      |||||:|||||:
DB      2  GCAAGCGAGUGCUCAU 18
```

```
RESULT 1161
US-11-083-784-371445/C
; Sequence 371445, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR APPLICATION NUMBER: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 371445
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-371445
```

```
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1;
```

```
QY      651 CAAAGTGTCTCTCTG 667
      |||||:|||||:
DB      18  CAAAGTGGCCATCTGTG 2
```

```
RESULT 1162
US-11-083-784-421451/C
; Sequence 421451, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR APPLICATION NUMBER: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 421451
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-421451
```

```
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1;
```

Oy 242 TCTCCCAACATCTCC 258
Db 17 TCTCCCAATATCTCC 1

RESULT 1163

US-11-083-784-425085
; Sequence 425085, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 425085
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-425085

Query Match 0.9%; Score 15.4; DB 1; Length 19;

Best Local Similarity 94.1%; Pred. No. 9e+02; Mismatches 1; Indels 0; Gaps 0;

Oy 1307 AGGAGGACCGAGGAC 1323

Db 1 AGGAGGACCGAGGAC 17

RESULT 1164

US-11-083-784-460346/c
; Sequence 460346, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 460346
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-460346

Query Match 0.9%; Score 15.4; DB 1; Length 19;

Best Local Similarity 94.1%; Pred. No. 9e+02; Mismatches 1; Indels 0; Gaps 0;

Oy 651 CAAAGTGTCATCTGTG 667

Db 18 CAAAGTGTCATCTGTG 2

RESULT 1165

US-11-083-784-460400/c
; Sequence 460400, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 460400
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-460400

Query Match 0.9%; Score 15.4; DB 1; Length 19;

Best Local Similarity 94.1%; Pred. No. 9e+02; Mismatches 1; Indels 0; Gaps 0;

Oy 651 CAAAGTGTCATCTGTG 667

Db 18 CAAAGTGTCATCTGTG 2

RESULT 1166

US-11-083-784-501423
; Sequence 501423, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 501423
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-501423

US-11-083-784-501423

Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 9e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 463 AATACAGTGTGACCTT 479
DB 3 AAGACAGUGUGAACU 19

RESULT 1167

US-11-083-784-578794/C
; Sequence 578794, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 578794
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-578794

Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1721 TTCTGGAAGTGACCTT 1737
DB 19 TTCTGGAAGTGACCTT 3

RESULT 1168
US-11-083-784-671090/C
; Sequence 671090, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 671090

; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-671090

Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1404 CTTGAGCTTCTCTCCA 1420
DB 17 CTTGAGCTTCTCTCCA 1

RESULT 1169
US-11-083-784-674587
; Sequence 674587, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 674587
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-674587

Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 9e+02;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1269 CTTGAGACCACTCT 1285
DB 1 CCAGAGACCACTCAU 17

RESULT 1170
US-11-083-784-688433/C
; Sequence 688433, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14

```
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 688433
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-688433
```

```
Query Match      0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy      404 CAGTACGACTATT 420
Db      18 CAGTACGACTATT 2
```

```
RESULT 1171
US-11-083-784-704511
; Sequence 704511, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18/714,333
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 704511
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-704511
```

```
Query Match      0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 58.8%; Pred. No. 9e+02;
Matches 10; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy      578 TGACGCTGTGCTTT 594
Db      1 TGACGAGUGGCGCCUU 17
```

```
RESULT 1172
US-11-083-784-704520
; Sequence 704520, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
```

```
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 704520
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-704520
```

```
Query Match      0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 58.8%; Pred. No. 9e+02;
Matches 10; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy      578 TGACGCTGTGCTTT 594
Db      3 TGACGAGUGGCGCCUU 19
```

```
RESULT 1173
US-11-083-784-751946/c
; Sequence 751946, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 751946
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-751946
```

```
Query Match      0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy      1659 TTTGCTGAGCTGTAA 1675
Db      17 TTTGCTGAGCTGTAA 1
```

```
RESULT 1174
US-11-083-784-820807/c
; Sequence 820807, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
```

```
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 820807
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-820807

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1721 TTCTGGAGTGAAGCTTT 1737
Db 19 TTCTGGAGGGAAGCTTT 3

RESULT 1175
US-11-083-784-896406/c
; Sequence 896406, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 896406
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-896406

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 261 TAACACTTCGGAACCA 277
Db 19 TAACACTTCGGAACCA 3

RESULT 1176
US-11-083-784-911965
; Sequence 911965, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
```

```
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 911965
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-911965

Query Match
Best Local Similarity 76.5%; Score 15.4; DB 1; Length 19;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1643 AACCAATCACTGAAGT 1659
Db 3 AACCAATCACTGAAGT 19

RESULT 1177
US-11-083-784-917716/c
; Sequence 917716, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 917716
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-917716

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 653 AAGTGTATCTGTGTC 669
Db 18 AAGTGTATCTGTGTC 2

RESULT 1178
US-11-083-784-926899/c
; Sequence 926899, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
```

```

; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 926899
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-926899
```

```

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1400 AGAGCTCAGCTCTCC 1416
Db      18  AGAGTTCAGCTCTCC 2
```

```

RESULT 1179
US-11-083-784-976398/C
; Sequence 976398, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18/714,333
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 976398
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-976398
```

```

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      998 CCTTCCACATCTTCTTC 1014
Db      18  CCTTCTCATCTCTCTC 2
```

```

RESULT 1180
US-11-083-784-1028300/C
; Sequence 1028300, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
```

```

; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1028300
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1028300
```

```

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      241 CTCTCCCAACATCTC 257
Db      18  CTCTCCCAACATCTC 2
```

```

RESULT 1181
US-11-083-784-1077507/C
; Sequence 1077507, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1077507
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1077507
```

```

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1575 CATTCATCCTTGAGTC 1591
Db      19  CATTCATCATTGAGTC 3
```

```

RESULT 1182
US-11-083-784-1098844
; Sequence 1098844, Application US/11083784
```

```
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 1098844
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-1098844
```

```
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 76.5%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 13; Conservative 3; Mismatches 1;
```

```
QY      1702 AAGAGCCCAATGATTC 1718
DB      3 AAGAGCCCAUUCAUUC 19
      |||||
      |||||
```

```
RESULT 1183
US-11-083-784-1245691/c
/ Sequence 1245691, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ CURRENT FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 1245691
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-1245691
```

```
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1;
```

```
QY      652 AAGGTGCTATCTGCT 668
DB      17 AAGGTGCTATCTGCT 1
      |||||
      |||||
```

```
RESULT 1184
US-11-083-784-1277052/c
/ Sequence 1277052, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ CURRENT FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 1277052
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-1277052
```

```
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1;
```

```
QY      802 ATCTGTGACTGTGCT 818
DB      19 ATCTGTGACTGTGCT 3
      |||||
      |||||
```

```
RESULT 1185
US-11-083-784-1277082/c
/ Sequence 1277082, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ CURRENT FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 1277082
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-1277082
```

```
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1;
```

```
QY      801 CATGTGTGACTGTGC 817
      |||||
      |||||
```


Db 17 CATCTGTGTGACTGTCC 1

RESULT 1186

US-11-083-784-1239074
; Sequence 1239074, Application US/11083784
; Publication No. US20050245475A1

GENERAL INFORMATION:

APPLICANT: Dharmacom, Inc.

APPLICANT: Khvorova, Anastasia

APPLICANT: Reynolds, Angela

APPLICANT: Leake, Devin

APPLICANT: Marshall, William

APPLICANT: Scaringe, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/083,784

PRIOR FILING DATE: 2005-03-18

PRIOR APPLICATION NUMBER: US/10/714,333

PRIOR FILING DATE: 2003-11-14

PRIOR APPLICATION NUMBER: 60/502,050

PRIOR FILING DATE: 2003-09-10

PRIOR APPLICATION NUMBER: 60/426,137

PRIOR FILING DATE: 2002-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO 1239074

LENGTH: 19

TYPE: RNA

ORGANISM: Homo sapiens

US-11-083-784-1239074

Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1306 GAGAGAGCCAGCA 1322

Db 2 GAGAGAGCCAGCA 18

RESULT 1187

US-11-083-784-1302380

; Sequence 1302380, Application US/11083784

; Publication No. US20050245475A1

GENERAL INFORMATION:

APPLICANT: Dharmacom, Inc.

APPLICANT: Khvorova, Anastasia

APPLICANT: Reynolds, Angela

APPLICANT: Leake, Devin

APPLICANT: Marshall, William

APPLICANT: Scaringe, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/083,784

PRIOR FILING DATE: 2005-03-18

PRIOR APPLICATION NUMBER: US/10/714,333

PRIOR FILING DATE: 2003-11-14

PRIOR APPLICATION NUMBER: 60/502,050

PRIOR FILING DATE: 2003-09-10

PRIOR APPLICATION NUMBER: 60/426,137

PRIOR FILING DATE: 2002-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO 1302380

LENGTH: 19

TYPE: RNA

ORGANISM: Homo sapiens

US-11-083-784-1302380

Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 9e+02;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 544 CCATGCGCGCTCTT 560

Db 2 CCCAUVGCCGCTGUCU 18

RESULT 1188

US-11-083-784-1335689/c

; Sequence 1335689, Application US/11083784

; Publication No. US20050245475A1

GENERAL INFORMATION:

APPLICANT: Dharmacom, Inc.

APPLICANT: Khvorova, Anastasia

APPLICANT: Reynolds, Angela

APPLICANT: Leake, Devin

APPLICANT: Marshall, William

APPLICANT: Scaringe, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/083,784

PRIOR FILING DATE: 2005-03-18

PRIOR APPLICATION NUMBER: US/10/714,333

PRIOR FILING DATE: 2003-11-14

PRIOR APPLICATION NUMBER: 60/502,050

PRIOR FILING DATE: 2003-09-10

PRIOR APPLICATION NUMBER: 60/426,137

PRIOR FILING DATE: 2002-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO 1335689

LENGTH: 19

TYPE: RNA

ORGANISM: Homo sapiens

US-11-083-784-1335689

Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1404 CTTGAGCTTCTCTCCA 1420

Db 17 CTCGAGTTCTCTCCA 1

RESULT 1189

US-11-083-784-1362687

; Sequence 1362687, Application US/11083784

; Publication No. US20050245475A1

GENERAL INFORMATION:

APPLICANT: Dharmacom, Inc.

APPLICANT: Khvorova, Anastasia

APPLICANT: Reynolds, Angela

APPLICANT: Leake, Devin

APPLICANT: Marshall, William

APPLICANT: Scaringe, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/083,784

PRIOR FILING DATE: 2005-03-18

PRIOR APPLICATION NUMBER: US/10/714,333

PRIOR FILING DATE: 2003-11-14

PRIOR APPLICATION NUMBER: 60/502,050

PRIOR FILING DATE: 2003-09-10

PRIOR APPLICATION NUMBER: 60/426,137

PRIOR FILING DATE: 2002-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO 1362687

LENGTH: 19

TYPE: RNA

ORGANISM: Homo sapiens

US-11-083-784-1362687


```
; SEQ ID NO 1464506
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1464506
```

```
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1529 CCTCAGCTGGGACTTG 1545
Db      17  CCACACACTGGGACTTG 1
```

```
RESULT 1194
US-11-083-784-1474304/c
; Sequence 1474304, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1474304
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1474304
```

```
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      418 TTCTGGGAACTGGC 434
Db      19  TTCTGGGAACTGGC 3
```

```
RESULT 1195
US-11-083-784-1485805/c
; Sequence 1485805, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
```

```
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1485805
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1485805
```

```
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1404 CTTGAGCTTCTCTCCA 1420
Db      17  CTTGAGCTTCTCTCCA 1
```

```
RESULT 1196
US-11-083-784-1498825
; Sequence 1498825, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1498825
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1498825
```

```
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 9e+02;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1651 CACTGAAGTTGCTGAG 1667
Db      2   CACUGAACUUGAUGAG 18
```

```
RESULT 1197
US-11-083-784-1498858
; Sequence 1498858, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
```

```

; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1498858
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1498858

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 11; Conservative 5; Mismatches 1;

Qy      1651 CACTGAACCTTGTGAG 1667
Db      1 CACUGAACUUUGAUGAG 17

RESULT 1198
US-11-083-784-1515526/c
; Sequence 1515526, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1515526
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1515526

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1;

Qy      1279 ACCATCTCCACAGTGT 1295
Db      19 ACCATCTCCACAGTGT 3

RESULT 1199
US-11-083-784-1515845/c
; Sequence 1515845, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
```

```

; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1515845
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1515845

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1;

Qy      1445 CTTGGCAGGTGCAGCC 1461
Db      17 CGTTGCAGGTGCAGCC 1

RESULT 1200
US-11-101-244-2195
; Sequence 2195, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 2195
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-2195

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 12; Conservative 4; Mismatches 1;

Qy      463 AATAcAGTGTGAACTT 479
Db      3 AAGACAGTGTGGAACUU 19

RESULT 1201
US-11-101-244-19634/c
; Sequence 19634, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
```

```
;; CURRENT APPLICATION NUMBER: US/11/101,244
;; PRIOR FILING DATE: 2005-04-07
;; PRIOR APPLICATION NUMBER: 60/502,050
;; PRIOR FILING DATE: 2003-09-10
;; PRIOR APPLICATION NUMBER: 60/426,137
;; PRIOR FILING DATE: 2002-11-14
;; NUMBER OF SEQ ID NOS: 1591911
;; SOFTWARE: Proprietary
;; SEQ ID NO 15634
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-11-101-244-19634
```

```
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1404 CTTGAGCTTCTCTCCA 1420
Db      17 CTTGAGCTTCTCTCCA 1
```

```
RESULT 1202
US-11-101-244-51038/C
;; Sequence 51038, Application US/11/101,244
;; Publication No. US20050246794A1
;; GENERAL INFORMATION:
;; APPLICANT: Dharmacon, Inc.
;; APPLICANT: Khvorova, Anastasia
;; APPLICANT: Reynolds, Angela
;; APPLICANT: Leake, Devin
;; APPLICANT: Marshall, William
;; APPLICANT: Scaringe, Stephen
;; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;; FILE REFERENCE: 13499US
;; CURRENT APPLICATION NUMBER: US/11/101,244
;; CURRENT FILING DATE: 2005-04-07
;; PRIOR APPLICATION NUMBER: 60/502,050
;; PRIOR FILING DATE: 2003-09-10
;; PRIOR APPLICATION NUMBER: 60/426,137
;; PRIOR FILING DATE: 2002-11-14
;; NUMBER OF SEQ ID NOS: 1591911
;; SOFTWARE: Proprietary
;; SEQ ID NO 51038
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-11-101-244-51038
```

```
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1005 CATCTTCTCTCTCTGC 1021
Db      17 CATCTTCTCTCTCTGC 1
```

```
RESULT 1203
US-11-101-244-61485/C
;; Sequence 61485, Application US/11/101,244
;; Publication No. US20050246794A1
;; GENERAL INFORMATION:
;; APPLICANT: Dharmacon, Inc.
;; APPLICANT: Khvorova, Anastasia
;; APPLICANT: Reynolds, Angela
;; APPLICANT: Leake, Devin
;; APPLICANT: Marshall, William
;; APPLICANT: Scaringe, Stephen
;; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;; FILE REFERENCE: 13499US
;; CURRENT APPLICATION NUMBER: US/11/101,244
```

```
;; CURRENT FILING DATE: 2005-04-07
;; PRIOR APPLICATION NUMBER: 60/502,050
;; PRIOR FILING DATE: 2003-09-10
;; PRIOR APPLICATION NUMBER: 60/426,137
;; PRIOR FILING DATE: 2002-11-14
;; NUMBER OF SEQ ID NOS: 1591911
;; SOFTWARE: Proprietary
;; SEQ ID NO 61485
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-11-101-244-61485
```

```
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1530 CTCGACTGGGACTTGC 1546
Db      17 CTCGACTGGGACTTGC 1
```

```
RESULT 1204
US-11-101-244-66269/C
;; Sequence 66269, Application US/11/101,244
;; Publication No. US20050246794A1
;; GENERAL INFORMATION:
;; APPLICANT: Dharmacon, Inc.
;; APPLICANT: Khvorova, Anastasia
;; APPLICANT: Reynolds, Angela
;; APPLICANT: Leake, Devin
;; APPLICANT: Marshall, William
;; APPLICANT: Scaringe, Stephen
;; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;; FILE REFERENCE: 13499US
;; CURRENT APPLICATION NUMBER: US/11/101,244
;; CURRENT FILING DATE: 2005-04-07
;; PRIOR APPLICATION NUMBER: 60/502,050
;; PRIOR FILING DATE: 2003-09-10
;; PRIOR APPLICATION NUMBER: 60/426,137
;; PRIOR FILING DATE: 2002-11-14
;; NUMBER OF SEQ ID NOS: 1591911
;; SOFTWARE: Proprietary
;; SEQ ID NO 66269
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-11-101-244-66269
```

```
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1067 TCTACCTGGCCATCATG 1083
Db      19 TCTTCTGGCCATCATG 3
```

```
RESULT 1205
US-11-101-244-66270/C
;; Sequence 66270, Application US/11/101,244
;; Publication No. US20050246794A1
;; GENERAL INFORMATION:
;; APPLICANT: Dharmacon, Inc.
;; APPLICANT: Khvorova, Anastasia
;; APPLICANT: Reynolds, Angela
;; APPLICANT: Leake, Devin
;; APPLICANT: Marshall, William
;; APPLICANT: Scaringe, Stephen
;; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;; FILE REFERENCE: 13499US
;; CURRENT APPLICATION NUMBER: US/11/101,244
;; CURRENT FILING DATE: 2005-04-07
```

```
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 66270
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-66270

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1067 TCTACCTGGCCATCATG 1083
Db 17 TCTTCTGCGCATCATG 1

RESULT 1206
US-11-101-244-119668/c
; Sequence 119668, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 119668
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-119668

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1358 CCTCAGCTGCTCTCA 1374
Db 18 CCTTCACTGCTCTCA 2

RESULT 1207
US-11-101-244-132395/c
; Sequence 132395, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
```

```
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 132395
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-132395

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1005 CATCTTCTCTCTCTG 1021
Db 17 CATCTTCTCTCTCTG 1

RESULT 1208
US-11-101-244-143402/c
; Sequence 143402, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 143402
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-143402

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1446 TTGGCAGTGCAGCCC 1462
Db 17 TTGGCAGTGCAGCCC 1

RESULT 1209
US-11-101-244-202084
; Sequence 202084, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
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; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 202084
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-202084

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 9e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      1033 CCAGATCTTACTCGAA 1049
        |||||:|:|:|:|:|
        1 CCAGATCUCUACUGGAA 17

RESULT 1210
US-11-101-244-202116
; Sequence 202116, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 202116
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-202116

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 9e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      1033 CCAGATCTTACTCGAA 1049
        |||||:|:|:|:|:|
        3 CCAGATCUCUACUGGAA 19

RESULT 1211
US-11-101-244-202174
; Sequence 202174, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
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; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 202174
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-202174

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 9e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      1033 CCAGATCTTACTCGAA 1049
        |||||:|:~|:|:|:|
        1 CCAGATCUCUACUGGAA 17

RESULT 1212
US-11-101-244-202197
; Sequence 202197, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 202197
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-202197

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 9e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      1033 CCAGATCTTACTCGAA 1049
        |||||:|:~|:|:|:|
        3 CCAGATCUCUACUGGAA 19

RESULT 1213
US-11-101-244-232135/c
; Sequence 232135, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
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; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 232135
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-232135

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1024 TACATCAACCCGATCT 1040
DB 17 TACATCAACCCGATCT 1

RESULT 1214
US-11-101-244-232235/c
; Sequence 232235, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 232235
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-232235

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1024 TACATCAACCCGATCT 1040
DB 17 TACATCAACCCGATCT 1

RESULT 1215
US-11-101-244-237477/c
; Sequence 237477, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
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; SOFTWARE: Proprietary
; SEQ ID NO 237477
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-237477

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1404 CTTGACGCTCTCCTCCA 1420
DB 17 CTTGACGCTCTCCTCCA 1

RESULT 1216
US-11-101-244-262644
; Sequence 262644, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 262644
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-262644

Query Match
Best Local Similarity 76.5%; Score 15.4; DB 1; Length 19;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 313 TGGGACGCTGCTACAC 329
DB 2 UGGGAGAGCTGCGCAC 18

RESULT 1217
US-11-101-244-304519
; Sequence 304519, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
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SEQ ID NO 304519
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-304519

Query Match
Best Local Similarity 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 993 GCTGCTTCCACATCT 1009
Db 3 GTCGCCGCCCAUVCU 19

RESULT 1218
US-11-101-244-360639
Sequence 360639, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:

APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 134950S
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 360639
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-360639

Query Match
Best Local Similarity 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 76.5%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1350 GGAAGTGTCTCCACT 1366
Db 1 GGACUCCGCCCAUVCU 17

RESULT 1219
US-11-101-244-368528
Sequence 368528, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:

APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 134950S
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 368528

LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-368528

Query Match
Best Local Similarity 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1742 GCATGCGAGTCTCAT 1758
Db 2 GCAAGCGAGGCCAUCU 18

RESULT 1220
US-11-101-244-371445/C
Sequence 371445, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:

APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 134950S
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 371445
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-371445

Query Match
Best Local Similarity 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 651 CAAAGTGTCTCTGTG 667
Db 18 CAAAGTGTCTCTGTG 2

RESULT 1221
US-11-101-244-421451/C
Sequence 421451, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:

APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 134950S
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 421451
LENGTH: 19

```
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-421451

Query Match      0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      242 TCTCCCAACATCTCC 258
Db      17 TCTCCCAATATCTCC 1

RESULT 1222
US-11-101-244-425085
; Sequence 425085, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 425085
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-425085

Query Match      0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1307 AGGAGGACCGAGGAC 1323
Db      1 AGGAGGACCGAGGAC 17

RESULT 1223
US-11-101-244-460346/C
; Sequence 460346, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 460346
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-11-101-244-460346

Query Match      0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      651 CAAAGTGTCATCTGTG 667
Db      18 CAAAGTGTCATCTGTG 2

RESULT 1224
US-11-101-244-460400/C
; Sequence 460400, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 460400
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-460400

Query Match      0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      651 CAAAGTGTCATCTGTG 667
Db      18 CAAAGTGTCATCTGTG 2

RESULT 1225
US-11-101-244-501423
; Sequence 501423, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 501423
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
```

US-11-101-244-501423

Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 9e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Oy 463 AATACAGTGTGACTT 479
|||:|:|:|:|:|:|:
Db 3 AAGACAGUGUGAACU 19

RESULT 1226

US-11-101-244-578794/C

; Sequence 578794, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmaco, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 578794
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-578794

Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1721 TTCTGGAAGTACTT 1737
|||:|:|:|:|:|:|:
Db 19 TTCTGGAAGTACTT 3

RESULT 1227

US-11-101-244-671090/C

; Sequence 671090, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmaco, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 671090
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-671090

Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1404 CTTGAGCTTCTCCCA 1420
|||:|:|:|:|:|:|:
Db 17 CTTGAGCTTCTCCCA 1

RESULT 1228

US-11-101-244-674587

; Sequence 674587, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmaco, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 674587
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-674587

Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 9e+02;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1269 CTTGAGACCACTT 1285
|||:|:|:|:|:|:|:
Db 1 CTTGAGACCACTT 17

RESULT 1229

US-11-101-244-688433/C

; Sequence 688433, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmaco, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 688433
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-688433

Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 16; Conservative 0;

OY 404 CAGTGACGAACCTATTTT 420
Db 18 CAGTGATGAACCTATTTT 2

RESULT 1230

US-11-101-244-704511
; Sequence 704511, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 704511
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-704511

Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 58.8%; Pred. No. 9e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 10; Conservative 6;

OY 578 TGACGGCTGTGGCCTTT 594
Db 1 UGACGGAUGUGGCCUUT 17

RESULT 1231

US-11-101-244-704520
; Sequence 704520, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 704520
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-704520

Query Match 0.9%; Score 15.4; DB 1; Length 19;

Best Local Similarity 58.8%; Pred. No. 9e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 10; Conservative 6;

OY 578 TGACGGCTGTGGCCTTT 594
Db 3 UGACGGAUGUGGCCUUT 19

RESULT 1232

US-11-101-244-751946/c
; Sequence 751946, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 751946
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-751946

Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 16; Conservative 0;

OY 1659 TTTCCTGACGCTGTAA 1675
Db 17 TTTCCTGACGCTGTAA 1

RESULT 1233

US-11-101-244-820807/c
; Sequence 820807, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 820807
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-820807

Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1721 TTTCTGGAAGTACTTT 1737
Db 19 TTTCTGGAAGGACTTT 3

RESULT 1234

US-11-101-244-896406/c
; Sequence 896406, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 896406
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-896406

Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 261 TAACACTTCGGAACCA 277
Db 19 TAACACTTCGGAACCA 3

RESULT 1235

US-11-101-244-911965
; Sequence 911965, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 911965
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-911965

Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 76.5%; Pred. No. 9e+02;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1643 AACCAATCACTGACT 1659
Db 3 AACCAAUCAUGAAAU 19

RESULT 1236

US-11-101-244-917716/c
; Sequence 917716, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 917716
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-917716

Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 653 AAGTGTCATCTGTGTC 669
Db 18 AAGTGTCATCTGTGTC 2

RESULT 1237

US-11-101-244-926899/c
; Sequence 926899, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 926899
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-926899

Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 AGAGCTTCAGCTCTCC 1416
 Db 18 AGAGTTCAGCTCTCC 2

RESULT 1238
 US-11-101-244-976398/c
 ; Sequence 976398, Application US/11101244
 ; Publication No. US20050246794A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmacon, Inc.
 ; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 134990S
 ; CURRENT APPLICATION NUMBER: US/11/101,244
 ; CURRENT FILING DATE: 2005-04-07
 ; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 976398
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-101-244-976398

Query Match 0.9%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 9e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 998 CCTTCCACATCTCTTC 1014
 Db 18 CCTTCCATCTCTTC 2

RESULT 1239
 US-11-101-244-1028300/c
 ; Sequence 1028300, Application US/11101244
 ; Publication No. US20050246794A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmacon, Inc.
 ; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 134990S
 ; CURRENT APPLICATION NUMBER: US/11/101,244
 ; CURRENT FILING DATE: 2005-04-07
 ; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 1028300
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-101-244-1028300

Query Match 0.9%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 9e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 241 CTCTCCCAACATCTC 257

Db 18 CTCTCCCAACATCTC 2

RESULT 1240
 US-11-101-244-1077507/c
 ; Sequence 1077507, Application US/11101244
 ; Publication No. US20050246794A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmacon, Inc.
 ; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 134990S
 ; CURRENT APPLICATION NUMBER: US/11/101,244
 ; CURRENT FILING DATE: 2005-04-07
 ; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 1077507
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-101-244-1077507

Query Match 0.9%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 9e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1575 CATTCCATCTTGATC 1591
 Db 19 CATTCCATCTTGATC 3

RESULT 1241
 US-11-101-244-1098844
 ; Sequence 1098844, Application US/11101244
 ; Publication No. US20050246794A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmacon, Inc.
 ; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 134990S
 ; CURRENT APPLICATION NUMBER: US/11/101,244
 ; CURRENT FILING DATE: 2005-04-07
 ; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 1098844
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-101-244-1098844

Query Match 0.9%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 76.5%; Pred. No. 9e+02;
 Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1702 AAGAGCCCATGATCTC 1718

Db 3 AAGAGCCCAUUCUUC 19

```
RESULT 1242
US-11-101-244-1245691/c
; Sequence 1245691, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OR INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1245691
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1245691
```

```
Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 652 AAGTGTGATCTGTGT 668
Db 17 AAGTGTGATCTGTGT 1

RESULT 1243
US-11-101-244-1277052/c
; Sequence 1277052, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OR INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1277052
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1277052
```

```
Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
RESULT 1244
US-11-101-244-1277082/c
; Sequence 1277082, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OR INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1277082
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1277082
```

```
Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 801 CATCTGTGTGACTGTGC 817
Db 17 CATCTGTGTGACTGTGC 1

RESULT 1245
US-11-101-244-1299074
; Sequence 1299074, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OR INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1299074
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1299074
```

```
Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

RESULT 1246

```

US-11-101-244-1302380
; Sequence 1302380, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1302380
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1302380

```

Query Match 0.9%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 64.7%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
 Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 544 CCATCGCCGCTGTCTT 560
 |||||:||||:|:
 DB 2 CCATCGCCGCTGTCTT 18

```

RESULT 1247
US-11-101-244-1335689/c
; Sequence 1335689, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1335689
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1335689

```

Query Match 0.9%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1404 CTTGAGTTCTCTTCCA 1420
 |||||:|||||:
 DB 17 CTTGAGTTCTCTTCCA 1

RESULT 1248

```

US-11-101-244-1362687
; Sequence 1362687, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1362687
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1362687

```

Query Match 0.9%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 76.5%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
 Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1029 CAACCCGATCTCTACC 1045
 |||||:||||:|:
 DB 1 CAUCCGAGUCUCCUACC 17

```

RESULT 1249
US-11-101-244-1374698/c
; Sequence 1374698, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1374698
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1374698

```

Query Match 0.9%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 999 CTTCCAGATCTTCTCC 1015
 |||||:|||||:
 DB 17 CTTCCAGATCTTCTCC 1

RESULT 1250


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US-11-101-244-1410088/c
; Sequence 1410088, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1410088
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1410088

Query Match
Best Local Similarity 0.9%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1402 AGCTTCAGCTTCCTC 1418
Db 17 AGCTTCGCTTCCTC 1

RESULT 1251
US-11-101-244-1450085
; Sequence 1450085, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1450085
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1450085

Query Match
Best Local Similarity 0.9%; Score 15.4; DB 1; Length 19;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Cy 1495 GGAATTCCTTCATCT 1511
Db 1 GGAATGCGCCUACACU 17

RESULT 1252
US-11-101-244-1464506/c

```

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; Sequence 1464506, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1464506
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1464506

Query Match
Best Local Similarity 0.9%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1529 CCTCACCTGGAGCTTG 1545
Db 17 CCACACACTGGAGCTTG 1

RESULT 1253
US-11-101-244-1474304/c
; Sequence 1474304, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1474304
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1474304

Query Match
Best Local Similarity 0.9%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 418 TTCTGTGAACCTGCG 434
Db 19 TTCTGTGAACCTGCG 3

RESULT 1254
US-11-101-244-1485805/c
; Sequence 1485805, Application US/11101244

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/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07,050
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 1498505
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-1498505

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1404 CTTGAGCTTCTCCTCCA 1420
DB      17 CTTGAGCTTCTCCTCCA 1

RESULT 1255
US-11-101-244-1498825
/ Sequence 1498825, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 1498825
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-1498825

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      1651 CACTGAACCTTTGCTGAG 1667
DB      2 CACUGAACUUGAUGAG 18

RESULT 1256
US-11-101-244-1498858
/ Sequence 1498858, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
```

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/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 1498858
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-1498858

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      1651 CACTGAACCTTTGCTGAG 1667
DB      1 CACUGAACUUGAUGAG 17

RESULT 1257
US-11-101-244-1515526/c
/ Sequence 1515526, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 1515526
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-1515526

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1279 ACCATCTCCACAGTGGT 1295
DB      19 ACCATCTCCACAGTGT 3

RESULT 1258
US-11-101-244-1515845/c
/ Sequence 1515845, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
```

```

; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorovaya, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leaake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scarsange, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1515845
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-1515845

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1445 CTTGGCAGGTGCAGCC 1461
Db      17  CGTTGGCAGGTGCAGCC 1

RESULT 1259
US-11-058-582-229
; Sequence 229, Application US/11058582
; Publication No. US20050260620A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwigen, James
; APPLICANT: Christiano, Angela
; TITLE OF INVENTION: RNA interference Mediated Inhibition Of Retinoblastoma (Rb1) Gene
; FILE REFERENCE: 400/250 (MBHB 05-059-A)
; CURRENT APPLICATION NUMBER: US/11/058,582
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: US 11/039,680
; PRIOR FILING DATE: 2005-01-18
; PRIOR APPLICATION NUMBER: US 10/923,536
; PRIOR FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 650
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 229
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-11-058-582-229
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US-11-058-582-229

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 9e+02;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Oy      1550 AAGGTCAGTATGGGTT 1566
Db      3  AAGGTCATTAAGGGUU 19

RESULT 1260
US-11-058-582-492/C
; Sequence 492, Application US/11058582
; Publication No. US20050260620A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwigen, James
; APPLICANT: Christiano, Angela
; TITLE OF INVENTION: RNA interference Mediated Inhibition Of Retinoblastoma (Rb1) Gene
; FILE REFERENCE: 400/250 (MBHB 05-059-A)
; CURRENT APPLICATION NUMBER: US/11/058,582
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: US 11/039,680
; PRIOR FILING DATE: 2005-01-18
; PRIOR APPLICATION NUMBER: US 10/923,536
; PRIOR FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 650
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 492
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-11-058-582-492

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1550 AAGGTCAGTATGGGTT 1566
Db      17  AAGGTCATTAAGGGTT 1

RESULT 1261
US-09-866-108-6966
; Sequence 6966, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; US-09-866-108-6966
```

```

; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 6966
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108-6966

Query Match      0.8%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      28 CAGTGCATCCAGAG 42
      |||
Db      3 CAGTGCATCCAGAG 17

RESULT 1262
US-09-866-108-6967
; Sequence 6967, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
```

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; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 6967
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108-6967

Query Match      0.8%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      28 CAGTGCATCCAGAG 42
      |||
Db      2 CAGTGCATCCAGAG 16

RESULT 1263
US-09-866-108-6968
; Sequence 6968, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
```

;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 60/266,860
;; PRIOR FILING DATE: 2001-02-05
;; NUMBER OF SEQ ID NOS: 15752
;; SOFTWARE: Aeomica Sequence Listing Engine
;; SEQ ID NO 6968
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-866-108-6968

Query Match 0.8%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 CAGTGATCCGAGAG 42
Db 1 CAGTGATCCGAGAG 15

RESULT 1264
US-09-780-164-702
;; Sequence 702, Application US/09780164
;; Publication No. US20030092646A1
;; GENERAL INFORMATION:
;; APPLICANT: Ribozyne Pharmaceuticals, Inc.
;; APPLICANT: Blatt, Larry
;; APPLICANT: Mswiggen, Jim
;; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
;; FILE REFERENCE: 400/010
;; CURRENT APPLICATION NUMBER: US/09/780,164
;; PRIOR FILING DATE: 2001-02-09
;; PRIOR APPLICATION NUMBER: 60/185,516
;; PRIOR FILING DATE: 2000-02-28
;; NUMBER OF SEQ ID NOS: 2603
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 702
;; LENGTH: 17
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-09-780-164-702

Query Match 0.8%; Score 15; DB 1; Length 17;
Best Local Similarity 60.0%; Pred. No. 8.5e+02;
Matches 9; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 802 ATGTGTGACTGTG 816
Db 1 AUCUGUGACUGUG 15

RESULT 1265
US-10-723-361-6966
;; Sequence 6966, Application US/10723361
;; Publication No. US20040137589A1
;; GENERAL INFORMATION:
;; APPLICANT: GU, Yizhong
;; APPLICANT: JI, Yongsang
;; APPLICANT: PENN, Sharon G.

;; APPLICANT: HANZEL, David K.
;; APPLICANT: RANK, David R.
;; APPLICANT: CHEN, Wensheng
;; APPLICANT: SHANNON, Mark
;; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
;; FILE REFERENCE: PB0105
;; CURRENT APPLICATION NUMBER: US/10/723,361
;; PRIOR FILING DATE: 2003-11-26
;; PRIOR APPLICATION NUMBER: US 09/866,108
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: GB 24263,6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 15755
;; SOFTWARE: Aeomica Sequence Listing Engine
;; SEQ ID NO 6966
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-723-361-6966

Query Match 0.8%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 CAGTGATCCGAGAG 42
Db 3 CAGTGATCCGAGAG 17

RESULT 1266
US-10-723-361-6967
;; Sequence 6967, Application US/10723361
;; Publication No. US20040137589A1
;; GENERAL INFORMATION:
;; APPLICANT: GU, Yizhong
;; APPLICANT: JI, Yongsang
;; APPLICANT: PENN, Sharon G.
;; APPLICANT: HANZEL, David K.
;; APPLICANT: RANK, David R.
;; APPLICANT: CHEN, Wensheng
;; APPLICANT: SHANNON, Mark
;; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
;; FILE REFERENCE: PB0105
;; CURRENT APPLICATION NUMBER: US/10/723,361
;; PRIOR FILING DATE: 2003-11-26
;; PRIOR APPLICATION NUMBER: US 09/866,108
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: GB 24263,6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00664
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 15755
 SOFTWARE: Aecomica Sequence Listing Engine
 SEQ ID NO 6967
 LENGTH: 17
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-723-361-6967

Query Match 0.8%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 CAGTGCATCCAGAG 42
 DB 2 CAGTGCATCCAGAG 16

RESULT 1267
 US-10-723-361-6968

Sequence 6968, Application US/10723361
 Publication No. US20040137589A1

GENERAL INFORMATION:
 APPLICANT: GU, Yizhong
 APPLICANT: JI, Yonggang
 APPLICANT: PENN, Sharon G.
 APPLICANT: HANZEL, David K.
 APPLICANT: RANK, David R.
 APPLICANT: CHEN, Wensheng
 APPLICANT: SHANNON, Mark
 TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
 FILE REFERENCE: PB0105
 CURRENT FILING DATE: 2003-11-26
 PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: US 09/866,108
 PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: GB 24263.6
 PRIOR FILING DATE: 2000-10-04
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: PCT/US01/00666
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00664
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 15755
 SOFTWARE: Aecomica Sequence Listing Engine
 SEQ ID NO 6968
 LENGTH: 17
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-723-361-6968

Query Match 0.8%; Score 15; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 8.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 CAGTGCATCCAGAG 42
 DB 1 CAGTGCATCCAGAG 15

RESULT 1268
 US-10-241-313-5

Sequence 5, Application US/10241313
 Publication No. US20030118506A1

GENERAL INFORMATION:
 APPLICANT: O'Malley, Karen L.
 APPLICANT: Todd, Richard D.
 TITLE OF INVENTION: Gene Encoding the Rat Dopamine D4 Receptor
 FILE REFERENCE: WU 102 CON DIV(2)
 CURRENT FILING DATE: 2002-09-11
 PRIOR FILING DATE: 2002-09-11
 PRIOR APPLICATION NUMBER: US 08/475,742
 PRIOR FILING DATE: 1995-06-07
 PRIOR APPLICATION NUMBER: US 08/261,293
 PRIOR FILING DATE: 1994-06-16
 PRIOR APPLICATION NUMBER: US 08/014,013
 PRIOR FILING DATE: 1993-01-28
 NUMBER OF SEQ ID NOS: 16
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 5
 LENGTH: 18
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: primer- TM
 OTHER INFORMATION: VI/VII primer set ord-403
 PUBLICATION INFORMATION:
 TITLE: The rat dopamine D4 receptor: sequence, gene structure
 TITLE: and demonstration of expression in the cardiovascular
 TITLE: system
 JOURNAL: New Biol.
 VOLUME: 4
 PAGES: 1-9
 DATE: 1992
 US-10-241-313-5

Query Match 0.8%; Score 15; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 9.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 988 TGCTGCTGCCCTTC 1002
 DB 1 TGCTGCTGCCCTTC 15

RESULT 1269
 US-10-854-018-3/c

Sequence 3, Application US/10854018
 Publication No. US20050014246A1

GENERAL INFORMATION:
 APPLICANT: Hitachi, Ltd.
 TITLE OF INVENTION: Chemical reaction apparatus
 FILE REFERENCE: H0300729
 CURRENT FILING DATE: 2004-05-26
 PRIOR FILING DATE: 2003-07-14
 PRIOR APPLICATION NUMBER: JP 2003-196178
 NUMBER OF SEQ ID NOS: 20
 SEQ ID NO 3
 LENGTH: 18
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-854-018-3

Query Match 0.8%; Score 15; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1144 TTCGCTGTGGGCTTC 1158
|||||

Db 17 TTCGCTGTGGGCTTC 3
|||||

RESULT 1270

US-10-854-018-13

; Sequence 13, Application US/10854018
; Publication No. US20050014246A1
; GENERAL INFORMATION:
; APPLICANT: Hitachi, Ltd.
; TITLE OF INVENTION: Chemical reaction apparatus
; FILE REFERENCE: H0300729
; CURRENT APPLICATION NUMBER: US/10/854, 018
; CURRENT FILING DATE: 2004-05-26
; PRIOR APPLICATION NUMBER: JP 2003-196178
; NUMBER OF SEQ ID NOS: 20
; NUMBER OF SEQ ID NOS: 20
; SEQ ID NO 13
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-854-018-13

Query Match 0.8%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1144 TTCGCTGTGGGCTTC 1158
|||||

Db 2 TTCGCTGTGGGCTTC 16
|||||

RESULT 1271

US-10-310-914A-449129/C

; Sequence 449129, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310, 914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 449129
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-449129

Query Match 0.8%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1325 GCCCAGGCCACAC 1339
|||||

Db 18 GCCCAGGCCACAC 4
|||||

RESULT 1272

US-10-310-914A-767846/C

; Sequence 767846, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310, 914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1357464
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1357464

Query Match 0.8%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310, 914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 767846
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-767846

Query Match 0.8%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1010 TCTTCTCTGCGCCT 1024
|||||

Db 18 TCTTCTCTGCGCCT 4
|||||

RESULT 1273

US-10-310-914A-1113869

; Sequence 1113869, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310, 914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1113869
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1113869

Query Match 0.8%; Score 15; DB 1; Length 18;
Best Local Similarity 80.0%; Pred. No. 9.1e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 249 AACATCTCCACTAA 263
|||||

Db 4 AACATCTCCACTAA 18
|||||

RESULT 1274

US-10-310-914A-1357464/C

; Sequence 1357464, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310, 914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1357464
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1357464

Query Match 0.8%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1404 CTCGCTTCTCCTC 1418
 DB 15 CTCGCTTCTCCTC 1

RESULT 1275

US-11-044-498-3/c
 ; Sequence 3, Application US/11044498
 ; Publication No. US20060083667A1
 ; GENERAL INFORMATION: Software Engineering Co., Ltd.
 ; APPLICANT: Hitachi Chemical Reaction Apparatus
 ; TITLE OF INVENTION: PH-2343
 ; FILE REFERENCE: PH-2343
 ; CURRENT APPLICATION NUMBER: US/11/044,498
 ; CURRENT FILING DATE: 2005-01-28
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthesized DNA
 US-11-044-498-3

Query Match 0.8%; Score 15; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 9.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1144 TTCGCTCTGGGCTTC 1158
 DB 17 TTCGCTCTGGGCTTC 3

RESULT 1276

US-09-067-638B-50/c
 ; Sequence 50, Application US/09067638B
 ; Patent No. US2002028923A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lex M. Cowsett
 ; APPLICANT: Brenda F. Baker
 ; APPLICANT: John McNeil
 ; APPLICANT: Susan M. Freier
 ; APPLICANT: Henry M. Sasnor
 ; APPLICANT: Douglas G. Brooks
 ; APPLICANT: Cara Ohashi
 ; APPLICANT: Jacqueline R. Wyatt
 ; APPLICANT: Alexander Borchers
 ; APPLICANT: Timothy A. Vickers
 ; TITLE OF INVENTION: Identification of Genetic
 ; TITLE OF INVENTION: Targets for Modulation By Oligonucleotides and
 ; TITLE OF INVENTION: Generation of Oligonucleotides for Gene
 ; TITLE OF INVENTION: Modulation
 ; NUMBER OF SEQUENCES: 112
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: WOODCOCK WASHURN KURTZ
 ; ADDRESSEE: MACKIEWICZ & NORRIS LLP
 ; STREET: 1 LIBERTY PLACE 46TH FLOOR
 ; CITY: PHILADELPHIA
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
 COMPUTER: IBM
 OPERATING SYSTEM: PC-Windows NT
 SOFTWARE: WORD PERFECT 6.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/067,638B
 FILING DATE: 28-APR-1998
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/081,483
 FILING DATE: 13-APR-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: John W. Caldwell
 REGISTRATION NUMBER: 28,937
 REFERENCE/DOCKET NUMBER: ISIS-2960
 TELEPHONE: (215) 568-3439
 TELEFAX: (215) 568-3100
 INFORMATION FOR SEQ ID NO: 50:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-09-067-638B-50

Query Match 0.8%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 9.4e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1406 TCAGCTTCTCTCCATG 1423
 DB 18 TCAGCTTCTCTCCATG 1

RESULT 1277

US-10-116-325-50/c
 ; Sequence 50, Application US/10116325
 ; Publication No. US2003011379A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cowsett, Lex M.
 ; APPLICANT: Baker, Brenda F.
 ; APPLICANT: McNeil, John
 ; APPLICANT: Freier, Susan M.
 ; APPLICANT: Sasnor, Henry M.
 ; APPLICANT: Brooks, Douglas G.
 ; APPLICANT: Ohashi, Cara
 ; APPLICANT: Wyatt, Jacqueline R.
 ; APPLICANT: Borchers, Alexander
 ; APPLICANT: Vickers, Timothy A.
 ; TITLE OF INVENTION: Identification of Genetic Targets For Modulation By Oligonucleotides
 ; TITLE OF INVENTION: Generation of Oligonucleotides for Gene Modulation
 ; FILE REFERENCE: ISIS5026
 ; CURRENT APPLICATION NUMBER: US/10/116,325
 ; CURRENT FILING DATE: 2002-04-04
 ; PRIOR APPLICATION NUMBER: 09/067,638
 ; PRIOR FILING DATE: 1998-04-28
 ; PRIOR APPLICATION NUMBER: 60/081,483
 ; PRIOR FILING DATE: 1998-04-13
 ; NUMBER OF SEQ ID NOS: 112
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 50
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: No. US2003011379A1e1 Sequence
 US-10-116-325-50

Query Match 0.8%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 9.4e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1406 TCAGCTTCTCTCCATG 1423
 DB 18 TCAGCTTCTCTCCATG 1

RESULT 1278

US-10-388-263-50/c
 ; Sequence 50, Application US/10388263
 ; Publication No. US20030228597A1


```
; GENERAL INFORMATION:
; APPLICANT: Cowser, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
; APPLICANT: Freiler, Susan M.
; APPLICANT: Sasnor, Henri M.
; APPLICANT: Brooke, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
; TITLE OF INVENTION: MODULATION BY OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
; FILE REFERENCE: ISIS-4503
; CURRENT APPLICATION NUMBER: US/10/388,263
; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-388-263-50
```

```
Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1406 TCAGCTTCTCTCCAAAG 1423
Db 18 TCGGCTTCTTCTCCAAAG 1
```

```
RESULT 1279
US-10-016-248-66
; Sequence 66, Application US/10016248
; Publication No. US2004003491A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-218
; CURRENT APPLICATION NUMBER: US/10/016,248
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/254,329
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/291,037
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/255,648
; PRIOR FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 60/297,173
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/309,258
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/326,393
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/315,639
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide primer
US-10-016-248-66
```

```
Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
```

```
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 315 GGCAGCTGCCTACACGGT 332
Db 1 GGCAGCGCCCTACACGGT 18
```

```
RESULT 1280
US-10-698-689-50/c
; Sequence 50, Application US/10698689
; Publication No. US20040186071A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Cowser, Lex M.
; APPLICANT: Malik, Leila
; APPLICANT: Siwkowski, Andrew
; APPLICANT: Eldrup, Anne B.
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD40 EXPRESSION
; FILE REFERENCE: ISIS-5315
; CURRENT APPLICATION NUMBER: US/10/698,689
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: PCT/US03/31166
; PRIOR FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US 10/261,382
; PRIOR FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US 09/067,638
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: US 60/081,483
; PRIOR FILING DATE: 1998-04-13
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-698-689-50
```

```
Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1406 TCAGCTTCTCTCCAAAG 1423
Db 18 TCGGCTTCTTCTCCAAAG 1
```

```
RESULT 1281
US-10-698-689-214
; Sequence 214, Application US/10698689
; Publication No. US20040186071A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Cowser, Lex M.
; APPLICANT: Malik, Leila
; APPLICANT: Siwkowski, Andrew
; APPLICANT: Eldrup, Anne B.
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD40 EXPRESSION
; FILE REFERENCE: ISIS-5315
; CURRENT APPLICATION NUMBER: US/10/698,689
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: PCT/US03/31166
; PRIOR FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US 10/261,382
; PRIOR FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US 09/067,638
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: US 60/081,483
; PRIOR FILING DATE: 1998-04-13
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 214
```

LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Construct
US-10-698-689-214

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1406 TCAGCTTCTCTCCATG 1423
DB 1 TCAGCTTCTCTCCATG 18

RESULT 1282

US-10-830-475-50/c
Sequence 50, Application US/10830475
Publication No. US2004019781A1

GENERAL INFORMATION:

APPLICANT: Lex M. Cowseert
Brenda F. Baker
John McNeill
Susan M. Freier
Henri M. Sasmor
Douglas G. Brooks
Cara Ohashi
Jacqueline R. Wyatt
Alexander Borchers
Timothy A. Vickers

TITLE OF INVENTION: Identification of Genetic
Targets for Modulation By Oligonucleotides and
Modulation
Generation of Oligonucleotides for Gene

NUMBER OF SEQUENCES: 112

CORRESPONDENCE ADDRESS:

ADDRESSEE: WOODCOCK WASHBURN KURTZ
MACKIEWICZ & NORRIS LLP
STREET: 1 LIBERTY PLACE 46TH FLOOR
CITY: PHILADELPHIA
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB

COMPUTER: IBM

OPERATING SYSTEM: PC-Windows NT

SOFTWARE: WORD PERFECT 6.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/830,475

FILING DATE: 21-Apr-2004

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/067,638B

FILING DATE: 28-APR-1998

APPLICATION NUMBER: 60/081,483

FILING DATE: 13-APR-1998

ATTORNEY/AGENT INFORMATION:

NAME: John W. Caldwell

REGISTRATION NUMBER: 28,937

REFERENCE/DOCKET NUMBER: ISIS-2960

TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTERISTICS:

LENGTH: 18

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 50:

US-10-830-475-50

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1406 TCAGCTTCTCTCCATG 1423
DB 18 TCAGCTTCTCTCCATG 1

RESULT 1283

US-10-649-467-50/c
Sequence 50, Application US/10649467
Publication No. US20050033524A1

GENERAL INFORMATION:

APPLICANT: Lex M. Cowseert
Brenda F. Baker
John McNeill
Susan M. Freier
Henri M. Sasmor
Douglas G. Brooks
Cara Ohashi
Jacqueline R. Wyatt
Alexander Borchers
Timothy A. Vickers
TITLE OF INVENTION: Identification of Genetic Targets for Modulation By Oligonucleotides
FILE REFERENCE: ISIS085-100 (ISIS2960US.C2)

CURRENT APPLICATION NUMBER: US/10/649,467

CURRENT FILING DATE: 2003-08-27

PRIOR APPLICATION NUMBER: 09/067,636

PRIOR FILING DATE: 1998-04-28

PRIOR APPLICATION NUMBER: 60/081,483

PRIOR FILING DATE: 1998-04-13

NUMBER OF SEQ ID NOS: 112

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 50

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: oligomeric compound

US-10-649-467-50

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1406 TCAGCTTCTCTCCATG 1423
DB 18 TCAGCTTCTCTCCATG 1

RESULT 1284

US-10-934-798-89/c
Sequence 89, Application US/10934798
Publication No. US20050142581A1

GENERAL INFORMATION:

APPLICANT: Richard H. Griffey
APPLICANT: C. Frank Bennett
APPLICANT: David J. Becker
APPLICANT: Donna T. Ward
APPLICANT: Susan M. Freier
TITLE OF INVENTION: MICRORNA AS LIGANDS AND TARGET MOLECULES
FILE REFERENCE: CORE0020US

CURRENT APPLICATION NUMBER: US/10/934,798

CURRENT FILING DATE: 2004-09-03

PRIOR APPLICATION NUMBER: 60/500,824

PRIOR FILING DATE: 2003-09-04

PRIOR APPLICATION NUMBER: 60/500,730

PRIOR FILING DATE: 2003-09-04

PRIOR APPLICATION NUMBER: 60/504,495

PRIOR FILING DATE: 2003-09-17

```

; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Compound
US-10-934-798-89

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1406 TCAGCTTCTCTCCCATG 1423
Db      18 TCGGCTTCTCTCCCATG 1

RESULT 1285
US-10-934-798-208/c
; Sequence 208, Application US/10934798
; Publication No. US20050142581A1
; GENERAL INFORMATION:
; APPLICANT: Richard H. Giffey
; APPLICANT: C. Frank Bennett
; APPLICANT: David J. Ecker
; APPLICANT: Donna T. Ward
; APPLICANT: Susan M. Freiler
; TITLE OF INVENTION: MICRORNA AS LIGANDS AND TARGET MOLECULES
; FILE REFERENCE: CORE0020US
; CURRENT APPLICATION NUMBER: US/10/934,798
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/500,824
; PRIOR FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: 60/500,730
; PRIOR FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: 60/504,495
; PRIOR FILING DATE: 2003-09-17
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 208
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Compound
US-10-934-798-208

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1406 TCAGCTTCTCTCCCATG 1423
Db      18 TCGGCTTCTCTCCCATG 1

RESULT 1286
US-10-310-914A-77047
; Sequence 77047, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77047

; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-101443

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 9.4e+02;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY      1511 TGGAACCATCAGAAACAC 1528
Db      1 UGGAACCAAAAGAAACAC 18

RESULT 1289
US-10-310-914A-83639
; Sequence 83639, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 83639
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-83639

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 9.4e+02;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY      1326 CCCCAAGGCCACACCTTC 1343
Db      1 CCUCAAGGCCACACCCCTTC 18

RESULT 1288
US-10-310-914A-101443
; Sequence 101443, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 101443
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-101443

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 9.4e+02;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY      1511 TGGAACCATCAGAAACAC 1528
Db      1 UGGAACCAAAAGAAACAC 18

RESULT 1289
```

```

US-10-310-914A-213729
; Sequence 213729, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 213729
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-213729

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Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 55.6%; Pred. No. 9.4e+02;
Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

```

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QY      984 CATCTGCTGCTGCCCTT 1001
      ||:||||:|:||||:|:
Db      1 CACUCGUCGACUCGACU 18

```

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RESULT 1290
US-10-310-914A-309009/c
; Sequence 309009, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 309009
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-309009

```

```

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      13 CCGGGGCGAGCGGCGAG 30
      ||:||||:|:||||:|:
Db      18 CCGGGGCGAGCGGCGAG 1

```

```

RESULT 1291
US-10-310-914A-336351
; Sequence 336351, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 336351
; LENGTH: 18

```

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; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-336351

```

```

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 72.2%; Pred. No. 9.4e+02;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      1284 CTCACAGTGTGGGGGC 1301
      ||:||||:|:||||:|:
Db      1 CUCCCGACGUCGCGGC 18

```

```

RESULT 1292
US-10-310-914A-427752/c
; Sequence 427752, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 427752
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-427752

```

```

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      1001 TCCACATCTTCTTCCTCC 1018
      ||:||||:|:||||:|:
Db      18 TCCCTCTCTTCTTCCTCC 1

```

```

RESULT 1293
US-10-310-914A-465296
; Sequence 465296, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 465296
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-465296

```

```

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 50.0%; Pred. No. 9.4e+02;
Matches 9; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      1001 TCCACATCTTCTTCCTCC 1018
      ||:||||:|:||||:|:
Db      1 UCUCUCUCUCUCUCUCUC 18

```

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RESULT 1294
US-10-310-914A-472856/c

```

```
; Sequence 472856, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 472856
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-472856

Query Match
Best Local Similarity 88.9%; Score 14.8; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GCCCAGCAGACTCGTGTG 749
Db 18 GCCCAGCAGAGACGTGGG 1

RESULT 1295
US-10-310-914A-519019
; Sequence 519019, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 519019
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-519019

Query Match
Best Local Similarity 83.3%; Score 14.8; DB 1; Length 18;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 128 CCTGAGCCCGAGCGGCC 145
Db 1 CCTGAGUGCCAGCGGCC 18

RESULT 1296
US-10-310-914A-519948/C
; Sequence 519948, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 519948
; LENGTH: 18
; TYPE: RNA

; ORGANISM: Human
US-10-310-914A-519948

Query Match
Best Local Similarity 88.9%; Score 14.8; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 694 GCCTCCCCCAGGCGTAC 711
Db 18 GCCATCCCCCAGGCGTCC 1

RESULT 1297
US-10-310-914A-519969
; Sequence 519969, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 519969
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-519969

Query Match
Best Local Similarity 72.2%; Score 14.8; DB 1; Length 18;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1283 TCTCCACAGTGGTGGGG 1300
Db 1 UCUCACAGGGGGUGGGG 18

RESULT 1298
US-10-310-914A-585840/C
; Sequence 585840, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 585840
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-585840

Query Match
Best Local Similarity 88.9%; Score 14.8; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 132 GAGCCCGAGCGCCAGCC 149
Db 18 GAGCCTCAGGCCCGAGCC 1

RESULT 1299
US-10-310-914A-601989/C
; Sequence 601989, Application US/10310914A
```

```
/ Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Knuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 601989
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-601989

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1168 TTCCGCTGCTGCCCCCTTC 1185
Db      18  TTCCGAGACTGCCCTTC 1

RESULT 1300
US-10-310-914A-645930/c
; Sequence 645930, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Knuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 645930
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-645930

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      685 CTCTGCTGCTGCCCCCTTC 702
Db      18  CTCTGCTGCTGCCCCCTTC 1

RESULT 1301
US-10-310-914A-696092/c
; Sequence 696092, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Knuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 696092
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human

US-10-310-914A-696092

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      984 CATCTGCTGCTGCCCCCTT 1001
Db      18  CATATGAGGCTTCCTTC 1

RESULT 1302
US-10-310-914A-707873/c
; Sequence 707873, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Knuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 707873
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-707873

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1592 AAAAATCTCAATCTTC 1609
Db      18  AAAAAGTCTATCTTC 1

RESULT 1303
US-10-310-914A-768979
; Sequence 768979, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Knuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 768979
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-768979

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 50.0%; Pred. No. 9.4e+02;
Matches 9; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY      1001 TCCACATCTGCTGCTTC 1018
Db      1  UCCUCUCUCUCUCUCUC 18

RESULT 1304
US-10-310-914A-795204/c
; Sequence 795204, Application US/10310914A
; Publication No. US20060003322A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 795204
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-795204

Query Match      0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      623 TCCAGCCCCGCGCTGCTCAG 640
Db      18 TCCATCCCCGCGAGCTCAG 1

RESULT 1305
US-10-310-914A-809520
; Sequence 809520, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 809520
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-809520

Query Match      0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 72.2%; Pred. No. 9.4e+02;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1638 ACTCAACCAATGACATG 1655
Db      1 ACUCAUCCCAUAUCACUG 18

RESULT 1306
US-10-310-914A-847106/c
; Sequence 847106, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 847106
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-847106

Query Match      0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 77.8%; Pred. No. 9.4e+02;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1243 CAGGCGAGTGTTACAAA 1260
Db      1 CAGGCGAGUAAGUACAAA 18

RESULT 1309
US-10-310-914A-923895/c
; Sequence 923895, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 874025
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-874025

Query Match      0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 50.0%; Pred. No. 9.4e+02;
Matches 9; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY      1007 TCTTCTCTCTGCGCCT 1024
Db      1 UCUGCUUCUCUCUCUCU 18

RESULT 1308
US-10-310-914A-885132
; Sequence 885132, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 885132
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-885132

Query Match      0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 77.8%; Pred. No. 9.4e+02;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1615 CTTGCGACCCCTCATGCT 1632
Db      18 CTTCGCACTCTCTGCT 1

RESULT 1307
US-10-310-914A-874025
; Sequence 874025, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 874025
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-874025

Query Match      0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1615 CTTGCGACCCCTCATGCT 1632
Db      18 CTTCGCACTCTCTGCT 1
```

```

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 923895
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-923895
```

```
Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      15 GCGGGCAGCGCGGCGATG 32
Db      18 GCGGGCAGCGCGGCGGAG 1
```

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RESULT 1310
US-10-310-914A-937032/c
; Sequence 937032, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 937032
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-937032
```

```
Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      685 CTCCTGCTGGCCTTCCCC 702
Db      18 CCCGAGCTGGCTTCCCC 1
```

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RESULT 1311
US-10-310-914A-946378/c
; Sequence 946378, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 946378
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-946378
```

```

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1165 GCCTCCGGTGTCTGCC 1182
Db      18 GCCTCCGGAGCTGCC 1
```

```

RESULT 1312
US-10-310-914A-965107/c
; Sequence 965107, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 965107
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-965107
```

```
Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      998 CCTTCCACATCTCTTCC 1015
Db      18 CCTTCCACATCTCTTCC 1
```

```

RESULT 1313
US-10-310-914A-971333
; Sequence 971333, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 971333
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-971333
```

```
Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 90.0%; Pred. No. 9.4e+02;
Matches 9; Conservative 7; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1001 TCACATCTTCTCTCC 1018
Db      1 UCUCUCUCUCUCUCUC 18
```

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RESULT 1314
US-10-310-914A-981336/c
; Sequence 981336, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
```


APPLICANT: Shiler, Kuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310.914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 981336
LENGTH: 18
TYPE: RNA
ORGANISM: Human
US-10-310-914A-981336

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1308 GGAGAGCCAGAGGCGG 1325
DB 18 GGAGAGCCAGCGCGG 1

RESULT 1315
US-10-310-914A-984119
Sequence 984119, Application US/10310914A
Publication No. US2006003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310.914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 984119
LENGTH: 18
TYPE: RNA
ORGANISM: Human
US-10-310-914A-984119

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 61.1%; Pred. No. 9.4e+02;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 676 GTCCTGGCTCTGCTGCTG 693
DB 1 GGCCTUGGCTCUCCTCUG 18

RESULT 1316
US-10-310-914A-990023/C
Sequence 990023, Application US/10310914A
Publication No. US2006003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310.914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 990023
LENGTH: 18
TYPE: RNA
ORGANISM: Human
US-10-310-914A-990023

Query Match 0.8%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1729 AGTGACTTTGGCTGCAGG 1746
DB 18 AGTGACTTTGGCTGCAGG 1

RESULT 1317
US-10-310-914A-999624
Sequence 999624, Application US/10310914A
Publication No. US2006003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310.914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 999624
LENGTH: 18
TYPE: RNA
ORGANISM: Human
US-10-310-914A-999624

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 72.2%; Pred. No. 9.4e+02;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1455 TGCAGCCCCCAGCTGCTT 1472
DB 1 TGCAGCCCCCAGCTGCTT 18

RESULT 1318
US-10-310-914A-1004988/C
Sequence 1004988, Application US/10310914A
Publication No. US2006003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310.914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1004988
LENGTH: 18
TYPE: RNA
ORGANISM: Human
US-10-310-914A-1004988

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 99 CTTCACCCCTCTGCTGCTG 116
DB 18 CTGCTTCCTCTGCTGCTG 1

RESULT 1319
US-10-310-914A-1093902/C
Sequence 1093902, Application US/10310914A
Publication No. US2006003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kuzat

```

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1093902
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
; US-10-310-914A-1093902

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      156 CTCTGCTGCAGAGGGGG 173
Db      18 CTGTGCTGCAGAGGGGG 1

RESULT 1320
US-10-310-914A-1169386
; Sequence 1169386, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1169386
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
; US-10-310-914A-1169386

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 61.1%; Pred. No. 9.4e+02;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      525 CAAGTCCACAACCTCTT 542
Db      1 CAGAATCCACAATUDCU 18

RESULT 1321
US-10-310-914A-1219917
; Sequence 1219917, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1219917
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
; US-10-310-914A-1219917

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 61.1%; Pred. No. 9.4e+02;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      1145 TCCGCTGTGGGCTTCAAGC 1162
Db      1 UCCUUCUGGCGUCCAGC 18

RESULT 1322
US-10-310-914A-1234776
; Sequence 1234776, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1234776
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
; US-10-310-914A-1234776

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 77.8%; Pred. No. 9.4e+02;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1436 CCACAGGGCCTTGGCAG 1453
Db      1 CUCACAGGGCCUCUGGCAG 18

RESULT 1323
US-10-310-914A-1249080/c
; Sequence 1249080, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1249080
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
; US-10-310-914A-1249080

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      134 GCCCCAGGCCCGCAGCCAC 151
Db      18 GCCCCAGGCCCGCAGCCAC 1

RESULT 1324
US-10-310-914A-1255023/c
; Sequence 1255023, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
```

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; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1255023
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1255023

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      685 CTCCTGCTGGCCTTCCCC 702
Db      18 CTCCTGCTGGCCTTCCCC 1

RESULT 1325
US-10-310-914A-1329744/c
; Sequence 1329744, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1329744
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1329744

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      685 CTCCTGCTGGCCTTCCCC 702
Db      18 CTCCTGCTGGCCTTCCCC 1

RESULT 1326
US-10-310-914A-1337516/c
; Sequence 1337516, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1337516
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1337516

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```

Qy      1181 CCTTCATCAGCGCGCGC 1198
Db      18 CTTTCAGCAGCGCGCGC 1

RESULT 1327
US-10-310-914A-1366802/c
; Sequence 1366802, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1366802
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1366802

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      366 AGTGATGTGATCATCTT 383
Db      18 AGTGATGTGATCATCTT 1

RESULT 1328
US-10-310-914A-1383827/c
; Sequence 1383827, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1383827
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1383827

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1434 GGCACAGGCGCTTTGGC 1451
Db      18 GGCACAGGCGCATCTGGC 1

RESULT 1329
US-11-069-908-3801/c
; Sequence 3801, Application US/11069908
; Publication No. US20050266432A1
; GENERAL INFORMATION:
; APPLICANT: OLIPHANT, ARNOLD
; APPLICANT: MORRAY, SARAH
; TITLE OF INVENTION: HAPLOTYPE MARKERS FOR DIAGNOSING SUSCEPTIBILITY TO IMMUNOLOGICAL
; TITLE OF INVENTION: CONDITIONS
```

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; FILE REFERENCE: 029011-0402
; CURRENT APPLICATION NUMBER: US/11/069,908
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 60/547,823
; PRIOR FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7098
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3801
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-11-069-908-3801

Query Match
Best Local Similarity 0.8%; Score 14.8; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1292 TGGTGGGGGCCACGAGG 1309
Db 18 TGGTGGAGGCGCTCGAGG 1

RESULT 1330
US-11-226-882A-50/c
; Sequence 50, Application US/11226882A
; Publication No. US20060069518A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowsett
; APPLICANT: Brenda F. Baker
; APPLICANT: John McNeil
; APPLICANT: Susan M. Freier
; APPLICANT: Henri M. Sasmor
; APPLICANT: Douglas G. Brooks
; APPLICANT: Cara Ohashi
; APPLICANT: Jacqueline R. Wyatt
; APPLICANT: Alexander Borchers
; APPLICANT: Timothy A. Vickers
; TITLE OF INVENTION: Identification of Genetic Targets for Modulation By Oligonucleotids
; TITLE OF INVENTION: Generation of Oligonucleotides for Gene Modulation
; FILE REFERENCE: US150085-104 (US152960US C4)
; CURRENT APPLICATION NUMBER: US/11/226,882A
; CURRENT FILING DATE: 2005-09-14
; PRIOR APPLICATION NUMBER: 09/067,638
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/081,483
; PRIOR FILING DATE: 1998-04-13
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: oligomeric compound
US-11-226-882A-50

Query Match
Best Local Similarity 0.8%; Score 14.8; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1406 TCAGCTTCTCTCCATG 1423
Db 18 TCAGCTTCTCTCCATG 1

RESULT 1331
US-10-310-914A-467163
; Sequence 467163, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
```

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; APPLICANT: Shiler, Kuvatz
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: Uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 138402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 467163
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-467163

Query Match
Best Local Similarity 0.8%; Score 14.6; DB 1; Length 22;
Matches 15; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 893 TCCCGGGAGCTCTCGACC 913
Db 1 TCCCGGGAGACCTCCUGGCC 21

RESULT 1332
US-10-310-914A-467164
; Sequence 467164, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuvatz
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: Uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 138402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 467164
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-467164

Query Match
Best Local Similarity 0.8%; Score 14.6; DB 1; Length 22;
Matches 15; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 893 TCCCGGGAGCTCTCGACC 913
Db 1 TCCCGGGAGACCTCCUGGCC 21

RESULT 1333
US-09-930-503-14/c
; Sequence 14, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREOF
; FILE REFERENCE: 39245-173913
; CURRENT APPLICATION NUMBER: US/09/930,503
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
; US-09-930-503-14

Query Match          0.8%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      207 CGAATGATACGTC 222
DB      16 CAAATGATACGTC 1

RESULT 1334
; US-10-712-672-1732
; Sequence 1732, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowitra, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MBH00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1732
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-10-712-672-1732

Query Match          0.8%; Score 14.4; DB 1; Length 16;
Best Local Similarity 68.8%; Pred. No. 8.8e+02;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      464 ATACAGTGTGAACCT 479
DB      1 AGACAGUGUGAACCU 16

RESULT 1335
; US-09-864-785-1566
; Sequence 1566, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to the Inhibition of Telomerase Enzyme
; FILE REFERENCE: 400/022 (MBH00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1566
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; US-09-864-785-1566
```

```
Query Match          0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      134 GCGCCAGCGCCGACC 149
DB      2 GCGCCAGCGCCGACC 17

RESULT 1336
; US-09-930-503-13/c
; Sequence 13, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; FILE REFERENCE: 39245-173913
; CURRENT APPLICATION NUMBER: US/09/930,503
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
; US-09-930-503-13

Query Match          0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      207 CGAATGATACGTC 222
DB      16 CAAATGATACGTC 1

RESULT 1337
; US-09-780-533A-920
; Sequence 920, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatz, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowitra, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00-878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 920
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-780-533A-920

Query Match          0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      619 CCGCTCAGCGCCGCGC 634
DB      1 CCGCTCAGCGCCGCGC 634
```

Db 2 CCCCCCAGCCCCGC 17

RESULT 1338

US-09-848-754A-3108/c
; Sequence 3108, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MHB00-958-1 (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3108
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-3108

Query Match 0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1694 TTTTCCTCAAGAGCC 1709

Db 17 TTTTCCTCCAGAGCC 2

RESULT 1339

US-09-930-423-1361/c
; Sequence 1361, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwigen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MHB00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1361
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-1361

Query Match 0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1275 GACCACCATCTCCACA 1290

Db 17 GTCACCATCTCCACA 2

RESULT 1340

US-09-780-164-769
; Sequence 769, Application US/09780164
; Publication No. US20030092646A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwigen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
; FILE REFERENCE: 400/010
; CURRENT APPLICATION NUMBER: US/09/780,164
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/185,516

; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 769
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-164-769

Query Match 0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 9.5e+02;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 799 CACATCTGTGTACTG 814

Db 2 CCCAUCUGUGACUG 17

RESULT 1341

US-09-745-237A-1361/c
; Sequence 1361, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwigen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1361
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-1361

Query Match 0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1275 GACCACCATCTCCACA 1290

Db 17 GTCACCATCTCCACA 2

RESULT 1342

US-10-238-700-1302/c
; Sequence 1302, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level;
; FILE REFERENCE: 400/057 (MHB01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1302
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-1302

Query Match 0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 834 CCTGCTGTGATTCGC 849
Db 17 CCTGCTGTGATTCGC 2

RESULT 1343
US-10-712-672-342
; Sequence 342, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowitra, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MBHB00-882-C (400/019)
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 342
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-342

Query Match 0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 9.5e+02;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1687 GACCAGCTTTCCCA 1702
Db 1 GGCCAGCUCUCCUCA 16

RESULT 1344
US-10-724-270-1302/C
; Sequence 1302, Application US/10724270
; Publication No. US20050080031A1
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; APPLICANT: Sirna Therapeutics, Inc.
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
; TITLE OF INVENTION: RAS, HER2 and HIV
; FILE REFERENCE: 400/046-US (MBHB02-326-A)
; CURRENT APPLICATION NUMBER: US/10/724,270
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: PCT/US02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/296,249
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/294,140
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 10/238,700
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: US 10/163,552
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 10/157,580
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012

; PRIOR FILING DATE: 2003-04-16
; Remaining Prior Application data removed - See File Wrapper or PAM.
; NUMBER OF SEQ ID NOS: 6810
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1302
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-724-270-1302

Query Match 0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 834 CCTGCTGTGATTCGC 849
Db 17 CCTGCTGTGATTCGC 2

RESULT 1345
US-09-930-503-12/C
; Sequence 12, Application US/0930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CARILL, CATHERINE
; APPLICANT: VASHEPL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; FILE REFERENCE: 39245-173913
; CURRENT APPLICATION NUMBER: US/09/930,503
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-12

Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 207 CGAATGATTAAGTC 222
Db 16 CGAATGATTAAGTC 1

RESULT 1346
US-09-774-381-11
; Sequence 11, Application US/09774381
; Publication No. US20030082677A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Pan, Yang
; APPLICANT: Geating, David P.
; TITLE OF INVENTION: NOVEL EDIRF, MTR-1, LSP-1, TAP-1, AND PA-I MOLECULES
; FILE REFERENCE: MNI-107CP2
; CURRENT APPLICATION NUMBER: US/09/774,381
; CURRENT FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 08/941,354
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/010,674
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 60/061,149
; PRIOR FILING DATE: 1997-10-06

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; PRIOR APPLICATION NUMBER: 09/014,347
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 60/061,159
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: 09/474,151
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 09/004,206
; PRIOR FILING DATE: 1998-01-08
; PRIOR APPLICATION NUMBER: 60/061,143
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: 09/483,414
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/213,571
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/994,890
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence:primer
US-09-774-381-11
```

```

Query Match          0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1450 GCAGTGCAGCCCCCA 1465
Db       2   GCAGTGCAGCCCA 17
```

```

RESULT 1347
US-10-133-779-42/c
; Sequence 42, Application US/10133779
; Publication No. US20030165884A1
; GENERAL INFORMATION:
; APPLICANT: Chow, Robert
; APPLICANT: Tonal, Richard
; APPLICANT: StemCyle, Inc.
; TITLE OF INVENTION: High Throughput Methods of HLA Typing
; FILE REFERENCE: 020035-000210US
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/10/133,779
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/172,768
; PRIOR FILING DATE: 1999-12-20
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-133-779-42
```

```

Query Match          0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      438 GCGGAGGCTTCATG 453
Db       18   GCGGAGGCTTCATG 3
```

```

RESULT 1348
US-10-349-143-10970
; Sequence 10970, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CEP1
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/10/349,143
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 10970
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURES:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-23427 for SEQ 3105, in compleme
US-10-349-143-10970
```

```

Query Match          0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      1404 CTTGAGCTTCTCTCC 1419
Db       2   CTTGATCTTCTCTCC 17
```

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RESULT 1349
US-10-138-674-3013/c
; Sequence 3013, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MSHB00-876-N (400/049)
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3013
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-138-674-3013
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```

Query Match          0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY      662 TCTGTGATCTGGAT 677
Db       18   TCTGTGATCTGAGT 3
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```

RESULT 1350
US-10-287-949A-3013/c
; Sequence 3013, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
```



```

; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3013
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-287-949A-3013

Query Match          0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          662 TCTGTGTCATCTGGGT 677
Db          18 TCTGTGTCATCTGAGT 3

RESULT 1351
US-10-702-817-9
; Sequence 9, Application US/10702817
; Publication No. US20040147471A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; TITLE OF INVENTION: ANTISENSE MODULATION OF TNFR1 EXPRESSION
; FILE REFERENCE: ISPH-0797
; CURRENT APPLICATION NUMBER: US/10/702, 817
; CURRENT FILING DATE: 2003-11-06
; PRIOR APPLICATION NUMBER: US 09/106, 038
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: PCT/US99/13763
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 09/695,451
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 247
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-702-817-9

Query Match          0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          105 CCTCTCTGTCTGCTTT 120
Db          3 CCTCTCTCTGCTTT 18

RESULT 1352
US-10-509-009-22/c
; Sequence 22, Application US/10509009
; Publication No. US20050202430A1
; GENERAL INFORMATION:
; APPLICANT: Chiquet-Ehrismann, Ruth
; APPLICANT: Scherberich, Arnaud
; TITLE OF INVENTION: TENASCIN-W COMPOSITIONS AND USES THEREOF
; FILE REFERENCE: 1/32411A/USN/FWI
; CURRENT APPLICATION NUMBER: US/10/509, 009
; CURRENT FILING DATE: 2004-09-24
; PRIOR APPLICATION NUMBER: PCT/EP03/03150
```

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; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: GB0207224.7
; PRIOR FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: (1)...(18)
; OTHER INFORMATION: hTNF6
US-10-509-009-22

Query Match          0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          1276 ACCACCATCTCCACAG 1291
Db          16 ACCACCTCTCCACAG 1

RESULT 1353
US-10-951-303-3013/C
; Sequence 3013, Application US/10951303
; Publication No. US20050227937A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related
; FILE REFERENCE: MBH00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/10/951,303
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/09/685,664
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3013
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-951-303-3013

Query Match          0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          662 TCTGTGTCATCTGGGT 677
Db          18 TCTGTGTCATCTGAGT 3

RESULT 1354
US-10-750-185-14622
; Sequence 14622, Application US/10750185
; Publication No. US2005026603A1
; GENERAL INFORMATION:
; APPLICANT: MMT GENOMICS, INC.
; APPLICANT: Denise, Sue K.
; APPLICANT: Kerr, Richard
; APPLICANT: ROSENFELD, David
```

APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14622
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Forward Primer
US-10-750-185-14622

Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 720 CACAGAGCACCATGCCAG 737
|||||:|
Db 1 CACAGAGCAGTGCACG 18

RESULT 1355
US-10-750-623-14622
Sequence 14622, Application US/10750623
Publication No. US2005028753A1
GENERAL INFORMATION:
APPLICANT: MMT GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14622
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Forward Primer
US-10-750-623-14622

Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 720 CACAGAGCACCATGCCAG 737
|||||:|
Db 1 CACAGAGCAGTGCACG 18

RESULT 1356
US-10-310-914A-72534
Sequence 72534, Application US/10310914A
Publication No. US2006000322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shlier, Kvuza
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 72534
LENGTH: 18
TYPE: RNA
ORGANISM: Human
US-10-310-914A-72534

Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 75.0%; Pred. No. 1e+03;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 151 CAGGACTGCTGCGAC 166
|||||:|
Db 2 CAGGCTCUCGUCGACG 17

RESULT 1357
US-10-310-914A-183276/C
Sequence 183276, Application US/10310914A
Publication No. US2006000322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shlier, Kvuza
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 183276
LENGTH: 18
TYPE: RNA
ORGANISM: Human
US-10-310-914A-183276

Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 826 TTCCTCCCTGCTGG 841
|||||:|
Db 18 TTCCTCAGCTGCTGG 3

RESULT 1358
US-10-310-914A-199415
Sequence 199415, Application US/10310914A
Publication No. US2006000322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shlier, Kvuza
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 199415
LENGTH: 18
TYPE: RNA
ORGANISM: Human
US-10-310-914A-199415

Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1e+03;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;


```

Qy      999  CTTCCACATCTCTTC 1014
Db      18  CTTCCCATCTTCTTC 3

RESULT 1364
US-10-310-914A-441528/c
; Sequence 441528, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzaat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 441528
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-441528

Query Match      0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      895  CCGGAGACTCCTCTG 910
Db      18  CCGGAGACTCCTCTG 3

RESULT 1365
US-10-310-914A-448431
; Sequence 448431, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzaat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 448431
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-448431

Query Match      0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      15  GCGGCGAGGCGGCGAG 30
Db      3  GCGGCGAGGCGGCGG 18

RESULT 1366
US-10-310-914A-572242/c
; Sequence 572242, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzaat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01

```

```

; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 572242
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-572242

Query Match      0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      835  CTGCTGTGATTGGCT 850
Db      18  CTGCTGTGATTGGCT 3

RESULT 1367
US-10-310-914A-581385
; Sequence 581385, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzaat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 581385
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-581385

Query Match      0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      727  ACCATGCCAGCAGAG 742
Db      2  ACCAGGCCAGCAGAG 17

RESULT 1368
US-10-310-914A-629984
; Sequence 629984, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzaat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 629984
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-629984

Query Match      0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1306  GAGGAGGAGCCAGAG 1321

```


Db 3 CGCCGCGCCGCGCC 18

RESULT 1374

US-10-310-914A-816050/C
; Sequence 816050, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 816050
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-816050

Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1;

QY 667 GTCATCTGGGCTCTGG 682

Db 17 CTCATTGGCTCTGG 2

RESULT 1375

US-10-310-914A-816837
; Sequence 816837, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 816837
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-816837

Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 75.0%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;
Matches 12; Conservative 3; Mismatches 1;

QY 687 CCTGCTGGCCTTCCCC 702

Db 1 CCUGCGGCGCGCCCC 16

RESULT 1376

US-10-310-914A-824133/C
; Sequence 824133, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 824133
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-824133

Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1;

QY 1283 TCTCCACAGTGTGGG 1298

Db 16 TCTCCAGAGTGTGGG 1

RESULT 1377

US-10-310-914A-824134/C
; Sequence 824134, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 824134
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-824134

Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1;

QY 1283 TCTCCACAGTGTGGG 1298

Db 16 TCTCCAGAGTGTGGG 1

RESULT 1378

US-10-310-914A-872243
; Sequence 872243, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 872243
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-872243

Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 81.2%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;
Matches 13; Conservative 2; Mismatches 1;

QY 287 TGCAACGAGCTGGCA 302

Db 3 UGCACCGAGCCUGGCA 18

```
RESULT 1379
US-10-310-914A-879849/c
; Sequence 879849, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; NUMBER OF SEQ ID NOS: 2002-12-06
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 879849
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-879849

Query Match
Best Local Similarity 93.8%; Score 14.4; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1421 ATGTCCTCTCTAGGC 1436
DB 17 ATGTCCTCTCTAGGC 2

RESULT 1380
US-10-310-914A-902588/c
; Sequence 902588, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; NUMBER OF SEQ ID NOS: 2002-12-06
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 902588
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-902588

Query Match
Best Local Similarity 93.8%; Score 14.4; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1148 GTCGCGCTTCACGA 1163
DB 16 GTTGGGCTTCACGA 1

RESULT 1381
US-10-310-914A-915824/c
; Sequence 915824, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; NUMBER OF SEQ ID NOS: 2002-12-06
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 915824
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-915824
```

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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 915824
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-915824

Query Match
Best Local Similarity 93.8%; Score 14.4; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1710 AATGATTCATTCT 1725
DB 17 AAGCATTCATTCT 2

RESULT 1382
US-10-310-914A-951224
; Sequence 951224, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; NUMBER OF SEQ ID NOS: 2002-12-06
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 951224
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-951224

Query Match
Best Local Similarity 93.8%; Score 14.4; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1430 CCTAGCCACAGGCC 1445
DB 2 CCAAGCCACAGGCC 17

RESULT 1383
US-10-310-914A-969334/c
; Sequence 969334, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; NUMBER OF SEQ ID NOS: 2002-12-06
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 969334
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-969334

Query Match
Best Local Similarity 93.8%; Score 14.4; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 619 CCCCTCAGCCCGGC 634
DB 17 CCTCTCAGCCCGGC 2
```

```
RESULT 1384
US-10-310-914A-1095570
; Sequence 1095570, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1095570
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1095570

Query Match          0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 62.5%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      676 GTCCTGCTCTCTGCG 691
      1 GUCCUGCCUCUCUGC 16
      |||:|:|:|:|:|:|
      |||:|:|:|:|:|:|

RESULT 1385
US-10-310-914A-1127203/c
; Sequence 1127203, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1127203
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1127203

Query Match          0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      990 CTGGCTGCGCTTCCAC 1005
      17 CTGGCTGCGCTTCCAC 2
      |||:|:|:|:|:|:|
      |||:|:|:|:|:|:|

RESULT 1386
US-10-310-914A-1197826/c
; Sequence 1197826, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 1197826
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1197826

Query Match          0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 81.2%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1455 TGCAGCCCCCACTGCC 1470
      3 UCCAGCCCCCACTGCC 18
      :|||:|:|:|:|:|:|
      :|||:|:|:|:|:|:|

; SEQ ID NO 1197826
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1197826

Query Match          0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      728 CCATGCCCAGCAGAGT 743
      16 CCATGCCCAGCAGAGT 1
      |||:|:|:|:|:|:|
      |||:|:|:|:|:|:|

RESULT 1387
US-10-310-914A-1202881/c
; Sequence 1202881, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1202881
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1202881

Query Match          0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1306 GAGGAGGAGCCAGNG 1321
      18 GAGGAGGAGCCAGNG 3
      |||:|:|:|:|:|:|
      |||:|:|:|:|:|:|

RESULT 1388
US-10-310-914A-1218505
; Sequence 1218505, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1218505
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1218505

Query Match          0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 81.2%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1455 TGCAGCCCCCACTGCC 1470
      3 UCCAGCCCCCACTGCC 18
      :|||:|:|:|:|:|:|
      :|||:|:~|:|:|:|:|
```



```
RESULT 1389
US-10-310-914A-123356
; Sequence 123356, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 123356
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-123356

Query Match
Best Local Similarity 93.8%; Score 14.4; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 132 GAGCCCGAGGCCGAG 147
Db 2 GAGCCCGAGGCCGAG 17

RESULT 1390
US-10-310-914A-124978
; Sequence 124978, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 124978
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-124978

Query Match
Best Local Similarity 87.5%; Score 14.4; DB 1; Length 18;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 628 CCCCGCTGTGAGCCA 643
Db 1 CCCCGCTGTGAGCCA 16

RESULT 1391
US-10-310-914A-1252017/c
; Sequence 1252017, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 1252017
```

```
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1252017

Query Match
Best Local Similarity 93.8%; Score 14.4; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1266 CCGCTGAGAGCACAC 1281
Db 18 CCGCTGAGAGCACAC 3

RESULT 1392
US-10-310-914A-1376270
; Sequence 1376270, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 1376270
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1376270

Query Match
Best Local Similarity 87.5%; Score 14.4; DB 1; Length 18;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 619 CCCCTCAGCCCGGCG 634
Db 1 CCCCTCAGCCCGGCG 16

RESULT 1393
US-11-090-617-509
; Sequence 509, Application US/11090617
; Publication No. US20060024692A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yusuke
; APPLICANT: Daigo, Yataro
; TITLE OF INVENTION: METHOD FOR DIAGNOSING NON-SMALL CELL LUNG CANCERS
; FILE REFERENCE: 082368-003500US
; CURRENT APPLICATION NUMBER: US/11/090.617
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: PCT/JP04/04075
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: PCT/JP03/12072
; PRIOR FILING DATE: 2003-09-22
; PRIOR APPLICATION NUMBER: US 60/555,757
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: US 60/466,100
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/451,374
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/414,673
; PRIOR FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 706
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 509
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial
```

```
; FEATURE:
; OTHER INFORMATION: Artificially synthesized S-oligonucleotide sequence for antisense
; OTHER INFORMATION: method
US-11-090-617-509
Query Match      0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1277 CCACCATCTCCACAGT 1292
Db      3 CCGCCATCTCCACAGT 18

RESULT 1394
US-09-847-601B-5
; Sequence 5, Application US/09847601B
; Publication No. US20050096282A1
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/847,601B
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-847-601B-5

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 71.4%; Pred. No. 8e+02;
Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      689 TGCTGGCGCTGCC 702
Db      1 UGCTUGGCTCCUCCCC 14

RESULT 1395
US-09-930-503-15/c
; Sequence 15, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREOF
; FILE REFERENCE: 39245-173913
; CURRENT APPLICATION NUMBER: US/09/930,503
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-15
Query Match      0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      209 AAATGATATACGTC 222
Db      14 AAATGATATACGTC 1

RESULT 1396
US-09-866-108-6965
; Sequence 6965, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ABOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecwica Sequence Listing Engine
; SEQ ID NO 6965
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-6965

Query Match      0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      28 CAGTGCATCCAGAA 41
          |||||
```

```
Db      4  CAGTCATCCAGAA 17

RESULT 1397
US-09-866-108-6969
; Sequence 6969, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wenheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ASCMCA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 6969
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-6969

Query Match      0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      29  AGTCATCCAGAG 42
Db      1  AGTCATCCAGAG 14

RESULT 1398
US-09-930-423-1550/C
; Sequence 1550, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry

US-09-930-423-1550
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MHB00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1550
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-1550

Query Match      0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1277 CCACCATCTCCACA 1290
Db      16  CCACCATCTCCACA 3

RESULT 1399
US-09-780-164-867
; Sequence 867, Application US/09780164
; Publication No. US20030092646A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
; FILE REFERENCE: 460/010
; CURRENT APPLICATION NUMBER: US/09/780,164
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/185,516
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 867
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-164-867

Query Match      0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 57.1%; Pred. No. 1e+03;
Matches 8; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy      803 TCTGTGTGACTGTG 816
Db      1  UCUGUGACUGUG 14

RESULT 1400
US-09-745-237A-1550/C
; Sequence 1550, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1550
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-1550
```

Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1277 CCACCATCTCCACA 1290
DB 16 CCACCATCTCCACA 3

RESULT 1401
US-10-339-782-265
; Sequence 265, Application US/10339782
; Publication No. US20030166026A1
; GENERAL INFORMATION:
; APPLICANT: Lynx Therapeutics, Inc.
; APPLICANT: Goodman, Laurie J.
; APPLICANT: Bowen, Benjamin A.
; TITLE OF INVENTION: Identification of Specific Biomarkers for Breast Cancer Cells
; FILE REFERENCE: 37-000110US
; CURRENT APPLICATION NUMBER: US/10/339,782
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 265
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-339-782-265

Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 617 ATCCCTCCAGCCC 630
DB 2 ATCCCTCCAGCCC 15

RESULT 1402
US-10-712-672-343
; Sequence 343, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MBH00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 343
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-343

Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 64.3%; Pred. No. 1e+03;
Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1689 CCAGCTTTCTCTCA 1702
DB 2 CCAGCTTTCTCTCA 15

RESULT 1403
US-10-712-672-344
; Sequence 344, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MBH00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 344
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-344

Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 64.3%; Pred. No. 1e+03;
Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1689 CCAGCTTTCTCTCA 1702
DB 1 CCAGCTTTCTCTCA 14

RESULT 1404
US-10-723-361-6965
; Sequence 6965, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART ANI
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30

Remaining Prior Application data removed - See File Wrapper or PALM.

;; NUMBER OF SEQ ID NOS: 15755
;; SOFTWARE: Aeomica Sequence Listing Engine
;; SEQ ID NO: 6965
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-723-361-6965

Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 28 CAGTCATCCAGAA 41
DB 4 CAGTCATCCAGAA 17

RESULT 1405

US-10-723-361-6969
; Sequence 6969, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:

;; APPLICANT: GU, Yizhong
;; APPLICANT: PENN, Sharon G.
;; APPLICANT: HANZEL, David K.
;; APPLICANT: RANK, David R.
;; APPLICANT: CHEN, Wensheng
;; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MROSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723, 361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO: 6969
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-6969

US-10-723-361-6969

Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 29 AGTCATCCAGAG 42
DB 1 AGTCATCCAGAG 14

RESULT 1406

US-11-090-866-22

;; Sequence 22, Application US/11090866
;; Publication No. US20050164294A1
;; GENERAL INFORMATION:

;; APPLICANT: Anderson, John P.
;; APPLICANT: Basi, Guripbal
;; APPLICANT: Doane, Minh Tam
;; APPLICANT: Frigon, Normand
;; APPLICANT: John, Varghese
;; APPLICANT: Power, Michael
;; APPLICANT: Sinha, Sukanto
;; APPLICANT: Tatsuno, Gwen
;; APPLICANT: Tung, Jay
;; APPLICANT: Wang, Shuwen
;; APPLICANT: McConlogue, Lisa

; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C12
; CURRENT APPLICATION NUMBER: US/11/090, 866
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 22
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

OTHER INFORMATION: Degenerate oligonucleotide primer

NAME/KEY: misc_feature

LOCATION: (1)..(17)

OTHER INFORMATION: n = A,T,C or G

US-11-090-866-22

Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1306 GAGGAGAGCCAGAGA 1322
DB 1 GAGGAGAGCCAGAGA 17

RESULT 1407

US-11-089-918-22
; Sequence 22, Application US/11089918
; Publication No. US20050164327A1
; GENERAL INFORMATION:

;; APPLICANT: Anderson, John P.
;; APPLICANT: Basi, Guripbal
;; APPLICANT: Doane, Minh Tam
;; APPLICANT: Frigon, Normand
;; APPLICANT: John, Varghese
;; APPLICANT: Power, Michael
;; APPLICANT: Sinha, Sukanto
;; APPLICANT: Tatsuno, Gwen
;; APPLICANT: Tung, Jay
;; APPLICANT: Wang, Shuwen
;; APPLICANT: McConlogue, Lisa

; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C9
; CURRENT APPLICATION NUMBER: US/11/089, 918

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; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Degenerate oligonucleotide primer
; NAME/KEY: misc_feature
; LOCATION: (1)...(17)
; OTHER INFORMATION: n = A,T,C or G
US-11-089-918-22

Query Match          0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1306 GAGGAGAGCCGAGGA 1322
DB      1 GAYGARAGCCGAGGA 17
      |||:|||||
RESULT 1408
US-11-069-377-22
; Sequence 22, Application US/11069377
; Publication No. US20050170489A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEM2C8
; CURRENT APPLICATION NUMBER: US/11/069,377
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Degenerate oligonucleotide primer
; NAME/KEY: misc_feature
; LOCATION: (1)...(17)
; OTHER INFORMATION: n = A,T,C or G
US-11-090-872-22
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; LOCATION: (1)...(17)
; OTHER INFORMATION: n = A,T,C or G
US-11-069-377-22

Query Match          0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1306 GAGGAGAGCCGAGGA 1322
DB      1 GAYGARAGCCGAGGA 17
      |||:|||||
RESULT 1409
US-11-090-872-22
; Sequence 22, Application US/11090872
; Publication No. US2005017888A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEM2C11
; CURRENT APPLICATION NUMBER: US/11/090,872
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Degenerate oligonucleotide primer
; NAME/KEY: misc_feature
; LOCATION: (1)...(17)
; OTHER INFORMATION: n = A,T,C or G
US-11-090-872-22

Query Match          0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1306 GAGGAGAGCCGAGGA 1322
DB      1 GAYGARAGCCGAGGA 17
      |||:|||||
RESULT 1410
US-11-090-399-22
; Sequence 22, Application US/11090399
; Publication No. US20050196839A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
```

```
APPLICANT: Baqi, Guribbal
APPLICANT: Doane, Minh Tam
APPLICANT: Frigon, Normand
APPLICANT: John, Varghese
APPLICANT: Power, Michael
APPLICANT: Sinha, Sukanto
APPLICANT: Tatsuno, Gwen
APPLICANT: Tung, Jay
APPLICANT: Wang, Shuwen
APPLICANT: McConlogue, Lisa
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
FILE REFERENCE: 228-US-NEW2C10
CURRENT APPLICATION NUMBER: US/11/090,399
CURRENT FILING DATE: 2005-03-25
PRIOR APPLICATION NUMBER: US 09/723,722
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 09/501,708
PRIOR FILING DATE: 2000-02-10
PRIOR APPLICATION NUMBER: US 09/471,669
PRIOR FILING DATE: 1999-12-24
PRIOR APPLICATION NUMBER: 60/119,571
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/139,172
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 104
SOFTWARE: PasteSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 17
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Degenerate oligonucleotide primer
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(17)
OTHER INFORMATION: n = A,T,C or G
US-11-090-399-22

Query Match      0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Cy      1306 GAGAGAGCGCAGGAGA 1322
Db      1 GAYGARGAGCCGAGGAGA 17

RESULT 1411
US-09-866-108-2756
Sequence 2756, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: ABOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
```

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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 2756
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-2756

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy      1196 GCGACTATGAGGCGCTG 1212
Db      1 GCGAGTATGAGAGCTG 17

RESULT 1412
US-09-866-108-7674/c
Sequence 7674, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: ABOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 7674
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-7674

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1404 CTCGAGCTTCTCCCA 1420
DB 17 CTCGCTTCTTCTCA 1

RESULT 1413
US-09-864-785-336
Sequence 336, Application US/09864785
Patent No. US20020177568A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Stinchcomb, Dan
APPLICANT: Draper, Ken
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
FILE REFERENCE: 400/022 (MBH00-812-D)
CURRENT APPLICATION NUMBER: US/09/864,785
CURRENT FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 3929
SOFTWARE: PatentIn version 3.0
SEQ ID NO 336
LENGTH: 17
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-336

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 135 CCCGAGCGCCGACAC 151
DB 1 CCCGAGCGCCGACCC 17

RESULT 1414
US-09-961-077-765/C
Sequence 765, Application US/09961077
Publication No. US20030014775A1
GENERAL INFORMATION:
APPLICANT: Zwick, Michael G.
Edington, Brent E.
McSwiggen, James A.
Merlo, Patricia Ann Owens
Guo, Lining
Skokut, Thomas A.
Young, Scott A.

Folkerts, Otto
Merlo, Donald J.
TITLE OF INVENTION: COMPOSITION AND METHODS FOR
MODULATION OF GENE EXPRESSION
IN PLANTS
NUMBER OF SEQUENCES: 1263
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/961,077
FILING DATE: 21-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/679,645
FILING DATE: July 12, 1996
APPLICATION NUMBER: 60/001,135
FILING DATE: July 13, 1995
APPLICATION NUMBER: 08/300,726
FILING DATE: September 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 219/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 765:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 765:
US-09-961-077-765

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 636 GTCAGCCAGCGACCA 652
DB 17 GTCAGCCAGCGACCA 1

RESULT 1415
US-09-780-533A-1580
Sequence 1580, Application US/09780533A
Publication No. US20030060611A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: Chowrira, Bharat
APPLICANT: Haeblerli, Pete
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
FILE REFERENCE: MBH00,878-A (400/011)
CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,797
PRIOR FILING DATE: 2000-02-11

NUMBER OF SEQ ID NOS: 6679
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1580
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-780-533A-1580

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 1.1e+03;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 545 CCATCGCCGCTGTCTTC 561
Db 1 CCAUCCCGGCGUCUC 17

RESULT 1416
US-09-780-533A-2357/c
Sequence 2357, Application US/09780533A
Publication No. US20030060611A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: McSwigen, Jim
APPLICANT: Chowitra, Bharat
APPLICANT: Haeblerli, Pete
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
FILE REFERENCE: MBH00-878-A (400/011)
CURRENT APPLICATION NUMBER: US/09/780,533A
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,797
NUMBER OF SEQ ID NOS: 6679
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2357
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-780-533A-2357

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1003 CACATCTTCTTCTCTCT 1019
Db 17 CTCCTCTTCTTCTCTCT 1

RESULT 1417
US-09-780-533A-2363
Sequence 2363, Application US/09780533A
Publication No. US20030060611A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: McSwigen, Jim
APPLICANT: Chowitra, Bharat
APPLICANT: Haeblerli, Pete
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
FILE REFERENCE: MBH00-878-A (400/011)
CURRENT APPLICATION NUMBER: US/09/780,533A
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,797
NUMBER OF SEQ ID NOS: 6679
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2363
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-780-533A-2363

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1306 GAGGAGGAGGAGGAGGA 1322
Db 1 GAGGAGGAGGAGGAGGA 17

RESULT 1418
US-09-877-478-2345
Sequence 2345, Application US/09877478
Publication No. US20030068301A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Draper, Kenneth
APPLICANT: Blatt, Larry
APPLICANT: McSwigen, Jim
APPLICANT: Morrissey, Dave
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REFERENCE: MBH00-845-H (400/029)
CURRENT APPLICATION NUMBER: US/09/877,478
PRIOR FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: US 07/882,712
PRIOR FILING DATE: 1992-05-14
PRIOR APPLICATION NUMBER: US 09/531,025
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: US 09/636,385
PRIOR FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: US 09/636,347
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 08/193,627
PRIOR FILING DATE: 1994-02-07
PRIOR APPLICATION NUMBER: US 08/433,993
PRIOR FILING DATE: 1995-05-04
PRIOR APPLICATION NUMBER: US 08/434,504
PRIOR FILING DATE: 1995-05-04
PRIOR APPLICATION NUMBER: US 09/436,430
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 6586
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2345
LENGTH: 17
TYPE: RNA
ORGANISM: Hepatitis B virus
US-09-877-478-2345

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.1e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1265 GCGCGCTGGAGACACC 1281
Db 1 GUGGCAUGGAGACACC 17

RESULT 1419
US-09-877-478-2346
Sequence 2346, Application US/09877478
Publication No. US20030068301A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Draper, Kenneth
APPLICANT: Blatt, Larry
APPLICANT: McSwigen, Jim
APPLICANT: Morrissey, Dave
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REFERENCE: MBH00-845-H (400/029)
CURRENT APPLICATION NUMBER: US/09/877,478
PRIOR FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: US 07/882,712
PRIOR FILING DATE: 1992-05-14

```
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2346
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
; US-09-877-478-2346
```

```
Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 1.1e+03;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1267 CGCCTGGAGACACCAT 1283
Db      1 CGCAUGGAGACACCGU 17
```

```
RESULT 1420
US-09-848-754A-243/c
; Sequence 243, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MEBB00-958-1 (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 243
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-848-754A-243
```

```
Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1313 AGCCAGAGACGCGCCC 1329
Db      17 AGCAAGAGAGCGGCC 1
```

```
RESULT 1421
US-09-848-754A-891/c
; Sequence 891, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MEBB00-958-1 (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 891
```

```
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-848-754A-891
```

```
Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1695 TTTCCTCAAGAGCCCA 1711
Db      17 TTTCCTCAAGAGCCCA 1
```

```
RESULT 1422
US-09-848-754A-990/c
; Sequence 990, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MEBB00-958-1 (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 990
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-848-754A-990
```

```
Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      310 CTTTGGGAGCTGCCTA 326
Db      17 CTTTGGGAGCTGCCA 1
```

```
RESULT 1423
US-09-848-754A-1483/c
; Sequence 1483, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MEBB00-958-1 (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1483
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-848-754A-1483
```

```
Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1224 CACCCGATATCCAGA 1240
Db      17 CACCCGATGCTCCAGA 1
```

```
RESULT 1424
US-09-848-754A-1525/c
; Sequence 1525, Application US/09848754A
```

```
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MHB00-958-1 (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1525
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-1525

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1646 CAATCTGAACTTTG 1662
DB      17 CAACTCAGGAAGCTTTG 1

RESULT 1425
US-09-776-474-250/C
; Sequence 250, Application US/09776474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Bocher, Robert
; APPLICANT: Holman, Patricia
; APPLICANT: Faltacy, Ali
; APPLICANT: McSwigen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK
; FILE REFERENCE: MHB00-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776,474
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 250
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-250

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1369 TCTTCACGAAGTGC 1385
DB      17 TCTTCAGGAAGTGTCTC 1

RESULT 1426
US-09-930-423-839
; Sequence 839, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwigen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MHB00-918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
```

```
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 839
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-839

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 1.1e+03;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1346 CCTGACCTGACCTCC 1362
DB      1 CCTCGACACACCCUCC 17

RESULT 1427
US-09-827-395A-381
; Sequence 381, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwigen
; APPLICANT: Bharat Chowitra
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor Ge
; FILE REFERENCE: MHB00-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 381
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-827-395A-381

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 1.1e+03;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      1084 TGGCTGGCAGTGC 1100
DB      1 UGGGUGGCGGACCCUC 17

RESULT 1428
US-09-740-332-964/C
; Sequence 964, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 964
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
```

US-09-740-332-964

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1254 GTACAAAGTCAGCGCC 1270
DB 17 GTACAAAGTCAGCGCC 1

RESULT 1429

US-09-745-237A-839
; Sequence 839, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blact, Larry
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBH00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 839
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-839

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 1.1e+03;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1346 CCCTGACCTGACCTCC 1362
DB 1 CCCTGACCTGACCTCC 17

RESULT 1430

US-09-817-879-964/c
; Sequence 964, Application US/09817879
; Publication No. US2003017311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBH00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 964
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-964

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1254 GTACAAAGTCAGCGCC 1270
DB 17 GTACAAAGTCAGCGCC 1

RESULT 1431

US-10-060-756A-4268/c

; Sequence 4268, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Neomica Sequence Listing Engine
; SEQ ID NO 4268
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-4268

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1089 GGCCATGAGCTCCACCA 1105
DB 17 GGCCATGAGCTCCACCA 1

RESULT 1432

US-10-156-306-6951/c
; Sequence 6951, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6951
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-6951

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1402 AGCTTCAGCTTCCTC 1418
DB 17 AGCTTCAGCTTCCTC 1

RESULT 1433
US-10-061-201-1453/c

```
; Sequence 1453, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1453
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-061-201-1453

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1444 CCTTGGCAGTGCAGC 1460
Db      17 CCTTTGCAGTCCAGC 1

RESULT 1434
US-10-430-882-381
; Sequence 381, Application US/10430882
; Publication No. US20030203870A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggan
; APPLICANT: Bharat Chawitra
; APPLICANT: Peter Haebel
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor G
; FILE REFERENCE: MBH00-878-H (400/112)
; CURRENT APPLICATION NUMBER: US/10/430,882
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 09/827,395
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PCT/US01/04273
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/10512
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 381
; LENGTH: 17
```

```
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-10-430-882-381

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 1.1e+03;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      1084 TGCGTGGCCATGAGCTC 1100
Db      1 UGCGUGCGCCUGACCTC 17

RESULT 1435
US-10-297-068-1039
; Sequence 1039, Application US/10297068
; Publication No. US20030228585A1
; GENERAL INFORMATION:
; APPLICANT: INOKO, Hidetoshi
; APPLICANT: KAGIYA, Taeko
; APPLICANT: ICHIHARA, Tatsuo
; APPLICANT: Matsumura, Yoshiyuki
; APPLICANT: MORIYA, Shogo
; APPLICANT: NISHIDA, Michio
; TITLE OF INVENTION: KIT AND METHOD FOR DETERMINING HLA TYPES
; FILE REFERENCE: 13140P1174
; CURRENT APPLICATION NUMBER: US/10/297,068
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: JP 2000-164798
; PRIOR FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 1298
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1039
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: capture
; US-10-297-068-1039

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1299 GCGCCACGAGGAGGAGC 1315
Db      1 GCGCCATGAGGCGGAGC 17

RESULT 1436
US-10-342-902-2345
; Sequence 2345, Application US/10342902
; Publication No. US20040054156A1
; GENERAL INFORMATION:
; APPLICANT: Sirta Therapeutics, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggan, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: 400/075 (MBH00-845-1)
; CURRENT APPLICATION NUMBER: US/10/342,902
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 09/877,478
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
```

PRIOR APPLICATION NUMBER: US 07/882,712
 PRIOR FILING DATE: 1992-05-14
 PRIOR APPLICATION NUMBER: US 09/436,430
 PRIOR FILING DATE: 1999-11-08
 NUMBER OF SEQ ID NOS: 6592
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 2345
 LENGTH: 17
 TYPE: RNA
 ORGANISM: Hepatitis B virus
 US-10-342-902-2345

Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 1.1e+03;
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1265 GCGCGCTGGAGACCAACC 1281
 DB 1 GCGCAUGGAGACCAACC 17

RESULT 1437
 US-10-342-902-2346
 Sequence 2346, Application US/10342902
 Publication No. US20040054156A1
 GENERAL INFORMATION:
 APPLICANT: Sima Therapeutics, Inc.
 APPLICANT: Draper, Kenneth
 APPLICANT: Blatt, Larry
 APPLICANT: McSwiggen, Jim
 APPLICANT: Morrissey, Dave
 TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
 FILE REFERENCE: 400/075 (MBH00-845-1)
 CURRENT APPLICATION NUMBER: US/10/342,902
 PRIOR FILING DATE: 2003-01-15
 PRIOR APPLICATION NUMBER: US 09/877,478
 PRIOR FILING DATE: 2001-06-08
 PRIOR APPLICATION NUMBER: US 09/531,025
 PRIOR FILING DATE: 2000-03-20
 PRIOR APPLICATION NUMBER: US 09/636,385
 PRIOR FILING DATE: 2000-08-09
 PRIOR APPLICATION NUMBER: US 09/696,347
 PRIOR FILING DATE: 2000-10-24
 PRIOR APPLICATION NUMBER: US 08/193,627
 PRIOR FILING DATE: 1994-02-07
 PRIOR APPLICATION NUMBER: US 07/882,712
 PRIOR FILING DATE: 1992-05-14
 PRIOR APPLICATION NUMBER: US 09/436,430
 PRIOR FILING DATE: 1999-11-08
 NUMBER OF SEQ ID NOS: 6592
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 2346
 LENGTH: 17
 TYPE: RNA
 ORGANISM: Hepatitis B virus
 US-10-342-902-2346

Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 76.5%; Pred. No. 1.1e+03;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1267 GCGCTGGAGACCAACC 1283
 DB 1 GCGCAUGGAGACCAACC 17

RESULT 1438
 US-10-138-674-1714/c
 Sequence 1714, Application US/10138674
 Publication No. US20040077565A1
 GENERAL INFORMATION:
 APPLICANT: Ribozyne Pharmaceuticals, Inc.
 APPLICANT: Pavco, Pam

APPLICANT: McSwiggen, Jim
 APPLICANT: Stinchcomb, Dan
 APPLICANT: Escobedo, Jaime
 TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
 TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
 FILE REFERENCE: MBH00-876-N (400/049)
 CURRENT APPLICATION NUMBER: US/10/138,674
 CURRENT FILING DATE: 2002-05-03
 NUMBER OF SEQ ID NOS: 20822
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 1714
 LENGTH: 17
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-10-138-674-1714

Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 714 CTCACCAAGAGAGCA 730
 DB 17 CACACCAAGAGAGCA 1

RESULT 1439
 US-10-138-674-1886/c
 Sequence 1886, Application US/10138674
 Publication No. US20040077565A1
 GENERAL INFORMATION:
 APPLICANT: Ribozyne Pharmaceuticals, Inc.
 APPLICANT: McSwiggen, Jim
 APPLICANT: Stinchcomb, Dan
 APPLICANT: Escobedo, Jaime
 TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
 TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
 FILE REFERENCE: MBH00-876-N (400/049)
 CURRENT APPLICATION NUMBER: US/10/138,674
 CURRENT FILING DATE: 2002-05-03
 NUMBER OF SEQ ID NOS: 20822
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 1886
 LENGTH: 17
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-10-138-674-1886

Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1505 TTCATCTGACCATCA 1521
 DB 17 TTCATCTGACCATCA 1

RESULT 1440
 US-10-138-674-6345/c
 Sequence 6345, Application US/10138674
 Publication No. US20040077565A1
 GENERAL INFORMATION:
 APPLICANT: Ribozyne Pharmaceuticals, Inc.
 APPLICANT: Pavco, Pam
 APPLICANT: McSwiggen, Jim
 APPLICANT: Stinchcomb, Dan
 APPLICANT: Escobedo, Jaime
 TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
 TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
 FILE REFERENCE: MBH00-876-N (400/049)
 CURRENT APPLICATION NUMBER: US/10/138,674
 CURRENT FILING DATE: 2002-05-03
 NUMBER OF SEQ ID NOS: 20822

SOFTWARE: PatentIn version 3.0
SEQ ID NO 6345
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-10-138-674-6345

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 713 ACTCACCACAGAGACC 729
Db 17 ACACACCAGAGAGACC 1

RESULT 1441
US-10-287-949A-1714/c
Sequence 1714, Application US/10287949A
Publication No. US20040102389A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwigen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
FILE REFERENCE: MBH00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/287,949A
CURRENT FILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1714
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-10-287-949A-1714

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 714 CTCACCACAGAGACC 730
Db 17 CACAACCAGAGAGACC 1

RESULT 1442
US-10-287-949A-1886/c
Sequence 1886, Application US/10287949A
Publication No. US20040102389A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwigen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
FILE REFERENCE: MBH00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/287,949A
CURRENT FILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1886
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-10-287-949A-1886

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1505 TTCATCTGGAACCATCA 1521
Db 17 TTCATCTGGAATCATGA 1

RESULT 1443
US-10-287-949A-6345/c
Sequence 6345, Application US/10287949A
Publication No. US20040102389A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwigen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
FILE REFERENCE: MBH00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/287,949A
CURRENT FILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6345
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-10-287-949A-6345

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 713 ACTCACCACAGAGACC 729
Db 17 ACACACCAGAGAGACC 1

RESULT 1444
US-10-712-672-345
Sequence 345, Application US/10712672
Publication No. US20040102413A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Chowitra, Bharat
APPLICANT: McSwigen, Jim
APPLICANT: Stinchcomb, Dan
TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
FILE REFERENCE: MBH00-882-C (400/019)
CURRENT APPLICATION NUMBER: US/10/712,672
CURRENT FILING DATE: 2003-11-13
PRIOR APPLICATION NUMBER: US/09/653,225
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/197,769
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/150,713
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 5586
SOFTWARE: PatentIn version 3.0
SEQ ID NO 345
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-10-712-672-345

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 1.1e+03;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 1690 CAGCTTTCCTCAAGAG 1706
Db 1 CAGCTTTCCTCAAGAG 17

```
RESULT 1445
US-10-712-672-506/c
; Sequence 506, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowitira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MHB00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 506
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-506
```

```
Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1450 GCAGGTGCAGCCCCCACC 1466
Db      17  GCAGCAGCAGCCCCCACC 1
```

```
RESULT 1446
US-10-712-672-763
; Sequence 763, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowitira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MHB00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 763
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-763
```

```
Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.1e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1294 GTGGGGGCCCAAGAGGA 1310
Db      1  GTGGGGGCCCAAGAGGA 17
```

```
RESULT 1447
US-10-712-672-764
; Sequence 764, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowitira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MHB00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 764
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-764
```

```
Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.1e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1295 TTGGGGGCCCAAGAGAG 1311
Db      1  TTGGGGGCCCAAGAGAG 17
```

```
RESULT 1448
US-10-712-672-765
; Sequence 765, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowitira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MHB00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 765
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-765
```

```
Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1296 GGGGGGCCCAAGAGAGG 1312
Db      1  GGGGGGCCCAAGAGAGG 17
```



```
RESULT 1449
US-10-712-672-766
; Sequence 766, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowitra, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MBH00-882-C (400/019)
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 766
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-766

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy      1297 GGGGCCCGAGGAGA 1313
Db      1 GCGGCCCGCGAGAGA 17

RESULT 1450
US-10-669-841-2148
; Sequence 2148, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blact
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patricia, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEP
; FILE REFERENCE: 400/042US (MBH02-249-E)
; CURRENT FILING DATE: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
```

```
;; PRIOR APPLICATION NUMBER: US 09/504,321
;; PRIOR FILING DATE: 2000-02-15
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 16207
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 2148
;; LENGTH: 17
;; TYPE: RNA
;; ORGANISM: Hepatitis B Virus
US-10-669-841-2148

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.1e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Cy      1265 GCGCCCTGAGACCACC 1281
Db      1 GCGCAUGAGACCACC 17

RESULT 1451
US-10-669-841-2149
; Sequence 2149, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blact
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patricia, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEP
; FILE REFERENCE: 400/042US (MBH02-249-E)
; CURRENT FILING DATE: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2149
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B Virus
US-10-669-841-2149

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 1.1e+03;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Cy      1267 GCGCTGAGACCACCAT 1283
```

Db 1 CGCAGGAGGACCCGU 17

```
RESULT 1452
US-10-669-841-3557/c
; Sequence 3557, Application US/10669841
; Publication No. US2004012746A1
GENERAL INFORMATION:
; APPLICANT: Sima Therapeutics, Inc.
; APPLICANT: Lawrence, Blac
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggan
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patrice, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEP
FILE REFERENCE: 400/042US (MHB02-249-E)
CURRENT FILING DATE: 2003-09-23
CURRENT FILING DATE: PCT/US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/335,059
PRIOR FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: US 60/337,055
PRIOR FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 09/817,879
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 09/740,332
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US 09/611,931
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 09/504,321
PRIOR FILING DATE: 2000-02-15
Remaining prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 16207
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3557
LENGTH: 17
TYPE: RNA
ORGANISM: Artificial Sequence
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
FEATURE:
NAME/KEY: misc_feature
LOCATION:
OTHER INFORMATION: oligonucleotide substrate
US-10-669-841-3557

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1254 GTTCAAGTCAGCGGCC 1270
DB 17 GTTCAAGTCAGCGGCC 1

RESULT 1453
US-10-723-361-2756
; Sequence 2756, Application US/10723361
; Publication No. US20040137589A1
GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
```

```
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART ANI
FILE REFERENCE: PB0105
CURRENT FILING DATE: US/10/723,361
CURRENT FILING DATE: 2003-11-26
PRIOR FILING DATE: US 09/866,108
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
Remaining prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 2756
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-10-723-361-2756

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1196 GCGACTATGAGGCGCTG 1212
DB 1 GCGACTATGAGGCGCTG 17

RESULT 1454
US-10-723-361-7674/c
; Sequence 7674, Application US/10723361
; Publication No. US20040137589A1
GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART ANI
FILE REFERENCE: PB0105
CURRENT FILING DATE: US/10/723,361
CURRENT FILING DATE: 2003-11-26
PRIOR FILING DATE: US 09/866,108
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
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;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 15755
;; SOFTWARE: Aeomica Sequence Listing Engine
;; SEQ ID NO: 7674
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-723-361-7674

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1404 CTCGAGCTTCCTCCCA 1420
Db 17 CTCGCTCTCTCTCCA 1

RESULT 1455
US-10-498-462-376
; Sequence 376, Application US/10498462
; Publication No. US20040259175A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Jinjiao
; TITLE OF INVENTION: HUMAN PROSTATE CANCER CANDIDATE PROTEIN 1
; FILE REFERENCE: PB01102
; CURRENT APPLICATION NUMBER: US/10/498,462
; CURRENT FILING DATE: 2004-06-10
; PRIOR APPLICATION NUMBER: US 60/339,764
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/US02/37506
; PRIOR FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 3320
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO: 376
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-498-462-376

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 786 TGAGAAAGTGTACCA 802
Db 1 TGAGAAAGTGTCCACA 17

RESULT 1456
US-10-498-462-1855
; Sequence 1855, Application US/10498462
; Publication No. US20040259175A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Jinjiao
; TITLE OF INVENTION: HUMAN PROSTATE CANCER CANDIDATE PROTEIN 1
; FILE REFERENCE: PB01102
; CURRENT APPLICATION NUMBER: US/10/498,462
; CURRENT FILING DATE: 2004-06-10
; PRIOR APPLICATION NUMBER: US 60/339,764
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/US02/37506

;; PRIOR FILING DATE: 2002-11-22
;; NUMBER OF SEQ ID NOS: 3320
;; SOFTWARE: Aeomica Sequence Listing Engine
;; SEQ ID NO: 1855
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-498-462-1855

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 987 CTCGCTGCTGCCCTCC 1003
Db 1 CTCGCTGCTGCTCCTCC 17

RESULT 1457
US-10-498-462-2044/c
; Sequence 2044, Application US/10498462
; Publication No. US20040259175A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Jinjiao
; TITLE OF INVENTION: HUMAN PROSTATE CANCER CANDIDATE PROTEIN 1
; FILE REFERENCE: PB01102
; CURRENT APPLICATION NUMBER: US/10/498,462
; CURRENT FILING DATE: 2004-06-10
; PRIOR APPLICATION NUMBER: US 60/339,764
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/US02/37506
; PRIOR FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 3320
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO: 2044
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-498-462-2044

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 255 CTCGACTTAACACTCGG 271
Db 17 CTCCTTAACACACGCG 1

RESULT 1458
US-10-890-776A-4268/c
; Sequence 4268, Application US/10890776A
; Publication No. US20050129683A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB01177
; CURRENT APPLICATION NUMBER: US/10/890,776A
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 10/060,756
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4809
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 4268
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-890-776a-4268

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1089 GGCCTAGAGCTCCACCA 1105
DB      17  GGCCTAGAGCTCCACCA 1

RESULT 1459
US-10-951-303-1714/c
; Sequence 1714, Application US/10951303
; Publication No. US20050227937A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBH00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/10/951,303
; PRIOR FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/09/685,664
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1714
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-951-303-1714

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      714  CTCACCAAGAGACCA 730
DB      17  CACACCAAGAGACCA 1

RESULT 1460
US-10-951-303-1886/c
; Sequence 1886, Application US/10951303
; Publication No. US20050227937A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Escobedo, Jaime
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBH00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/10/951,303
; PRIOR FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/09/685,664
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1886
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-951-303-1886

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1505 TTCATCTGAACCATCA 1521
DB      17  TTCATCTGAACCATCA 1

RESULT 1461
US-10-492-570-396
; Sequence 396, Application US/10492570
; Publication No. US20060057666A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: A HUMAN G PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: PB0180
; CURRENT APPLICATION NUMBER: US/10/492,570
; PRIOR FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: US 60/329,000
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 1926
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 396
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-492-570-396

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1336 CTGGACTTGCAAAAG 1552
DB      1  CTGGACTTGCAAAAG 17

RESULT 1462
US-10-492-570-397
; Sequence 397, Application US/10492570
; Publication No. US20060057666A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: A HUMAN G PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: PB0180
; CURRENT APPLICATION NUMBER: US/10/492,570
; PRIOR FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: US 60/329,000
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 1926
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 397
; LENGTH: 17

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; FILE REFERENCE: MBH00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/10/951,303
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/09/685,664
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1886
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-951-303-1886

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1505 TTCATCTGAACCATCA 1521
DB      17  TTCATCTGAACCATCA 1

RESULT 1461
US-10-492-570-396
; Sequence 396, Application US/10492570
; Publication No. US20060057666A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: A HUMAN G PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: PB0180
; CURRENT APPLICATION NUMBER: US/10/492,570
; PRIOR FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: US 60/329,000
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 1926
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 396
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-492-570-396

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1336 CTGGACTTGCAAAAG 1552
DB      1  CTGGACTTGCAAAAG 17

RESULT 1462
US-10-492-570-397
; Sequence 397, Application US/10492570
; Publication No. US20060057666A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: A HUMAN G PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: PB0180
; CURRENT APPLICATION NUMBER: US/10/492,570
; PRIOR FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: US 60/329,000
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 1926
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 397
; LENGTH: 17

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TYPE: DNA
ORGANISM: Homo sapiens
US-10-492-570-397

Query Match
Best Local Similarity 0.8%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1537 TGGGACTTGCAGAAAGG 1553
Db 1 TGGGACTGCGAATATAGG 17

RESULT 1463
US-10-492-570-1002
Sequence 1002, Application US/10492570
Publication No. US20060057666A1
GENERAL INFORMATION:
APPLICANT: Zhang, Jian
TITLE OF INVENTION: A HUMAN G PROTEIN COUPLED RECEPTOR
FILE REFERENCE: PB0180
CURRENT APPLICATION NUMBER: US/10/492,570
CURRENT FILING DATE: 2004-04-12
PRIOR APPLICATION NUMBER: US 60/329,000
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 1926
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 1002
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-10-492-570-1002

Query Match
Best Local Similarity 0.8%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 455 CTGCATCATCACTACTG 471
Db 1 CTGCATCATCACTACTG 17

RESULT 1464
US-11-189-546-9/C
Sequence 9, Application US/11189546
Publication No. US20060057613A1
GENERAL INFORMATION:
APPLICANT: Nanosphere, Inc
APPLICANT: Ramakrishnan, Ramesh
APPLICANT: Riccielli, Peter V
TITLE OF INVENTION: Method For Distinguishing Methicillin Resistant S. Aureus From
FILE REFERENCE: 04-437-A
CURRENT APPLICATION NUMBER: US/11/189,546
CURRENT FILING DATE: 2005-07-26
PRIOR APPLICATION NUMBER: 60/591,127
PRIOR FILING DATE: 2004-07-26
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.3
SEQ ID NO 9
LENGTH: 17
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic sequence that is a capture probe for the MRSA gene.
US-11-189-546-9

Db 17 AACGCATCATCACTG 1

Search completed: June 12, 2006, 06:22:21
Job time : 36 secs

Query Match
Best Local Similarity 0.8%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1111 AACCCATCATCTACTG 1127
1111 AACCCATCATCTACTG 1127

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OM nucleic - nucleic search, using sw model

Run on: June 12, 2006, 06:18:10 ; Search time 0.001 Seconds
(without alignments)
533.332 Million cell updates/sec

Title: US-09-930-503A-6

Perfect score: 1766
Sequence: 1 aatcagagccaccgcgggc.....cgagtcctcattccagatg 1766

Scoring table: IDENTITY/MUC
Gapop 10.0 , Gapext 0.5

Searched: 11 segs, 151 residues

Total number of hits satisfying chosen parameters: 22

Minimum DB seq length: 8
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 11 summaries

Database : us-09-930-503a-6.sl.rnpbns4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15.8	0.9	19	US-10-533-300-10	Sequence 10, Appl
2	15.8	0.9	19	US-10-533-300-12	Sequence 12, Appl
3	12.4	0.7	14	US-11-303-896-1	Sequence 1, Appl
4	12.4	0.7	14	US-11-303-896-2	Sequence 2, Appl
5	12.4	0.7	15	US-10-559-415-172	Sequence 172, Appl
6	12	0.6	12	US-11-113-534-39	Sequence 39, Appl
7	11	0.6	11	US-11-158-209-139	Sequence 139, Appl
8	11	0.6	11	US-11-158-209-234	Sequence 234, Appl
9	11	0.6	12	US-11-158-209-936	Sequence 936, Appl
10	11	0.6	12	US-11-113-534-33	Sequence 33, Appl
11	11	0.6	13	US-11-238-162-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-10-533-300-10/c
; Sequence 10, Application US/10533300
; Publication No. US20060100145A1
; GENERAL INFORMATION:
; APPLICANT: Meder, Wolfgang
; APPLICANT: Wendland, Martin
; APPLICANT: John, Harald
; APPLICANT: Richter, Rudolf
; APPLICANT: Meyer, Markus
; APPLICANT: Forssmann, Wolf-Georg
; TITLE OF INVENTION: Human Chondroosteomodulin (TIG2), Production, and Use for the
; TITLE OF INVENTION: Treatment or Diagnosis of Bone Diseases, Cartilage Diseases,
; FILE REFERENCE: 2388-0010000/SRL/BL5
; CURRENT APPLICATION NUMBER: US/10/533.300
; CURRENT FILING DATE: 2005-04-29

PRIOR APPLICATION NUMBER: PCT/EP03/11799
; PRIOR FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence: Primer mDEZol14
US-10-533-300-10

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.4;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 671 TCTGGGTCTGCTCTCTCT 689
Db 19 TCTGGGTCTGCTCTCTCT 1

RESULT 2
US-10-533-300-12/c
; Sequence 12, Application US/10533300
; Publication No. US20060100145A1
; GENERAL INFORMATION:
; APPLICANT: Meder, Wolfgang
; APPLICANT: Wendland, Martin
; APPLICANT: John, Harald
; APPLICANT: Richter, Rudolf
; APPLICANT: Meyer, Markus
; APPLICANT: Forssmann, Wolf-Georg
; TITLE OF INVENTION: Human Chondroosteomodulin (TIG2), Production, and Use for the
; TITLE OF INVENTION: Treatment or Diagnosis of Bone Diseases, Cartilage Diseases,
; FILE REFERENCE: 2388-0010000/SRL/BL5
; CURRENT APPLICATION NUMBER: US/10/533.300
; CURRENT FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: PCT/EP03/11799
; PRIOR FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence: Primer hDEZ_a_0114
US-10-533-300-12

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.4;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 671 TCTGGGTCTGCTCTCTCT 689
Db 19 TCTGGGTCTGCTCTCTCT 1

RESULT 3
US-11-303-896-1
; Sequence 1, Application US/11303896
; Publication No. US20060099184A1
; GENERAL INFORMATION:
; APPLICANT: PODSAKOFF, GREGORY M.
; APPLICANT: KESSLER, PAUL D.
; APPLICANT: BYRNE, BARRY J.
; APPLICANT: KURTZMAN, GARY J.
; TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE
; CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS
; VIRIONS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESSES:

Mon Jun 12 07:03:37 200

US-09-930-503a-6.e1.rnpbns

Page 2

ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
OPERATING SYSTEM: IBM PC compatible
CURRENT APPLICATION: Patent Release #1.0, Version #1.30
APPLICATION NUMBER: US/11/303,896
CLASSIFICATION: <Unknown>
PRIORITY: 15-Dec-2005
APPLICATION DATE: US/10/445,088
APPLICATION NUMBER: US/09/969,204A
FILING DATE: 01-Oct-2001
APPLICATION DATE: 28-Sep-1999
FILING DATE: 08/784,757
ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, Thomas P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 0800-0009.20
TELEPHONE: (415) 325-7812
TELEFAX: (415) 325-7812
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
Query Match
Best Local Similarity 0.7%; Score 12.4; DB 1; Length 14;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 1 GGCAGCTGCTTCA 14
RESULT 4
US-11-305-629-2
Sequence 2, Application US/11305629
Publication No. US2006009185A1
GENERAL INFORMATION:
APPLICANT: HODSAKOFF, GREGORY M.
TITLE OF INVENTION: METHOD OF TREATING ANEMIA USING
CORRESPONDENCE ADDRESS:
ADDRESS: ROBINS & ASSOCIATES
CITY: 90 MIDDLEFIELD ROAD, SUITE 200
STATE: MENLO PARK
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
OPERATING SYSTEM: IBM PC compatible
CURRENT APPLICATION: Patent Release #1.0, Version #1.30
APPLICATION DATA:
PRIORITY: 15-Dec-2005
APPLICATION DATE: US/10/445,088
APPLICATION NUMBER: US/09/969,204A
FILING DATE: 01-Oct-2001
APPLICATION DATE: 28-Sep-1999
FILING DATE: 08/784,757
ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, Thomas P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 0800-0009.20
TELEPHONE: (415) 325-7812
TELEFAX: (415) 325-7812
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
Query Match
Best Local Similarity 0.7%; Score 12.4; DB 1; Length 14;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 1 GGCAGCTGCTTCA 14

APPLICATION NUMBER: US/11/305,629
FILING DATE: 15-Dec-2005
CLASSIFICATION: 514
APPLICATION DATA:
APPLICATION NUMBER: US/10/458,857
FILING DATE: 10-Jun-2003
APPLICATION NUMBER: US/08/785,750
FILING DATE: 16-Jan-1997
APPLICATION DATE: 18-Jan-1996
FILING DATE: 08/588,355
ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, Thomas P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 0800-0009.21
TELEPHONE: (415) 325-7812
TELEFAX: (415) 325-7812
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
Query Match
Best Local Similarity 0.7%; Score 12.4; DB 1; Length 14;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 1 GGCAGCTGCTTCA 14
RESULT 5
US-10-559-415-172/c
Sequence 172, Application US/10559415
Publication No. US20060100132A1
GENERAL INFORMATION:
APPLICANT: Abetazene, AB et al
TITLE OF INVENTION: Diagnostic Method
CURRENT APPLICATION: 101073-IP WO
PRIOR FILING DATE: 2005-12-06
PRIOR APPLICATION NUMBER: US/10/559,415
NUMBER OF SEQ ID NOS: 191
SOFTWARE: Patent version 3.2
SEQ ID NO: 172
LENGTH: 15
TYPE: DNA
ORGANISM: Homo sapiens
US-10-559-415-172
Query Match
Best Local Similarity 0.7%; Score 12.4; DB 1; Length 15;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 14 GGCAGCTGCTTCA 14
RESULT 6
US-11-113-534-39/c
Sequence 39, Application US/11113534
Publication No. US20060115825A1
GENERAL INFORMATION:
APPLICANT: Park, Hyun Gyu
TITLE OF INVENTION: PNA CHIP USING ZIP-CODES AND FABRICATION METHOD THEREOF

FILE REFERENCE: 4240-120
CURRENT APPLICATION NUMBER: US/11/113,534
CURRENT FILING DATE: 2005-04-25
PRIOR APPLICATION NUMBER: KR 10-2004-0099514
PRIOR FILING DATE: 2004-11-30
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn version 3.2
SEQ ID NO 39
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Construct
US-11-113-534-39

Query Match 0.7%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 940 CGCAGGTGTC 951
DB 12 CGCAGGTGTC 1

RESULT 7
US-11-158-209-139
Sequence 139, Application US/11158209
Publication No. US20060088852A1
GENERAL INFORMATION:
APPLICANT: Dirk Petersohn
APPLICANT: Kordula Schlotmann
APPLICANT: Thomas Gassenmeier
APPLICANT: Olaf Holtkotter
APPLICANT: Marcus Conradt
APPLICANT: Kay Hofmann
TITLE OF INVENTION: Method for Determining the Homeostasis of Hairy Skin
FILE REFERENCE: H 05667 PCT
CURRENT APPLICATION NUMBER: US/11/158,209
CURRENT FILING DATE: 2005-06-20
PRIOR APPLICATION NUMBER: PCT/EP2003/014070
PRIOR FILING DATE: 2003-12-11
PRIOR APPLICATION NUMBER: 102 60 931.4-41
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 1335
SOFTWARE: SeqWin99, version 1.02
SEQ ID NO 139
LENGTH: 11
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-158-209-139

Query Match 0.6%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1674 AAATAAAGCT 1684
DB 1 AAATAAAGCT 11

RESULT 8
US-11-158-209-234
Sequence 234, Application US/11158209
Publication No. US20060088852A1
GENERAL INFORMATION:
APPLICANT: Dirk Petersohn
APPLICANT: Kordula Schlotmann
APPLICANT: Thomas Gassenmeier
APPLICANT: Olaf Holtkotter
APPLICANT: Marcus Conradt
APPLICANT: Kay Hofmann
TITLE OF INVENTION: Method for Determining the Homeostasis of Hairy Skin
FILE REFERENCE: H 05667 PCT

CURRENT APPLICATION NUMBER: US/11/158,209
CURRENT FILING DATE: 2005-06-20
PRIOR APPLICATION NUMBER: PCT/EP2003/014070
PRIOR FILING DATE: 2003-12-11
PRIOR APPLICATION NUMBER: 102 60 931.4-41
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 1335
SOFTWARE: SeqWin99, version 1.02
SEQ ID NO 234
LENGTH: 11
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-158-209-234

Query Match 0.6%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 969 GGTTGTCACCT 979
DB 1 GGTTGTCACCT 11

RESULT 9
US-11-158-209-936
Sequence 936, Application US/11158209
Publication No. US20060088852A1
GENERAL INFORMATION:
APPLICANT: Dirk Petersohn
APPLICANT: Kordula Schlotmann
APPLICANT: Thomas Gassenmeier
APPLICANT: Olaf Holtkotter
APPLICANT: Marcus Conradt
APPLICANT: Kay Hofmann
TITLE OF INVENTION: Method for Determining the Homeostasis of Hairy Skin
FILE REFERENCE: H 05667 PCT
CURRENT APPLICATION NUMBER: US/11/158,209
CURRENT FILING DATE: 2005-06-20
PRIOR APPLICATION NUMBER: PCT/EP2003/014070
PRIOR FILING DATE: 2003-12-11
PRIOR APPLICATION NUMBER: 102 60 931.4-41
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 1335
SOFTWARE: SeqWin99, version 1.02
SEQ ID NO 936
LENGTH: 11
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-158-209-936

Query Match 0.6%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 355 GGCACGTGCT 365
DB 1 GGCACGTGCT 11

RESULT 10
US-11-113-534-33/C
Sequence 33, Application US/11113534
Publication No. US20060115825A1
GENERAL INFORMATION:
APPLICANT: Park, Hyun Gyu
APPLICANT: Song, Jae Yang
TITLE OF INVENTION: PNA CHIP USING ZIP-CODES AND FABRICATION METHOD THEREOF
FILE REFERENCE: 4240-120
CURRENT APPLICATION NUMBER: US/11/113,534
CURRENT FILING DATE: 2005-04-25
PRIOR APPLICATION NUMBER: KR 10-2004-0099514
PRIOR FILING DATE: 2004-11-30
NUMBER OF SEQ ID NOS: 55

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; SOFTWARE: Patentin version 3.2
; SEQ ID NO 33
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-113-534-33
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Query Match          0.6%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1062 GCAGGCTCTACC 1072
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Db       11 GCAGGCTCTACC 1
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RESULT 11
US-11-238-162-28
; Sequence 28, Application US/11238162
; Publication No. US20060099618A1
; GENERAL INFORMATION:
; APPLICANT: INNOGENETICS N.V.
; TITLE OF INVENTION: DETECTION, IDENTIFICATION AND DIFFERENTIATION OF SERRATIA SPECIES
; TITLE OF INVENTION: THE SPACER REGION.
; FILE REFERENCE: 2551-177
; CURRENT APPLICATION NUMBER: US/11/238,162
; PRIOR FILING DATE: 2005-09-29
; PRIOR APPLICATION NUMBER: 04447218.1
; PRIOR FILING DATE: 2005-09-30
; PRIOR APPLICATION NUMBER: 60/634,106
; PRIOR FILING DATE: 2004-12-08
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 28
; LENGTH: 13
; TYPE: DNA
; ORGANISM: S. marcescens
US-11-238-162-28
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Query Match          0.6%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db       1 CATGACGGCTG 11
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Search completed: June 12, 2006, 06:18:11
Job time : 0.001 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2006, 06:15:31 ; Search time 12 Seconds

(without alignments)

3.239 Million cell updates/sec

Title: US-09-930-503A-6

Perfect score: 1766

Sequence: 1 aattcagagccaccgcgggc.....cgagtcctcattcaggatg 1766

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 612 seqs, 11005 residues

Total number of hits satisfying chosen parameters: 1224

Minimum DB seq length: 8

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 621 summaries

Database : us-09-930-503a-6.sl.rng4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	28	1.6	28	1	AED31523
3	27	1.5	27	1	ABS60998
4	27	1.5	27	1	ADN12184
5	27	1.5	27	1	ADN12182
6	27	1.5	27	1	AED31524
7	26	1.5	27	1	ABS61087
8	25.8	1.5	30	1	ADN12193
9	25	1.4	25	1	AAH26071
10	25	1.4	25	1	AAH26070
11	25	1.4	25	1	ABS60907
12	25	1.4	25	1	ABS61082
13	25	1.4	27	1	ABS61088
14	24	1.4	24	1	AAO37209
15	24	1.4	24	1	AED51264
16	24	1.4	27	1	ABS61086
17	24	1.4	29	1	AAT36738
18	24	1.4	29	1	AAV02408
19	24	1.4	29	1	AAV81238
20	24	1.4	29	1	AAH15513
21	23.6	1.3	24	1	ABS60997
22	23.4	1.3	29	1	ABX95641
23	23.4	1.3	29	1	ABX22120
24	23	1.3	23	1	ABS60910
25	23	1.3	24	1	AAO30776
26	23	1.3	24	1	ABK63862
27	22.4	1.3	22	1	AAO30777
28	22	1.2	24	1	ABS60912
29	22	1.2	22	1	ABS61083
30	21.8	1.2	27	1	AAT18348
31	21.8	1.2	27	1	AAT27220
32	21.8	1.2	27	1	AAT29438
33	21.8	1.2	27	1	AAT98800

C 34	21.8	1.2	27	1	AAV02406	Receptor protein d
C 35	21.8	1.2	27	1	AAV81236	Human G-protein co
C 36	21.8	1.2	27	1	AAH83875	G-protein-coupled
C 37	21.8	1.2	27	1	AAH15511	Probe used to scre
C 38	21	1.2	21	1	AAO30782	PCR primer hsp13a1
C 39	21	1.2	21	1	AAO30790	PCR primer hsp16a2
C 40	21	1.2	21	1	AAO30785	PCR primer hsp15a1
C 41	21	1.2	21	1	AAO30789	PCR primer hsp16a1
C 42	21	1.2	21	1	AAO30787	PCR primer hsp16a1
C 43	21	1.2	21	1	AAO29678	hsp13a1 primer 1
C 44	21	1.2	21	1	AAO29679	hsp16a2 primer 868
C 45	21	1.2	21	1	AAO29674	hsp16a1 primer 768
C 46	21	1.2	21	1	AAO29676	hsp16a1 primer 888
C 47	21	1.2	21	1	AAO29671	hsp13a1 primer 491
C 48	21	1.2	21	1	AAO29678	hsp16a1 primer 836
C 50	21	1.2	21	1	ABS60219	Human polymorphism
C 51	21	1.2	21	1	ABS60218	Human polymorphism
C 52	21	1.2	21	1	ABS60277	Human polymorphism
C 53	21	1.2	21	1	ABS60343	Human polymorphism
C 54	21	1.2	21	1	ABS60999	Human genotyping p
C 55	21	1.2	21	1	ABS60214	Human polymorphism
C 56	21	1.2	21	1	ABS60345	Human polymorphism
C 57	21	1.2	21	1	ABS60217	Human polymorphism
C 58	21	1.2	21	1	ABS60283	Human polymorphism
C 59	21	1.2	21	1	ABS60344	Human polymorphism
C 60	21	1.2	21	1	ABS60994	Human genotyping p
C 61	21	1.2	21	1	ABK63856	Neurokinin 1 recep
C 62	21	1.2	21	1	ABK63871	Neurokinin 1 recep
C 63	21	1.2	21	1	ABK63894	Neurokinin 1 recep
C 64	21	1.2	21	1	ABK63875	Neurokinin 1 recep
C 65	21	1.2	21	1	ABK63890	Neurokinin 1 recep
C 66	21	1.2	21	1	ABK63904	Neurokinin 1 recep
C 67	21	1.2	21	1	ABK63851	Neurokinin 1 recep
C 68	21	1.2	21	1	ABK63885	Neurokinin 1 recep
C 69	21	1.2	21	1	ABK63889	Neurokinin 1 recep
C 70	21	1.2	21	1	ABK63870	Neurokinin 1 recep
C 71	21	1.2	21	1	ABK63878	Neurokinin 1 recep
C 72	21	1.2	21	1	ABK63866	Neurokinin 1 recep
C 73	21	1.2	21	1	ABK63880	Neurokinin 1 recep
C 74	21	1.2	21	1	ABK63887	Neurokinin 1 recep
C 75	21	1.2	21	1	ABK63868	Neurokinin 1 recep
C 76	21	1.2	21	1	ABK63897	Neurokinin 1 recep
C 77	21	1.2	21	1	ABK63852	Neurokinin 1 recep
C 78	21	1.2	21	1	ABK63852	Neurokinin 1 recep
C 79	21	1.2	21	1	ABK63906	Neurokinin 1 recep
C 80	21	1.2	21	1	ABK63854	Neurokinin 1 recep
C 81	21	1.2	21	1	ABK63873	Neurokinin 1 recep
C 82	21	1.2	21	1	ABK63861	Neurokinin 1 recep
C 83	21	1.2	21	1	ABK63881	Neurokinin 1 recep
C 84	21	1.2	21	1	ABK63859	Neurokinin 1 recep
C 85	21	1.2	21	1	ABK63892	Neurokinin 1 recep
C 86	21	1.2	21	1	ABK63900	Neurokinin 1 recep
C 87	21	1.2	21	1	ADU26730	Knock-down target
C 88	21	1.2	21	1	ADU26729	Knock-down target
C 89	21	1.2	26	1	AAO37208	PCR primer #1 to a
C 90	20.8	1.2	24	1	AAO30778	Human genotyping p
C 91	20.6	1.2	24	1	AAT18361	G-protein coupled
C 92	20.6	1.2	21	1	AAH18361	PCR primer hsp16a2
C 93	20	1.1	20	1	AAO30792	PCR primer hsp16a2
C 94	20	1.1	20	1	AAO30788	PCR primer hsp16a2
C 95	20	1.1	20	1	AAO30791	PCR primer hsp16a2
C 96	20	1.1	20	1	AAO30786	PCR primer hsp15a2
C 97	20	1.1	20	1	AAO30783	PCR primer hsp13a4
C 98	20	1.1	20	1	AAO30784	PCR primer hsp13a5
C 99	20	1.1	20	1	AAO29672	hsp13a4 primer 532
C 100	20	1.1	20	1	AAO29675	hsp16a2 primer 793
C 101	20	1.1	20	1	AAO29680	hsp16a2 primer 912
C 102	20	1.1	20	1	AAO29677	hsp16a2 primer 943
C 103	20	1.1	20	1	AAO29681	hsp16a4 primer 935
C 104	20	1.1	20	1	AAO29673	hsp16a5 primer 568
C 105	20	1.1	20	1	AAZ92287	Allele specific pr
C 106	20	1.1	20	1	ABS60995	Human genotyping p

C 107	20	1.1	20	1	ABSG0996	Human genotyping p	C 180	17.4	1.0	19	1	ABSS59900	Human DNA represen
C 108	20	1.1	20	1	ABK63858	Neurokinin 1 recep	181	17	1.0	20	1	ABE77697	Human dopamine rec
C 109	20	1.1	20	1	ABK63876	Neurokinin 1 recep	182	17	1.0	20	1	AEET7702	Human dopamine rec
C 110	20	1.1	20	1	ABK63857	Neurokinin 1 recep	C 183	17	1.0	21	1	AAQ36818	Oligomer SM 82 use
C 111	20	1.1	20	1	ABK63893	Neurokinin 1 recep	C 184	17	1.0	21	1	AAQ36820	Oligomer SM 86 use
C 112	20	1.1	20	1	ABK63895	Neurokinin 1 recep	C 185	17	1.0	21	1	AAQ36822	Oligomer SM 88 use
C 113	20	1.1	20	1	ABK63869	Neurokinin 1 recep	C 186	17	1.0	21	1	AAQ94986	SSP Oligonucleoti
C 114	20	1.1	20	1	ABK63877	Neurokinin 1 recep	C 187	17	1.0	21	1	AAQ94984	SSP Oligonucleoti
C 115	20	1.1	20	1	ABK63891	Neurokinin 1 recep	C 188	17	1.0	21	1	AAQ94976	SSP Oligonucleoti
C 116	20	1.1	20	1	ABK63850	Neurokinin 1 recep	C 189	17	1.0	21	1	AAV99519	Oligonucleotide SM
C 117	20	1.1	20	1	ABK63888	Neurokinin 1 recep	C 190	17	1.0	21	1	AAV99509	Oligonucleotide SM
C 118	20	1.1	20	1	ABK63853	Neurokinin 1 recep	C 191	17	1.0	21	1	ADA15939	Oligonucleotide SM
C 119	20	1.1	20	1	ABK63874	Neurokinin 1 recep	C 192	17	1.0	21	1	ADA15937	Synthetic storage
C 120	20	1.1	20	1	ABK63896	Neurokinin 1 recep	C 193	17	1.0	21	1	ADA15921	Synthetic storage
C 121	20	1.1	20	1	ABK63872	Neurokinin 1 recep	C 194	17	1.0	21	1	ACHO3695	Ear I-based lysine
C 122	20	1.1	20	1	ABK63855	Neurokinin 1 recep	C 195	17	1.0	21	1	ACHO3695	Ear I-based lysine
C 123	20	1.1	20	1	ABT16453	Human neurokinin 1	C 196	17	1.0	21	1	ACHO3685	Ear I-based lysine
C 124	20	1.1	20	1	ABT16465	Human neurokinin 1	C 197	17	1.0	21	1	ACHO3693	Oligonucleotide SM
C 125	20	1.1	20	1	ABT16467	Human neurokinin 1	C 198	17	1.0	21	1	ADW71666	Oligonucleotide SM
C 126	20	1.1	20	1	ABT16466	Human neurokinin 1	C 199	17	1.0	21	1	ADW71648	Oligonucleotide SM
C 127	20	1.1	20	1	ABD51262	Human tachykinin r	C 200	17	1.0	21	1	ADW71664	Oligonucleotide SM
C 128	20	1.1	20	1	AAQ30781	Probe hsp3a2 to h	C 201	16.8	1.0	20	1	ABT44412	Chimeric antisense
C 129	20	1.1	20	1	AAQ29670	hep3a2 primer 455	C 202	16.8	1.0	20	1	ABD90814	Human selenophosph
C 130	20	1.1	20	1	ABK63898	Neurokinin 1 recep	C 203	16.8	1.0	20	1	AEET77695	Human dopamine rec
C 131	20	1.1	20	1	ABK63879	Neurokinin 1 recep	C 204	16.8	1.0	20	1	AEET77704	Human dopamine rec
C 132	20	1.1	20	1	ABK63860	Neurokinin 1 recep	C 205	16.8	1.0	20	1	AEET77703	Human dopamine rec
C 133	20	1.1	20	1	ABQ81645	Oligonucleotide se	C 206	16.8	1.0	20	1	AEET77696	Human dopamine rec
C 134	19.4	1.1	21	1	ADU41834	Knock-down target	C 207	16.8	1.0	20	1	AEET77705	Human dopamine rec
C 135	19.4	1.1	21	1	ADU41833	Knock-down target	C 208	16.8	1.0	21	1	AAZ50619	PCR primer 3-AS to
C 136	19.2	1.1	24	1	AAQ67148	Primer for amplify	C 209	16.4	0.9	18	1	AAQ30774	PCR primer rspr284
C 137	19.2	1.1	24	1	AAT00836	HTLV-1 strains TSP	C 210	16.4	0.9	18	1	AAWX3459	Mouse flk-1 VEGF r
C 138	19	1.1	19	1	ABSS5989	Human DNA represen	C 211	16.4	0.9	19	1	AD147994	Human OGR-1 probe1
C 139	19	1.1	19	1	ABSS5983	Human DNA represen	C 212	16.4	0.9	20	1	ACCT0594	Sphingosine-1-phos
C 140	19	1.1	19	1	ABSS5985	Human DNA represen	C 213	16.4	0.9	20	1	ADFB3183	Antisense oligonuc
C 141	19	1.1	19	1	ABSS59901	Human DNA represen	C 214	16.4	0.9	20	1	ADFB3001	Antisense oligonuc
C 142	19	1.1	19	1	ABSS59959	Human DNA represen	C 215	16	0.9	17	1	ABL53529	Human CD20 Zinyme
C 143	19	1.1	19	1	ABK63901	Human DNA represen	C 216	16	0.9	20	1	ABL53527	Mouse SMIb antis
C 144	19	1.1	19	1	ABK63865	Neurokinin 1 recep	C 217	16	0.9	20	1	ACF79553	Mouse SMIb antis
C 145	19	1.1	19	1	ABK63882	Neurokinin 1 recep	C 218	16	0.9	20	1	ACF79551	Oligonucleotide an
C 146	19	1.1	19	1	ABK63863	Neurokinin 1 recep	C 219	16	0.9	20	1	ACF79551	Oligonucleotide an
C 147	19	1.1	19	1	ABK63903	Neurokinin 1 recep	C 220	16	0.9	20	1	ADH49395	MAS-signalling tra
C 148	19	1.1	19	1	ABK63884	Neurokinin 1 recep	C 221	16	0.9	20	1	ADH49397	MAS-signalling tra
C 149	19	1.1	19	1	ABE29146	Human siRNA molecu	C 222	15.8	0.9	19	1	AAV01172	Adrenergic recepto
C 150	19	1.1	19	1	ABE54827	Human siRNA molecu	C 223	15.8	0.9	19	1	ADOC6346	Haemofiltrate-cho
C 151	19	1.1	19	1	ABD51263	Human tachykinin r	C 224	15.8	0.9	19	1	ADOC6348	Haemofiltrate-cho
C 152	19	1.1	20	1	ABE77699	Human dopamine rec	C 225	15.8	0.9	19	1	AEC90914	STAT-3 siRNA anti
C 153	19	1.1	20	1	AEET77700	Human dopamine rec	C 226	15.8	0.9	19	1	AEC90637	STAT-3 siRNA targe
C 154	18.4	1.0	20	1	AAQ47254	Sequence of PCR pr	C 227	15.8	0.9	19	1	AEC73577	RNAi sense strand,
C 155	18.2	1.0	20	1	AAQ55048	Oligo probe hsp66	C 228	15.8	0.9	19	1	ABE41027	Human hairless hom
C 156	18	1.0	18	1	AAQ30793	hsp665 primer 950	C 229	15.8	0.9	19	1	ABE41028	Human hairless hom
C 157	18	1.0	18	1	AAQ29682	Substance p recep	C 230	15.8	0.9	19	1	AEF75464	Human NCOG-A trans
C 158	18	1.0	18	1	AAT76448	Substance p recep	C 231	15.8	0.9	19	1	AEF75690	Human NCOG-A trans
C 159	18	1.0	18	1	AAAX54239	Low adenosine anti	C 232	15.4	0.9	17	1	AAK72794	Mouse flk-1 VEGF r
C 160	18	1.0	18	1	AAAX3683	Human substance p	C 233	15.4	0.9	17	1	ABK01841	Human NCOG Zinyme
C 161	18	1.0	18	1	AAF19805	Human substance p	C 234	15.4	0.9	17	1	ADU94309	Human OGR1 gene sp
C 162	18	1.0	18	1	ABSG1000	Human genotyping p	C 235	15.4	0.9	18	1	ADU50872	Human OGR1 gene sp
C 163	18	1.0	18	1	ABSG0906	Human genotyping p	C 236	15.4	0.9	18	1	ADRI5253	Human HGPBMY9 PCR
C 164	18	1.0	18	1	ABK63886	Neurokinin 1 recep	C 237	15.4	0.9	18	1	AEF82508	Common marmoset 18
C 165	18	1.0	18	1	ABK63905	Neurokinin 1 recep	C 238	15.4	0.9	19	1	ADF37473	Human VEGFR3 short
C 166	18	1.0	18	1	ABK63867	Neurokinin 1 recep	C 239	15.4	0.9	19	1	ADF37226	Human VEGFR3 short
C 167	18	1.0	18	1	ABT16451	Human neurokinin 1	C 240	15.4	0.9	19	1	ADFP3722	Human TERT siNA 10
C 168	18	1.0	18	1	ABZ95499	Human substance p	C 241	15.4	0.9	19	1	ADFP3468	Human TERT transcr
C 169	18	1.0	18	1	ABD19638	Human substance p	C 242	15.4	0.9	19	1	ADK97381	Primer of the inve
C 170	18	1.0	20	1	AEET7698	Human dopamine rec	C 243	15.4	0.9	19	1	ADOC62492	Anti-TERT siRNA SE
C 171	18	1.0	20	1	AEET7701	Human dopamine rec	C 244	15.4	0.9	19	1	ADRO5766	Ribosome binding s
C 172	18	1.0	22	1	ABSG1085	Human automated ge	C 245	15.4	0.9	19	1	ADY88479	VEGFR siRNA SEQ ID
C 173	17.8	1.0	21	1	ABT4Q254	Human Chem23 PCR p	C 246	15.4	0.9	19	1	ADY88726	VEGFR siRNA SEQ ID
C 174	17.8	1.0	21	1	ADW43814	Human Chem23 PCR p	C 247	15.4	0.9	19	1	AEAD06712	G protein-coupled
C 175	17.8	1.0	22	1	AAQ47385	Substance p recep	C 248	15.4	0.9	19	1	AEAD06625	G protein-coupled
C 176	17.4	1.0	19	1	ABSS5964	Human DNA represen	C 249	15.4	0.9	19	1	AEAD1650	Short interfering
C 177	17.4	1.0	19	1	ABSS5962	Human DNA represen	C 250	15.4	0.9	19	1	AEAD1651	Short interfering
C 178	17.4	1.0	19	1	ABSS5986	Human DNA represen	C 251	15.4	0.9	19	1	AEAD1649	Short interfering
C 179	17.4	1.0	19	1	ABSS5958	Human DNA represen	C 252	15.4	0.9	19	1	ABE15725	Human telomerase-t

399	13.8	0.8	17	1	ACN01273	WNV Hammerhead Rib	472	13	0.7	13	1	ABCI0998	Oligonucleotide SE
400	13.8	0.8	17	1	ACN07407	WNV minus strand H	473	13	0.7	13	1	ABF29163	Oligonucleotide SE
401	13.8	0.8	17	1	ACN12112	WNV minus strand I	474	13	0.7	13	1	ABF98356	Oligonucleotide SE
402	13.8	0.8	17	1	ACN07336	WNV Amberzyme subs	475	13	0.7	13	1	ABC94324	Oligonucleotide SE
403	13.8	0.8	17	1	ACN09339	WNV minus strand B	476	13	0.7	13	1	ABF73245	Oligonucleotide SE
404	13.8	0.8	17	1	ACN13675	WNV minus strand D	477	13	0.7	13	1	AAT33386	Human vascular end
405	13.8	0.8	17	1	ACN03237	WNV inozyme subctr	478	13	0.7	13	1	AAT48401	Oligonucleotide H-
406	13.8	0.8	17	1	ACN15211	WNV minus strand A	479	13	0.7	13	1	AAK33621	Thrombin inhibitor
407	13.8	0.8	17	1	ACD00505	G-protein coupled	480	13	0.7	13	1	ABK55500	Selectin L Lymphoc
408	13.8	0.8	17	1	ACA98879	G-protein coupled	481	13	0.7	13	1	ABK95827	Solute Carrier Fam
409	13.8	0.8	17	1	ACA99880	G-protein coupled	482	13	0.7	13	1	ABK95804	Pyridoxal (Pyridox
410	13.8	0.8	17	1	ABT35050	Tumour suppression	483	13	0.7	13	1	ABN80579	Human P450(Cytochr
411	13.8	0.8	17	1	ABT36411	Tumour suppression	484	13	0.7	13	1	ABK92616	ASO primer #14 to
412	13.8	0.8	17	1	ACA06517	NFKB sub-unit modu	485	13	0.7	13	1	ABLS2021	Human SRC1842 alle
413	13.8	0.8	17	1	ADA989853	Human MD27 scannin	486	13	0.7	13	1	AAK37335	Human CRYBB1 gene
414	13.8	0.8	17	1	ADB03782	Human MD27 scannin	487	13	0.7	13	1	AAK16726	Human APOA4 allele
415	13.8	0.8	17	1	ACD55641	HBV amberzyme subs	488	13	0.7	13	1	ABK81517	Human CASP5 gene a
416	13.8	0.8	17	1	ACD55640	HBV amberzyme subs	489	13	0.7	13	1	ABA97329	CCR5 allele-specific
417	13.8	0.8	17	1	ACD58714	HCV DNAzyme subctr	490	13	0.7	13	1	ABA97329	Human lysosomal ac
418	13.8	0.8	17	1	ACC62777	Marine oligonucleo	491	13	0.7	13	1	AB163318	SMOH polymorphism
419	13.8	0.8	17	1	ACA89989	Cardiovascular dis	492	13	0.7	13	1	AAI39772	Allele-specific ol
420	13.8	0.8	17	1	ADB42998	Tumour suppression	493	13	0.7	13	1	ADP74524	Hyperlipidemia tre
421	13.8	0.8	17	1	ADP64140	Human PCCP1 DNA fr	494	13	0.7	13	1	ADN89026	Primer for second
422	13.8	0.8	17	1	ADP63951	Human PCCP1 DNA fr	495	13	0.7	13	1	ADS88857	Tachykinin recepto
423	13.8	0.8	17	1	ADP62472	Human PCCP1 DNA fr	496	13	0.7	13	1	ADN12185	Endothelial nitric
424	13.8	0.8	17	1	AD151353	Human tumour suppr	497	13	0.7	13	1	AAV70488	Control probe hybr
425	13.8	0.8	17	1	ACC53250	Human tumour suppr	498	12.8	0.7	16	1	AAZ09807	p53 exon 8 PCR pri
426	13.8	0.8	17	1	ACC53982	Human tumour suppr	499	12.8	0.7	16	1	AAZ09807	Inducible nitric o
427	13.8	0.8	17	1	ADL46848	Human NCOG recepto	500	12.8	0.7	16	1	AAK54320	Endothelial nitric o
428	13.8	0.8	17	1	ADL46896	Human IKK-gamma su	501	12.8	0.7	16	1	AAK54275	Inducible nitric o
429	13.8	0.8	17	1	ADM60212	Hepatitis B virus	502	12.8	0.7	16	1	AAK54321	Low adenosine anti
430	13.8	0.8	17	1	ADM60212	Hepatitis B virus	503	12.8	0.7	16	1	AAK33719	Low adenosine anti
431	13.8	0.8	17	1	ACN70772	Human GDMW-1 prob	504	12.8	0.7	16	1	AAK33764	Low adenosine anti
432	13.8	0.8	17	1	ACN65854	Gastric cancer rel	505	12.8	0.7	16	1	AAK33765	HIV-1 protease gen
433	13.8	0.8	17	1	ADW29146	HIA-C allele ident	506	12.8	0.7	16	1	AAZ97920	Human inducible ni
434	13.8	0.8	17	1	ADB23914	Human Leukocyte An	507	12.8	0.7	16	1	AAK19886	Human inducible ni
435	13.8	0.8	17	1	ADB288144	Chicken Pyrin Ligh	508	12.8	0.7	16	1	AAK19887	Human endothelial
436	13.8	0.8	17	1	AEF42068	Human ASO PCR prim	509	12.8	0.7	16	1	AAK19841	Human TERT G-cleav
437	13.6	0.8	15	1	AAK15285	Human dexametha rec	510	12.8	0.7	16	1	ADU94873	Human TERT G-cleav
438	13.6	0.8	15	1	AEF77703	Human CD40 hammerh	511	12.8	0.7	16	1	ADU94732	Human TERT G-cleav
439	13.4	0.8	15	1	AAK66607	Human CD40 hammerh	512	12.8	0.7	16	1	ADU94557	Control probe SEQ
440	13.4	0.8	15	1	AAK66606	IGF-1 oligonucleot	513	12.8	0.7	16	1	ABL46099	Human CYP4501A2 Ex
441	13.4	0.8	15	1	AAK49867	IGF-1 oligonucleot	514	12.8	0.7	16	1	ABS971178	Human H1A genotypi
442	13.4	0.8	15	1	AAK45173	IGF-1 oligonucleot	515	12.8	0.7	16	1	ABL131409	Human H1A genotypi
443	13.4	0.8	15	1	AAK49642	IGF-1 oligonucleot	516	12.8	0.7	16	1	ABL131307	Human hypoxia-indu
444	13.4	0.8	15	1	AAK52680	IGF-1 oligonucleot	517	12.8	0.7	16	1	AAK56914	Human inducible ni
445	13.4	0.8	15	1	AAK52481	IGF-1 oligonucleot	518	12.8	0.7	16	1	ABZ95580	Human inducible ni
446	13.4	0.8	15	1	AAK45224	IGFBP2 oligonucleo	519	12.8	0.7	16	1	ABZ95581	Human inducible ni
447	13.4	0.8	15	1	AAK45223	IGFBP2 oligonucleo	520	12.8	0.7	16	1	ABZ95581	Human endothelial
448	13.4	0.8	15	1	ABK5643	Human Omi/HtrA2 ex	521	12.8	0.7	16	1	ABD19740	Human endothelial
449	13.4	0.8	15	1	ABK5643	Human Leukocyte An	522	12.8	0.7	16	1	ABD19685	Human endothelial
450	13.4	0.8	15	1	AAQ95705	Primer A (Group 7,	523	12.8	0.7	16	1	ABD19739	Human inducible ni
451	13.4	0.8	16	1	ADC84377	Human papillomavir	524	12.8	0.7	16	1	ADK82289	Nucleic acid analy
452	13.4	0.8	16	1	ADU44279	HPV WM7 detecting	525	12.8	0.7	16	1	ADK82289	Glutathione S-tran
453	13.4	0.8	16	1	ADU76209	HPV WM7 probe SRQ	526	12.8	0.7	16	1	ADQ30169	Mutline VRI exon 1d
454	13.4	0.8	16	1	ABK56195	Oligonucleotide SE	527	12.8	0.7	16	1	ADQ62808	Aptamer-related pe
455	13	0.7	13	1	ABF73244	Oligonucleotide SE	528	12.8	0.7	16	1	ADQ62809	Oligonucleotide of
456	13	0.7	13	1	ABH37834	Oligonucleotide SE	529	12.8	0.7	16	1	ADQ62809	Hepatitis C virus-
457	13	0.7	13	1	ABK89691	Oligonucleotide SE	530	12.8	0.7	16	1	ADY03782	Human nucleic acid
458	13	0.7	13	1	ABH06065	Oligonucleotide SE	531	12.8	0.7	16	1	ABK50577	Human leukocyte an
459	13	0.7	13	1	ABF59772	Oligonucleotide SE	532	12.8	0.7	16	1	ABK52878	Oligonucleotide SE
460	13	0.7	13	1	ABF29162	Oligonucleotide SE	533	12.6	0.7	13	1	ABF46499	Oligonucleotide SE
461	13	0.7	13	1	ABC98834	Oligonucleotide SE	534	12.6	0.7	13	1	ABH39848	Oligonucleotide SE
462	13	0.7	13	1	ABC98835	Oligonucleotide SE	535	12.6	0.7	13	1	ABH39849	Oligonucleotide SE
463	13	0.7	13	1	ABC77569	Oligonucleotide SE	536	12.6	0.7	13	1	ABF46498	Oligonucleotide SE
464	13	0.7	13	1	ABF98357	Oligonucleotide SE	537	12.6	0.7	13	1	ABA96358	SCN2B gene polymor
465	13	0.7	13	1	ABC89690	Oligonucleotide SE	538	12.6	0.7	13	1	ABK27519	Human CTLA4 gene a
466	13	0.7	13	1	ABC77568	Oligonucleotide SE	539	12.6	0.7	15	1	ABK70728	ASO primer #9 to d
467	13	0.7	13	1	ABCI0989	Oligonucleotide SE	540	12.6	0.7	15	1	AAH99963	ASO primer for det
468	13	0.7	13	1	ABH06064	Oligonucleotide SE	541	12.6	0.7	20	1	AAO30786	PCR primer hsp5a2
469	13	0.7	13	1	ABF59773	Oligonucleotide SE	542	12.6	0.7	20	1	AAQ28675	hsp15a2 primer 793
470	13	0.7	13	1	ABH37835	Oligonucleotide SE	543	12.6	0.7	20	1	ABK63893	Neurokinin 1 recep
471	13	0.7	13	1	ABC34325	Oligonucleotide SE	544	12.6	0.7	20	1	ABK63874	Neurokinin 1 recep

545	12.6	0.7	20	1	ABK63855	Neurokinin 1 recep
546	12.6	0.7	20	1	ABE77702	Human dopamine rec
547	12.6	0.7	20	1	ABE77704	Human dopamine rec
548	12.4	0.7	14	1	ABZ58817	Nucleotide sequenc
549	12.4	0.7	14	1	AAAT79147	Human VEGF cDNA an
550	12.4	0.7	14	1	AAK54378	NK-kB antisense ol
551	12.4	0.7	14	1	AAA33822	Low adenosine anti
552	12.4	0.7	14	1	AAZ64750	Substrate for hair
553	12.4	0.7	14	1	AAZ65593	Immunosuppressant
554	12.4	0.7	14	1	ABX19944	Human NF-kB polyru
555	12.4	0.7	14	1	ABX01587	Hepatitis C virus
556	12.4	0.7	14	1	ABE76511	Hepatitis C virus
557	12.4	0.7	14	1	ABZ72766	Rod opsin hairpin
558	12.4	0.7	14	1	ABZ95638	Human NF-kappaB an
559	12.4	0.7	14	1	ABD15802	Human NF-kB DNA fr
560	12.4	0.7	14	1	ADZ85160	MODY 3 diabetes-as
561	12.4	0.7	14	1	ABE01280	VEGF inhibition ol
562	12.4	0.7	14	1	AEC63812	Novel microarray-r
563	12.4	0.7	15	1	AAO70347	Antisense oligonuc
564	12.4	0.7	15	1	AAK66605	Human CD40 hammerh
565	12.4	0.7	15	1	AAK66802	Mouse CD40 hammerh
566	12.4	0.7	15	1	AAK65304	Mouse B7-1 hammerh
567	12.4	0.7	15	1	AAK66801	Mouse CD40 hammerh
568	12.4	0.7	15	1	AAK65303	Mouse B7-1 hammerh
569	12.4	0.7	15	1	AAT15256	Antisense sequence
570	12.4	0.7	15	1	AAT50255	Rabbit CERP NH rib
571	12.4	0.7	15	1	AAV45771	Transcriptional sy
572	12.4	0.7	15	1	AAV48607	jund gene antisens
573	12.4	0.7	15	1	AAK31113	Tag sequence of a
574	12.4	0.7	15	1	AAK07158	Probe for XELF1-al
575	12.4	0.7	15	1	AAA65946	Human leukocyte an
576	12.4	0.7	15	1	AAK45174	ICG1P2 oligonucleo
577	12.4	0.7	15	1	AAK49868	ICG-1 oligonucleot
578	12.4	0.7	15	1	AAK52635	ICG-1 oligonucleot
579	12.4	0.7	15	1	AAK54012	ICG-1 oligonucleot
580	12.4	0.7	15	1	AAK49641	ICG-1 oligonucleot
581	12.4	0.7	15	1	AAK49643	ICG-1 oligonucleot
582	12.4	0.7	15	1	AAK54013	ICG-1 oligonucleot
583	12.4	0.7	15	1	AAK45225	ICG1P2 oligonucleo
584	12.4	0.7	15	1	AAK52480	ICG-1 oligonucleot
585	12.4	0.7	15	1	AAK52681	ICG-1 oligonucleot
586	12.4	0.7	15	1	AAK54011	ICG-1 oligonucleot
587	12.4	0.7	15	1	AAK49866	ICG-1 oligonucleot
588	12.4	0.7	15	1	AAK52634	ICG-1 oligonucleot
589	12.4	0.7	15	1	AAK54010	ICG-1 oligonucleot
590	12.4	0.7	15	1	AAK52622	ICG1P2 oligonucleo
591	12.4	0.7	15	1	AAK52679	ICG-1 oligonucleot
592	12.4	0.7	15	1	AAK45172	ICG1P2 oligonucleo
593	12.4	0.7	15	1	AAK54882	ICG-1 oligonucleot
594	12.4	0.7	15	1	AAK70390	Human DRD2 allele
595	12.4	0.7	15	1	AAK69430	Human IL4R1pha ge
596	12.4	0.7	15	1	AAK69387	Human IL4R1pha ge
597	12.4	0.7	15	1	AAK69537	Human IL4R1pha ge
598	12.4	0.7	15	1	AAK73926	Human SLC6A4 allel
599	12.4	0.7	15	1	AAK73930	Human SLC6A4 allel
600	12.4	0.7	15	1	ADK35833	Human anti-HER2 NC
601	12.4	0.7	15	1	ABL46309	Mouse scaveenger re
602	12.4	0.7	15	1	AAK43755	Human AGTR2 gene p
603	12.4	0.7	15	1	ABK32066	Human colon cancer
604	12.4	0.7	15	1	ACA09887	Necrosis factor ka
605	12.4	0.7	15	1	ACA09888	Necrosis factor ka
606	12.4	0.7	15	1	ABX94796	Beta-actin PCR pri
607	12.4	0.7	15	1	ADL50873	Human PKR substat
608	12.4	0.7	15	1	ADP64570	Human PKR substat
609	12.4	0.7	15	1	ADQ31062	C-fos mRNA detecti
610	12.4	0.7	15	1	ADQ11821	Poly Gly linker co
611	12.4	0.7	15	1	ADSI2596	Reverse RT-PCR pri
612	12.4	0.7	15	1	ADV95329	Sequence #1 from h
613	12.4	0.7	15	1	ADV25280	Human beta-actin c
614	12.4	0.7	15	1	ADY25936	Exemplary vector a
615	12.4	0.7	15	1	ADY50285	Randomized DNA poo
616	12.4	0.7	15	1	ADY52800	Human CHRNA2 gene
617	12.4	0.7	15	1	ADZ45541	Marine factor IX d

c 618 12.4 0.7 15 1 AEA40005
c 619 12.4 0.7 15 1 AEB21700
c 620 12.4 0.7 15 1 AEB08734
621 12.4 0.7 15 1 ABE99140

DNA encoding TNF r
Anti-Nogo-antibody
antibody 2A10 heav
Human c-fos FRET q

ALIGNMENTS

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RESULT 1
ADN12185/c
ID ADN12185 standard; DNA; 30 BP.
XX
AC ADN12185;
XX
DT 01-JUN-2004 (first entry)
XX
DE Tachykinin receptor NK1 amplifying primer NK13' (nested).
XX
KM Tachykinin; vascular disease; platelet aggregation; vulnery;
KM Thrombolytic; neurokinin; thrombosis; wound healing; PCR; primer; NK1;
KM NK3; tachykinin receptor; ss.
XX
OS Synthetic.
XX
PN W02004030695-A1.
XX
PD 15-APR-2004.
XX
PF 06-OCT-2003; 2003WO-GB004335.
XX
PR 04-OCT-2002; 2002GB-00023077.
XX
PA (UYRE-) UNIV READING.
XX
PI Gibbline JM, Lowry PJ, Graham GJ, Page NM;
XX WPI; 2004-330076/30.
XX
PT Use of tachykinin antagonist or agonist for treating diseases mediated by
PT binding of tachykinin ligand to its platelet associated receptor and
PT failure of platelet having tachykinin receptor to aggregate normally in
PT presence of tachykinin.
XX
PS Disclosure; Page 21; 46pp; English.
XX
CC The invention relates to the use of a tachykinin antagonist in the
CC manufacture of a medicament for treating e.g. a disease mediated by
CC binding of a tachykinin ligand to its platelet associated receptor. A
CC method of identifying an antagonist or agonist of tachykinin having a
CC platelet associated tachykinin receptor involves contacting a compound to
CC be evaluated with platelets expressing the tachykinin receptor in the
CC presence of the tachykinin and monitoring for an increase or decrease of
CC platelet aggregation. The agonist is useful in the manufacture of a
CC medicament in bulk quantities for treating a disease or conditions
CC mediated by binding of a tachykinin ligand to its platelet-associated
CC receptor (e.g. thrombosis), and by a failure of or a reduced ability of
CC platelet having a tachykinin receptor to aggregate normally in the
CC presence of the tachykinin; antagonizing or stimulating the effect of
CC tachykinin on platelet associated tachykinin receptor; and stimulating
CC platelet aggregation (e.g. wound healing). Sequences ADN12182-ADN12193
CC represent PCR primers for amplifying tachykinin receptors NK1, NK2 and
CC NK3.
XX
SQ Sequence 30 BP; 7 A; 8 C; 14 G; 1 T; 0 U; 0 Other;
XX
Query Match 1.7%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

RESULT 2
ID AED31523 standard; DNA; 28 BP.
XX AED31523;
AC
XX AED31523;
DT 15-DEC-2005 (first entry)
XX
DE Gerbil neurokinin 1 receptor (GNK1r) PCR primer SEQ ID NO:3.
XX
XX ss; gerbil neurokinin 1 receptor; GNK1r; schizophrenia; neuroleptic;
KM psychiatric disorder; micronutrient disorder; uropathic;
KM genitourinary disease; asthma; antiasthmatic; immune disorder;
KM inflammation; respiratory disease; pain; analgesic; neurological disease;
KM major depressive disorder; antidepressant; anxiety disorder;
KM tranquilizer; emesis; antiemetic; gastrointestinal disease;
KM inflammatory bowel disease; antiinflammatory; gastrointestinal-gen.;
KM gastrointestinal disease; irritable bowel syndrome; dyspepsia; migraine;
KM antiinigraine; primer; PCR.
XX
XX Homo sapiens.
OS Mus sp.
OS Cavia sp.
OS Synthetic.
XX WO2005090401-A1.
XX
XX 29-SEP-2005.
PD
XX 16-MAR-2005; 2005WO-GB001008.
PF
XX 20-MAR-2004; 2004GB-00006342.
PR
XX (ASTR) ASTRAZENCA AB.
PA (ASTR) ASTRAZENCA UK LTD.
XX
XX Drmotca T, Engberg S, Von Mentzer B;
PI
XX WPI; 2005-702670/72.
DR
XX
XX New polynucleotide comprising a sequence encoding gerbil neurokinin 1
PT receptor (GNK1r) polypeptide, useful in preparing a composition for
PT treating e.g., asthma, pain, depression, emesis, urine incontinence or
PT schizophrenia.
XX
XX Example 1; SEQ ID NO 3; 37pp; English.
PS
XX The invention relates to a new isolated polynucleotide molecule
XX comprising a nucleic acid sequence which encodes gerbil neurokinin 1
XX receptor (GNK1r) polypeptide or a polypeptide having at least 98%
XX sequence identity with AED31522. Also included are the following: an
XX expression vector comprising the polynucleotide molecule; a host cell
XX transformed or transfected with the expression vector; a method for
XX producing a polypeptide; an isolated or purified polypeptide comprising
XX the GNK1r amino acid sequence (see AED31522) or its variant having at
XX least 98% identity to the sequence, or its N-terminal or C-terminal
XX fragment of at least 350 amino acids in length; a method for identifying
XX a chemical compound capable of modulating the activity of GNK1r; a method
XX for identifying a therapeutic agent capable of modulating the activity of
XX GNK1r; a method of making a pharmaceutical composition; and a
XX pharmaceutical composition comprising a GNK1r modulator; and a
XX association with a diluent or carrier. The polynucleotide is useful in
XX preparing a composition for treating asthma, pain, depression, anxiety,
XX emesis, inflammatory bowel disease, irritable bowel syndrome, functional
XX dyspepsia, migraine, urine incontinence or schizophrenia. The present
XX sequence represents a PCR primer based on conserved regions identified by
XX alignment of human, mouse and guinea pig NK1r sequences and used to clone
XX gerbil neurokinin 1 receptor (GNK1r) cDNA.
XX
XX Sequence 28 BP; 2 A; 13 C; 3 G; 10 T; 0 U; 0 Other;
SQ

Query Match 1.6%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 993 GCTGCCCTTCACATCTCTCTCCTG 1020
DB 1 GCTGCCCTTCACATCTCTCTCCTG 28
RESULT 3
ID ABS60998 standard; DNA; 27 BP.
XX ABS60998;
AC
XX ABS60998;
DT 05-NOV-2002 (first entry)
XX
XX Human genotyping PCR primer #151.
DE
XX Human; ss; aminopeptidase P; XPNP2; bradykinin receptor B1; primer;
KM BDKRB1; tachykinin receptor B1; TACR1; Cl esterase inhibitor; C1NH;
KM kallikrein 1; KLK1; bradykinin receptor B2; BDKRB2; gene therapy;
KM angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;
KM polymorphisms; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
KM cardiovascular disease; angina pectoris; hypertension; heart failure;
KM myocardial infarction; ventricular hypertrophy; vascular disease;
KM aneurysm; embolism; thrombosis; coronary artery disease; angioedema;
KM arteriosclerosis; atherosclerosis; hypersensitivity; sepsis; PCR;
KM autoimmune disease; inflammatory arthritis; cancer; wound; genotyping;
KM viral infection; bacterial infection; fungal infection; CORD;
KM Chronic obstructive pulmonary disease; enterocolitis.
XX
XX Homo sapiens.
OS
XX WO200261131-A2.
PN
XX 08-AUG-2002.
PD
XX 03-DEC-2001; 2001WO-US047235.
PE
XX 04-DEC-2000; 2000US-0251015P.
PR 23-JAN-2001; 2001US-0263678P.
PR 02-MAR-2001; 2001US-0273037P.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
PA (TSUC/) TSUCHIHASHI Z.
PA (HUI/) HUI L.
XX
XX Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;
PI Swanson BN, Powell JR;
PI WPI; 2002-619265/66.
DR
XX
XX New isolated nucleic acid with at least one polymorphic position, useful
PT for detecting, diagnosing and treating disorders such as angioedema,
PT cancer, viral, bacterial or fungal infection, cardiovascular and
PT autoimmune diseases.
XX
XX Example 3; Page 913; 977pp; English.
PS
XX The invention relates to an isolated nucleic acid from a human gene
XX encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDKRB1),
XX tachykinin receptor B1 (TACR1), Cl esterase inhibitor (C1NH), kallikrein
XX 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme
XX 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one
XX polymorphic position. Also included are (1) a probe that hybridizes to a
XX polynucleotide position as provided in the detailed summary of single
XX nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
XX sequence; (2) analysing (M) at least one nucleic acid sample comprising
XX the sample from one or more individuals and determining the
XX nucleic acid sequence at one or more polymorphic positions in a gene
XX encoding a protein selected from the group above; (3) constructing (M2)
XX haplotypes using the genes comprising grouping at least two nucleic acids

CC : (4) identifying (M3) an individual at risk of developing a disorder
CC upon administration of an ACE inhibitor and/or vasopeptidase inhibitor.
CC using the polymorphic data; (5) a library of nucleic acids, each of which
CC comprises one or more polymorphic positions within a gene encoding a
CC human protein selected from the group above; and (6) genotyping (M4) an
CC individual comprising obtaining a nucleic acid sample, determining the
CC nucleotide present in at least one polymorphic position, and comparing at
CC least one position with a known data set. The genes, (M1, M2, M3 and M4)
CC and compositions are useful for detecting, diagnosing, treating,
CC preventing various disorders such as angiodema and diseases which
CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's
CC disease, trachomas, and cardiovascular diseases like angina pectoris,
CC hypertension, heart failure, myocardial infarction, ventricular
CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
CC artery disease, arteriosclerosis and/or atherosclerosis, and
CC hyperreactivity reactions, sepsis, autoimmune diseases, inflammatory
CC arthritis, cancer, wounds, viral, bacterial and fungal infection. Chronic
CC obstructive pulmonary disease (COPD) and enterocolitis (many other
CC diseases and disorders are listed in the specification). The
CC polynucleotides are also useful for chromosome identification. Antibodies
CC against the proteins may be utilised for immunophenotyping of cell lines
CC and biological samples. The present sequence is a genotyping PCR primer
CC for the gene encoding one of the proteins listed above
XX
SQ Sequence 27 BP; 9 A; 8 C; 0 G; 10 T; 0 U; 0 Other;
Query Match 1.5%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1590 TCAAAAATCTCATCTCTCCCTATCT 1616
Db 1 TCAAAAATCTCATCTCTCCCTATCT 27
RESULT 4
ADN12184
ID ADN12184 standard; DNA, 27 BP.
XX
AC ADN12184;
XX
DT 01-JUL-2004 (first entry)
XX
DE Tachykinin receptor NK1 amplifying primer NK15' (nested).
XX
XX Tachykinin; vascular disease; platelet aggregation; vulnery;
KM thrombolytic; neurokinin; thrombosis; wound healing; PCR; primer; NK1;
KM NK3; tachykinin receptor; SS.
XX
OS Synthetic.
XX
PN WO2004030695-A1.
XX
PD 15-APR-2004.
XX
PF 06-OCT-2003; 2003WO-GB004335.
XX
PR 04-OCT-2002; 2002GB-00023077.
XX
PA (UYRE-) UNIV READING.
XX
PI Gibbins JM, Lowry PJ, Graham GJ, Page NM;
XX
DR WPI; 2004-330076/30.
XX
XX Use of tachykinin antagonist or agonist for treating diseases mediated by
PT binding of tachykinin ligand to its platelet associated receptor and
PT failure of platelet having tachykinin receptor to aggregate normally in
PT presence of tachykinin.
XX
PS Disclosure; Page 21; 46pp; English.
XX
CC The invention relates to the use of a tachykinin antagonist in the

CC manufacture of a medicament for treating e.g. a disease mediated by
CC binding of a tachykinin ligand to its platelet associated receptor. A
CC method of identifying an antagonist or agonist of tachykinin having a
CC platelet associated tachykinin receptor involves contacting a compound to
CC be evaluated with platelets expressing the tachykinin receptor in the
CC presence of the tachykinin and monitoring for an increase or decrease of
CC platelet aggregation. The agonist is useful in the manufacture of a
CC medicament in bulk quantities for treating a disease or conditions
CC mediated by binding of a tachykinin ligand to its platelet-associated
CC receptor (e.g. thrombosis), and by a failure of or a reduced ability of
CC platelet having a tachykinin receptor to aggregate normally in the
CC presence of the tachykinin; antagonizing or stimulating the effect of
CC tachykinin on platelet associated tachykinin receptor; and stimulating
CC platelet aggregation (e.g. wound healing). Sequences ADN12182-ADN12193
CC represent PCR primers for amplifying tachykinin receptors NK1, NK2 and
CC NK3.
XX
SQ Sequence 27 BP; 6 A; 8 C; 8 G; 5 T; 0 U; 0 Other;
Query Match 1.5%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 213 GGATPACGTCCTCCGGTGACTCAGA 239
Db 1 GGATPACGTCCTCCGGTGACTCAGA 27
RESULT 5
ADN12182/c
ID ADN12182 standard; DNA, 27 BP.
XX
AC ADN12182;
XX
DT 01-JUL-2004 (first entry)
XX
DE Tachykinin receptor NK1 amplifying primer NK15'.
XX
XX Tachykinin; vascular disease; platelet aggregation; vulnery;
KM thrombolytic; neurokinin; thrombosis; wound healing; PCR; primer; NK1;
KM NK3; tachykinin receptor; SS.
XX
OS Synthetic.
XX
PN WO2004030695-A1.
XX
PD 15-APR-2004.
XX
PF 06-OCT-2003; 2003WO-GB004335.
XX
PR 04-OCT-2002; 2002GB-00023077.
XX
PA (UYRE-) UNIV READING.
XX
PI Gibbins JM, Lowry PJ, Graham GJ, Page NM;
XX
DR WPI; 2004-330076/30.
XX
XX Use of tachykinin antagonist or agonist for treating diseases mediated by
PT binding of tachykinin ligand to its platelet associated receptor and
PT failure of platelet having tachykinin receptor to aggregate normally in
PT presence of tachykinin.
XX
PS Disclosure; Page 21; 46pp; English.
XX
XX The invention relates to the use of a tachykinin antagonist in the
CC manufacture of a medicament for treating e.g. a disease mediated by
CC binding of a tachykinin ligand to its platelet associated receptor. A
CC method of identifying an antagonist or agonist of tachykinin having a
CC platelet associated tachykinin receptor involves contacting a compound to
CC be evaluated with platelets expressing the tachykinin receptor in the
CC presence of the tachykinin and monitoring for an increase or decrease of
CC platelet aggregation. The agonist is useful in the manufacture of a

CC medicament in bulk quantities for treating a disease or conditions
CC mediated by binding of a tachykinin ligand to its platelet-associated
CC receptor (e.g. thrombosis), and by a failure of or a reduced ability of
CC platelet having a tachykinin receptor to aggregate normally in the
CC presence of the tachykinin; antagonizing or stimulating the effect of
CC tachykinin on platelet associated tachykinin receptor; and stimulating
CC platelet aggregation (e.g. wound healing). Sequences ADN12182-ADN12193
CC represent PCR primers for amplifying tachykinin receptors NK1, NK2 and
CC NK3.
XX
SQ Sequence 27 BP; 3 A; 4 C; 11 G; 9 T; 0 U; 0 Other;
Query Match 1.5%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 711 CTACTCAACGACGAGACCATGCCAG 737
Db 27 CTACTCAACGACGAGACCATGCCAG 1
RESULT 6
AED31524/c
ID AED31524 standard; DNA; 27 BP.
XX
AC AED31524;
XX
DT 15-DEC-2005 (first entry)
XX
DE Gerbil neurokinin 1 receptor (GNK1r) PCR primer SEQ ID NO:4.
XX
XX ss: gerbil neurokinin 1 receptor; GNK1r; schizophrenia; neuroleptic;
KW psychiatric disorder; micturition disorder; uropathic;
KW genitourinary disease; asthma; antispasmodic; immune disorder;
KW inflammation; respiratory disease; antidepressant; anxiety disorder;
KW major depressive disorder; antiemetic; gastrointestinal disease;
KW tranquilizer; emesis; antiemetic; gastrointestinal disease;
KW inflammatory bowel disease; antiinflammatory; gastrointestinal gen.;
KW gastrointestinal disease; irritable bowel syndrome; dyspepsia; migraine;
KW antimigraine; primer; PCR.
XX
XX Homo sapiens.
OS Mus sp.
OS Rattus sp.
OS Synthetic.
XX
XX WO2005090401-A1.
XX
XX 29-SEP-2005.
XX
XX 16-MAR-2005; 2005WO-GB001008.
XX
XX 20-MAR-2004; 2004GB-00006342.
XX
XX (ASTR) ASTRAZENECA AB.
XX (ASTR) ASTRAZENECA UK LTD.
XX
XX Drmotca T, Engberg S, Von Mentzer B;
XX
XX WPI; 2005-702670/72.
XX
XX New polynucleotide comprising a sequence encoding gerbil neurokinin 1
XX receptor (GNK1r) polypeptide, useful in preparing a composition for
XX treating e.g., asthma, pain, depression, emesis, urine incontinence or
XX schizophrenia.
XX
XX Example 1; SEQ ID NO 4; 37bp; English.
XX
XX The invention relates to a new isolated polynucleotide molecule
XX comprising a nucleic acid sequence which encodes gerbil neurokinin 1
XX receptor (GNK1r) polypeptide or a polypeptide having at least 98%
XX sequence identity with AED31522. Also included are the following: an
XX expression vector comprising the polynucleotide molecule; a host cell

CC transformed or transfected with the expression vector; a method for
CC producing a polypeptide; an isolated or purified polypeptide comprising
CC the GNK1r amino acid sequence (see AED31522) or its variant having at
CC least 98% identity to the sequence, or its N-terminal or C-terminal
CC fragment of at least 350 amino acids in length; a method for identifying
CC a chemical compound capable of modulating the activity of GNK1r; a method
CC for identifying a therapeutic agent capable of modulating the activity of
CC GNK1r; a method of making a pharmaceutical composition; and a
CC pharmaceutical composition comprising a GNK1r modulator, or its salt in
CC association with a diluent or carrier. The polynucleotide is useful in
CC preparing a composition for treating asthma, pain, depression, anxiety,
CC emesis, inflammatory bowel disease, irritable bowel syndrome, functional
CC dyspepsia, migraine, urine incontinence or schizophrenia. The present
CC sequence represents a PCR primer based on conserved regions identified by
CC alignment of human, mouse and rat NK1r sequences and used to clone gerbil
CC neurokinin 1 receptor (GNK1r) cDNA.
XX
SQ Sequence 27 BP; 8 A; 8 C; 10 G; 1 T; 0 U; 0 Other;
Query Match 1.5%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 669 CATCTGGGCTCTGCTCTCTCTCTGTC 695
Db 27 CATCTGGGCTCTGCTCTCTCTCTGTC 1
RESULT 7
ABS61087/c
ID ABS61087 standard; DNA; 27 BP.
XX
AC ABS61087;
XX
DT 05-NOV-2002 (first entry)
XX
XX Human automated genomic bit analysis (GBA) PCR primer #64.
XX
XX Human; ss: aminopeptidase P; XPNBP2; bradykinin receptor B1; primer;
KW BDKRB1; tachykinin receptor B1; TACR1; Cl esterase inhibitor; C1NH;
KW kallikrein 1; KKL1; bradykinin receptor B2; BDKRB2; gene therapy;
KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;
KW polypeptidase; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
KW cardiovascular disease; angina pectoris; hypertension; heart failure;
KW myocardial infarction; ventricular hypertrophy; vascular disease;
KW aneurysm; embolism; thrombosis; coronary artery disease; angioedema;
KW arteriosclerosis; atherosclerosis; hypersensitivity; sepsis; PCR;
KW autoimmune disease; inflammatory arthritis; cancer; genotyping;
KW viral infection; bacterial infection; fungal infection; COPD; GBA;
KW Chronic obstructive pulmonary disease; enterocolitis;
KW automated genetic bit analysis.
XX
XX Homo sapiens.
XX
XX WO200261131-A2.
XX
XX 08-AUG-2002.
XX
XX 03-DEC-2001; 2001WO-US047235.
XX
XX 04-DEC-2000; 2000US-0251015P.
XX 23-JAN-2001; 2001US-0263678P.
XX 02-MAR-2001; 2001US-0273037P.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX (TSUC/) TSUCHIHASHI Z.
XX (HUTL/) HUT L.
XX
XX Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;
XX Swanson BN, Powell JR;
XX WPI; 2002-619265/66.
XX

PT New isolated nucleic acid with at least one polymorphic position, useful
PT for detecting, diagnosing and treating disorders such as angioedema,
PT cancer, viral, bacterial or fungal infection, cardiovascular and
PT autoimmune diseases.

XX Example 3; Page 932; 977pp; English.

CC The invention relates to an isolated nucleic acid from a human gene
CC encoding aminopeptidase P (APNBP2), bradykinin receptor B1 (BDRB1),
CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein
CC 1 (KLK1), bradykinin receptor B2 (BDRB2), angiotensin converting enzyme
CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one
CC polymorphic position. Also included are (1) a probe that hybridises to a
CC polymorphic position as provided in the detailed summary of single
CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising
CC obtaining the sample from one or more individuals and determining the
CC nucleic acid sequence at one or more polymorphic positions in a gene
CC encoding a protein selected from the group above; (3) constructing (M2)
CC haplotypes using the genes comprising grouping at least two nucleic acids
CC; (4) identifying (M3) an individual at risk of developing a disorder
CC upon administration of an ACE inhibitor and/or vasopeptidase inhibitor
CC using the polymorphic data; (5) a library of nucleic acids, each of which
CC comprises one or more polymorphic positions within a gene encoding a
CC human protein selected from the group above; and (6) genotyping (M4) an
CC individual comprising obtaining a nucleic acid sample, determining the
CC nucleotide present in at least one polymorphic position, and comparing at
CC least one position with a known data set. The genes, (M1, M2, M3 and M4)
CC and compositions are useful for detecting, diagnosing, treating,
CC preventing various disorders such as angioedema and diseases which
CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's
CC disease, trachomas, and cardiovascular diseases like angina pectoris,
CC hypertension, heart failure, myocardial infarction, ventricular
CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
CC artery disease, arteriosclerosis and/or atherosclerosis, and
CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory
CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic
CC obstructive pulmonary disease (COPD) and enterocolitis (many other
CC diseases and disorders are listed in the specification). The
CC polynucleotides are also useful for chromosome identification. Antibodies
CC against the proteins may be utilised for immunophenotyping of cell lines
CC and biological samples. The present sequence is a genotyping PCR primer
CC for the gene encoding one of the proteins listed above, using the method
CC of automated genetic bit analysis, GBA

XX SQ Sequence 27 BP; 6 A; 10 C; 3 G; 7 T; 0 U; 1 Other;

Query Match 1.5%; Score 26; DB 1; Length 27;
Best Local Similarity 96.3%; Pred. No. 12;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1539 GGAAGTGGCAAAAGGTCAGTATGGGT 1565

Db 27 GGAAGTGGCAAAAGGTCAGTATGGGT 1

RESULT 8

ID ADN12193/c standard; DNA; 30 BP.

AC ADN12193;

XX 01-JUL-2004 (first entry)

DE Tachykinin receptor NK3 amplifying primer NK3' (nested).

XX Tachykinin; vascular disease; platelet aggregation; vulnary;

KW thrombolytic; neurokinin; thrombosis; wound healing; PCR; primer; NK1;

XX NK3; tachykinin receptor; ss.

OS Synthetic.

XX WO2004030695-A1.

XX 15-APR-2004.

XX 06-OCT-2003; 2003WO-GB004335.

XX 04-OCT-2002; 2002GB-00023077.

XX (UTRE-) UNIV READING.

PI Gibbins JM, Lowry PJ, Graham GJ, Page NM;

DR WPI, 2004-330076/30.

PT Use of tachykinin antagonist or agonist for treating diseases mediated by
PT binding of tachykinin ligand to its platelet associated receptor and
PT failure of platelet having tachykinin receptor to aggregate normally in
PT presence of tachykinin.

PS Disclosure; Page 21; 46pp; English.

CC The invention relates to the use of a tachykinin antagonist in the
CC manufacture of a medicament for treating e.g. a disease mediated by
CC binding of a tachykinin ligand to its platelet associated receptor. A
CC method of identifying an antagonist or agonist of tachykinin having a
CC platelet associated tachykinin receptor involves contacting a compound to
CC be evaluated with platelets expressing the tachykinin receptor in the
CC presence of the tachykinin and monitoring for an increase or decrease of
CC platelet aggregation. The agonist is useful in the manufacture of a
CC medicament in bulk quantities for treating a disease or conditions
CC mediated by binding of a tachykinin ligand to its platelet-associated
CC receptor (e.g. thrombosis), and by a failure of or a reduced ability of
CC platelet having a tachykinin receptor to aggregate normally in the
CC presence of the tachykinin; antagonizing or stimulating the effect of
CC tachykinin on platelet associated tachykinin receptor; and stimulating
CC platelet aggregation (e.g. wound healing). Sequences ADN12182-ADN12193
CC represent PCR primers for amplifying tachykinin receptors NK1, NK2 and
CC NK3.

XX SQ Sequence 30 BP; 7 A; 7 C; 11 G; 5 T; 0 U; 0 Other;

Query Match 1.5%; Score 25.8; DB 1; Length 30;
Best Local Similarity 93.1%; Pred. No. 17;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 556 GTCTTCGCCAGTATCTCATGACGCGC 584

Db 30 GTCTTCGCCAGTATCTCATGACGCGC 2

RESULT 9

ID AAH26071 standard; DNA; 25 BP.

AC AAH26071;

XX 05-SEP-2001 (first entry)

DE Human NK-1 gene antisense PCR primer.

XX NK-1; neurokinin receptor; PPT-1; human; preprotachykinin; cytostatic;
KW analgesic; antiarthritic; antiasthmatic; antidepressant; breast cancer;
KW metastasis; pain; arthritis; aggression; depression;
KW haematopoietic disorder; gene therapy; PCR primer; ss.

XX Homo sapiens.

OS WO200146399-A1.

XX 28-JUN-2001.

XX 23-DEC-2000; 2000WO-US035047.

XX 23-DEC-1999; 99US-0171970P.

XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
PA Rameshwar P, Gascon P;
PI WPI; 2001-408640/43.
XX
XX
XX Novel promoters and 3' regulatory region of preprotrachykinin gene, useful
PT for treating pain, asthma, arthritis; aggressive behavior, depression,
PT bone marrow metastasis, and hematopoietic disorders.
XX
XX Example; Page 35; 78pp; English.
XX The present sequence is that of the antisense primer used in the PCR
CC amplification of a fragment of the human neurokinin NK-1 receptor gene.
CC The sense primer is given in AAH26070. Quantitative PCR was performed on
CC total RNA extracted from breast cancer cells. The results showed that NK-
CC 1 expression is up-regulated in breast cancers. Agonists and antagonists
CC that influence expression of NK-1 can be used for the treatment of breast
CC cancer, bone marrow metastasis, pain, asthma, arthritis, aggressive
CC behaviour and depression associated with NK-1 imbalance
CC
CC
SQ Sequence 25 BP; 7 A; 4 C; 7 G; 7 T; 0 U; 0 Other;
Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 400 AGGACAGTGCAGCACTATTCTTCTGG 424
DB 1 AGGACAGTGCAGCACTATTCTTCTGG 25
RESULT 10
AAH26070/c
ID AAH26070 standard; DNA; 25 BP.
XX
XX AAH26070;
AC
XX
DT 05-SRP-2001 (first entry)
XX
XX Human NK-1 gene sense PCR primer.
DE
XX NK-1; neurokinin receptor; PPT-1; human; preprotrachykinin; cytostatic;
KW analgesic; antiarthritic; antiasthmatic; antidepressant; breast cancer;
KW metastasis; pain; arthritis; aggression; depression;
KW haematopoietic disorder; gene therapy; PCR primer; ss.
XX
OS Homo sapiens.
XX
XX WO200146399-A1.
XX
XX 28-JUN-2001.
PD
XX 23-DEC-2000; 2000WO-US035047.
PF
XX 23-DEC-1999; 99US-0171970P.
PR
XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
PA
XX Rameshwar P, Gascon P;
PI
XX WPI; 2001-408640/43.
DR
XX Novel promoters and 3' regulatory region of preprotrachykinin gene, useful
PT for treating pain, asthma, arthritis, aggressive behavior, depression,
PT bone marrow metastasis, and hematopoietic disorders.
XX
XX Example; Page 35; 78pp; English.
XX The present sequence is that of the sense primer used in the PCR
CC amplification of a fragment of the human neurokinin NK-1 receptor gene.
CC The antisense primer is given in AAH26071. Quantitative PCR was performed

CC on total RNA extracted from breast cancer cells. The results showed that
CC NK-1 expression is up-regulated in breast cancers. Agonists and
CC antagonists that influence expression of NK-1 can be used for the
CC treatment of breast cancer, bone marrow metastasis, pain, asthma,
CC arthritis, aggressive behaviour and depression associated with NK-1
CC imbalance
CC
SQ Sequence 25 BP; 6 A; 5 C; 6 G; 8 T; 0 U; 0 Other;
Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1041 CTACTGGAAGAACTTTATCCAGCAG 1065
DB 25 CTACTGGAAGAACTTTATCCAGCAG 1
RESULT 11
ABS60907/c
ID ABS60907 standard; DNA; 25 BP.
XX
XX ABS60907;
AC
XX
DT 05-NOV-2002 (first entry)
XX
XX Human genotyping PCR primer #60.
DE
XX
XX Human; ss; aminopeptidase P; XPNBP2; bradykinin receptor B1; primer;
KW BDKRB1; tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH;
KW kallikrein 1; KLK1; bradykinin receptor B2; BDKRB2; gene therapy;
KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;
KW polymorphisms; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
KW cardiovascular disease; angina pectoris; hypertension; heart failure;
KW myocardial infarction; ventricular hypertrophy; vascular disease;
KW aneurysm; embolism; thrombosis; coronary artery disease; angioedema;
KW arteriosclerosis; atherosclerosis; hypersensitivity; sepsis; PCR;
KW autoimmune disease; inflammatory arthritis; cancer; wound; genotyping;
KW viral infection; bacterial infection; fungal infection; COPD;
KW Chronic obstructive pulmonary disease; enterocolitis.
XX
XX Homo sapiens.
OS
XX
XX WO200261131-A2.
XX
XX 08-AUG-2002.
PD
XX
XX 03-DEC-2001; 2001WO-US047235.
PF
XX 04-DEC-2000; 2000US-0251015P.
PR
XX 23-JAN-2001; 2001US-0263678P.
PR
XX 02-MAR-2001; 2001US-0273037P.
PR
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
PA
XX (TSUC/) TSUCHIHASHI Z.
PA
XX (HUTL/) HUTI L.
XX
XX Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;
PI Swanson BN, Powell JR;
XX
XX WPI; 2002-619265/66.
DR
XX
XX New isolated nucleic acid with at least one polymorphic position, useful
PT for detecting, diagnosing and treating disorders such as angioedema,
PT cancer, viral, bacterial or fungal infection, cardiovascular and
PT autoimmune diseases.
XX
XX Example 3; Page 898; 977pp; English.
XX The invention relates to an isolated nucleic acid from a human gene
CC encoding aminopeptidase P (XPNBP2), bradykinin receptor B1 (BDKRB1),
CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein
CC 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme

2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one polymorphic position. Also included are (1) a probe that hybridises to a polymorphic position as provided in the detailed summary of single nucleotide polymorphisms comprising additional 5' and 3' flanking genomic sequence; (2) analysing (M1) at least one nucleic acid sample comprising obtaining the sample from one or more individuals and determining the nucleic acid sequence at one or more polymorphic positions in a gene encoding a protein selected from the group above; (3) constructing (M2) haplotypes using the genes comprising grouping at least two nucleic acids; (4) identifying (M3) an individual at risk of developing a disorder upon administration of an ACE inhibitor and/or vasopeptidase inhibitor using the polymorphic data; (5) a library of nucleic acids, each of which comprises one or more polymorphic positions within a gene encoding a human protein selected from the group above; and (6) genotyping (M4) an individual comprising obtaining a nucleic acid sample, determining the nucleotide present in at least one polymorphic position, and comparing at least one position with a known data set. The genes, (M1, M2, M3 and M4) and compositions are useful for detecting, diagnosing, treating, and preventing various disorders such as angioedema and diseases which involve angioedema like haemangiomas, tumours, sarcomas, Crohn's disease, trachomas, and cardiovascular diseases like angina pectoris, coronary artery disease, arteriosclerosis and/or atherosclerosis, and hyperresponsivity reactions, sepsis, autoimmune diseases, inflammatory arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic obstructive pulmonary disease (COPD) and enterocolitis (many other diseases and disorders are listed in the specification). The polymorphisms are also useful for chromosome identification. Antibodies against the proteins may be utilised for immunophenotyping of cell lines and biological samples. The present sequence is a genotyping PCR primer for the gene encoding one of the proteins listed above

Sequence 25 BP; 4 A; 3 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

707 GCTACTACTCAACGACGACCAT 731
Db 25 GCTACTACTCAACGACGACCAT 1

RESULT 12
ABS61082/c
ID ABS61082 standard; DNA; 25 BP.

AC ABS61082;

XX 05-NOV-2002 (first entry)

DE Human automated genomic bit analysis (GBA) PCR primer #59.

XX
KW Human; ss; antipeptidase P; XPNRP2; bradykinin receptor B1; primer;
BMRB1; tachykinin receptor B1; TRACR1; Cl esterase inhibitor; CLNH;
Kallikrein 1; KKL1; bradykinin receptor B2; BDKRB2; gene therapy;
KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;
KW polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
KW cardiovascular disease; angina pectoris; hyperextension; heart failure;
KW myocardial infarction; ventricular hypertrophy; vascular disease;
KW aneurysm; embolism; thrombosis; coronary artery disease; angioedema;
KW arteriosclerosis; atherosclerosis; hyperresponsivity; sepsis; PCR;
KW autoimmune disease; inflammatory arthritis; cancer; wound; genotyping;
KW viral infection; bacterial infection; fungal infection; COPD; GBA;
KW Chronic obstructive pulmonary disease; enterocolitis;
KW automated genetic bit analysis.

XX Homo sapiens.
XX OS
XX FN WO200261131-A2.
XX PD 08-AUG-2002.

XX 03-DEC-2001; 2001WO-US047235.

PF 04-DEC-2000; 2000US-0251015P.
XX 23-JAN-2001; 2001US-0263678P.
PR 02-MAR-2001; 2001US-0273037P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.
PA (TSUC/) TSUCHIHASHI Z.
PA (HUI/L) HUI L.

PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;
PI Swanson EM, Powell JR;

DR WPI; 2002-619265/66.

XX New isolated nucleic acid with at least one polymorphic position, useful
PT for detecting, diagnosing and treating disorders such as angioedema,
PT cancer, viral, bacterial or fungal infection, cardiovascular and
PT autoimmune diseases.

XX Example 3; Page 931; 977pp; English.

XX The invention relates to an isolated nucleic acid from a human gene
CC encoding antipeptidase P (XPNRP2), bradykinin receptor B1 (BDKRB1),
CC tachykinin receptor B1 (TRACR1), Cl esterase inhibitor (CLNH), kallikrein
CC 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme
CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one
CC polymorphic position. Also included are (1) a probe that hybridises to a
CC polymorphic position as provided in the detailed summary of single
CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising
CC obtaining the sample from one or more individuals and determining the
CC nucleic acid sequence at one or more polymorphic positions in a gene
CC encoding a protein selected from the group above; (3) constructing (M2)
CC haplotypes using the genes comprising grouping at least two nucleic acids
CC; (4) identifying (M3) an individual at risk of developing a disorder
CC upon administration of an ACE inhibitor and/or vasopeptidase inhibitor
CC using the polymorphic data; (5) a library of nucleic acids, each of which
CC comprises one or more polymorphic positions within a gene encoding a
CC human protein selected from the group above; and (6) genotyping (M4) an
CC individual comprising obtaining a nucleic acid sample, determining the
CC nucleotide present in at least one polymorphic position, and comparing at
CC least one position with a known data set. The genes, (M1, M2, M3 and M4)
CC and compositions are useful for detecting, diagnosing, treating,
CC preventing various disorders such as angioedema and diseases which
CC involve angioedema like haemangiomas, tumours, sarcomas, Crohn's
CC disease, trachomas, and cardiovascular diseases like angina pectoris,
CC hypertension, heart failure, myocardial infarction, ventricular
CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
CC artery disease, arteriosclerosis and/or atherosclerosis, and
CC hyperresponsivity reactions, sepsis, autoimmune diseases, inflammatory
CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic
CC obstructive pulmonary disease (COPD) and enterocolitis (many other
CC diseases and disorders are listed in the specification). The
CC polymorphisms are also useful for chromosome identification. Antibodies
CC against the proteins may be utilised for immunophenotyping of cell lines
CC and biological samples. The present sequence is a genotyping PCR primer
CC for the gene encoding one of the proteins listed above, using the method
CC of automated genetic bit analysis, GBA

XX Sequence 25 BP; 6 A; 5 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 544 CCCATGCGCGCTGCTTCCGACGTA 568
Db 25 CCCATGCGCGCTGCTTCCGACGTA 1

RESULT 13

AB61088/c
ID AB61088 standard; DNA; 27 BP.
XX
AC AB61088;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human automated genomic b1t analysis (GBA) PCR primer #65.
XX
KW Human; ss; aminopeptidase P; XPNBP2; bradykinin receptor B1; primer;
KW BDKRB1; tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH;
KW kallikrein 1; KKL1; bradykinin receptor B2; BDKRB2; gene therapy;
KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;
KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;
KW cardiovascular disease; angina pectoris; hypertension; heart failure;
KW myocardial infarction; ventricular hypertrophy; vascular disease;
KW aneurysm; embolism; thrombosis; coronary artery disease; angiodema;
KW arteriosclerosis; atherosclerosis; hypersensitivity; sepsis; PCR;
KW autoimmune disease; inflammatory arthritis; cancer; wound; genotyping;
KW viral infection; bacterial infection; fungal infection; COPD; GBA;
KW chronic obstructive pulmonary disease; enterocolitis;
KW automated genetic b1t analysis.
OS Homo sapiens.
XX
PN WO200261131-A2.
XX
PD 08-AUG-2002.
XX
PF 03-DEC-2001; 2001WO-US047235.
XX
PR 04-DEC-2000; 2000US-0251015P.
PR 23-JAN-2001; 2001US-0263678P.
PR 02-MAR-2001; 2001US-0273037P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
PA (TSUC/) TSUCHIHASHI Z.
XX
HU1 L.
PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;
PI Shannon BN, Powell JR;
XX
DR WPI; 2002-619265/66.
XX
PT New isolated nucleic acid with at least one polymorphic position, useful
PT for detecting, diagnosing and treating disorders such as angioedema,
PT cancer, viral, bacterial or fungal infection, cardiovascular and
PT autoimmune diseases.
XX
PS Example 3; Page 932; 977pp; English.
XX
CC The invention relates to an isolated nucleic acid from a human gene
CC encoding aminopeptidase P (XPNBP2), bradykinin receptor B1 (BDKRB1),
CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein
CC 1 (KKL1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme
CC 2 (ACE2) or protease inhibitor 4 (P14), comprising at least one
CC polymorphic position. Also included in the detailed summary of single
CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising
CC obtaining the sample from one or more individuals and determining the
CC nucleic acid sequence at one or more polymorphic positions in a gene
CC encoding a protein selected from the group above; (3) constructing (M2)
CC haplotypes using the genes comprising grouping at least two nucleic acids
CC; (4) identifying (M3) an individual at risk of developing a disorder
CC upon administration of an ACE inhibitor and/or vasopressinase inhibitor
CC using the polymorphic data; (5) a library of nucleic acids, each of which
CC comprises one or more polymorphic positions within a gene encoding a
CC human protein selected from the group above; and (6) genotyping (M4) an
CC individual comprising obtaining a nucleic acid sample, determining the
CC nucleotide present in at least one polymorphic position, and comparing at
CC least one position with a known data set. The genes, (M1, M2, M3 and M4)
CC and compositions are useful for detecting, diagnosing, treating,

CC preventing various disorders such as angioedema and diseases which
CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's
CC disease, trachomas, and cardiovascular diseases like angina pectoris,
CC hypertension, heart failure, myocardial infarction, ventricular
CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
CC artery disease, arteriosclerosis and/or atherosclerosis, and
CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory
CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic
CC obstructive pulmonary disease (COPD) and enterocolitis (many other
CC diseases and disorders are listed in the specification). The
CC polynucleotides are also useful for chromosome identification. Antibodies
CC against the proteins may be utilised for immunophenotyping of cell lines
CC and biological samples. The present sequence is a genotyping PCR primer
CC for the gene encoding one of the proteins listed above, using the method
CC of automated genetic b1t analysis, GBA
XX
SQ Sequence 27 BP; 7 A; 3 C; 11 G; 4 T; 0 U; 2 Other;
XX
Query Match 1.4%; Score 25; DB 1; Length 27;
Best Local Similarity 92.6%; Pred. No. 17;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
CY 1345 TCCCTGACCTGACCTGCAACTGCTCT 1371
Db 27 TCCCTGACCTGACCTGCAACTGCTCT 1
XX
RESULT 14
ID AAQ37209/c
XX AAQ37209 standard; DNA; 24 BP.
XX
AC AAQ37209;
XX
DT 25-MAR-2003 (revised)
DT 17-JUN-1993 (first entry)
XX
DE PCR primer #2 to amplify substance P receptor coding region.
XX
KW human substance P receptor protein; SP; neurotransmitter; neuromodulator;
KW central nervous system; peripheral nervous system;
KW gastrointestinal disorders; inflammation; immune disease.
XX
OS Synthetic.
XX
PN WO9303137-A1.
XX
PD 18-FEB-1993.
XX
PF 05-AUG-1992; 92WO-US006532.
XX
PR 07-AUG-1991; 91US-00741200.
XX
PA (UNITW) UNIV WASHINGTON.
XX
PI Krause JE;
XX
DR WPI; 1993-076495/09.
XX
PT New human substance P receptor protein and DNA encoding it - used e.g.
PT for screening substance P antagonists.
XX
PS Example; Page 9; 40pp; English.
XX
CC This PCR primer was used with AAQ37208 to amplify the predicted human
CC substance P receptor coding region from IM-9 cDNA. The amplified fragment
CC was blunt end ligated into SmaI-digested pBS. Transformsants were further
CC analysed by restriction mapping and by sequence analysis. One cDNA was
CC isolated after restriction with HindIII and BamHI (present in the pBS
CC polylinker) and made blunt ended with Klenow, as was pM2 after BamHI
CC digestion. The cDNA was ligated to pM2 and used to transform E. coli XL-1
CC Blue cells by electroporation. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX

Sequence 24 BP; 9 A; 3 C; 9 G; 3 T; 0 U; 0 Other;
Query Match 1.4%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1411 TTCCTCCAAATGTCCTCTCTAG 1434
24 TTCCTCCAAATGTCCTCTCTAG 1
Db

RESULT 15
AED51264
ID AED51264 standard; DNA; 24 BP.
XX AED51264;
AC
XX
DT 29-DEC-2005 (first entry)
XX

Human tachykinin receptor 1 (TACR1) cDNA probe.
XX
XX Screening; diagnosis; tachykinin receptor 1; TACR1;
KW cardiovascular disease; infection; dermatological disease;
KW gastrointestinal disease; cancer; neoplasm; inflammation;
KW metabolic disorder; hematological disease; respiratory disease;
KW musculoskeletal disease; neurological disease; gynecological disorder;
KW gynecology and obstetrics; genitourinary disease; cardiovascular disorder;
KW cardiac; hypotensive; antimicrobial; antibacterial; fungicide; virucide;
KW dermatological; antiparasitic; gastrointestinal-gen.; antineoplastic;
KW cytostatic; immunosuppressive; anorectic; antidiabetic; antianemic;
KW respiratory-gen.; asthmatic; muscular-gen.; osteopathic;
KW antiarthritic; neuroprotective; nootropic; antiparkinsonian;
KW gynecological; antifertility; nephrotropic; metabolic; uropathic;
KW probe; ss.
XX
XX Homo sapiens.
OS
XX
XX W02005100986-A1.
PN
XX
XX 27-OCT-2005.
PD
XX
XX 02-APR-2005; 2005WO-EP003465.
PF
XX
XX 15-APR-2004; 2004EP-00008923.
PR
XX
XX (FARB) BAYER HEALTHCARE AG.
PA
XX
XX Golz S, Brueggemeier U, Geerts A;
PI
XX
XX WPI; 2005-758663/77.
DR

Screening for therapeutic agents, useful for treating a disease, e.g.
PT cardiovascular, infections, dermatological, cancer, inflammation,
PT respiratory, or neurological, comprises contacting a test compound with a
PT tachykinin receptor 1.
XX
XX Example 2; SEQ ID NO 5; 118bp; English.
XX

The invention relates to a method of screening for therapeutic agents
CC useful for treating a disease, comprising contacting a test compound with
CC a tachykinin receptor 1 (TACR1) polypeptide or polynucleotide, detecting
CC binding of the polypeptide or polynucleotide, determining the activity of
CC TACR1 at a certain concentration of the test compound, in the absence of
CC the compound or in the presence of a known regulator of the TACR1
CC polypeptide. The invention also relates to a method of diagnosing a
CC disease in a mammal comprising determining the amount of a TACR1
CC polynucleotide in a sample taken from the mammal and determining the
CC amount of TACR1 polynucleotide in healthy and/or diseased mammals, a
CC pharmaceutical composition for treating diseases in a mammal comprising a
CC TACR1 polynucleotide or polypeptide or a therapeutic agent which binds to
CC or regulates the activity of a TACR1 polypeptide, and preparing a
CC pharmaceutical composition useful for treating diseases in a mammal. The
CC disease is chosen from cardiovascular diseases, infections,

dermatological diseases, gastrointestinal diseases, cancer, inflammation,
CC metabolic disorders, hematological diseases, respiratory diseases,
CC musculoskeletal diseases, neurological diseases, gynecological disorders
CC and genitourinary diseases. This sequence represents a probe used in
CC expression profiling of the human TACR1 cDNA of the invention. The probe
CC is labeled with FAM (carboxyfluorescein succinimidyl ester) as a reporter
CC dye and TAMRA (carboxytetramethylrhodamine) as a quencher.
XX

Sequence 24 BP; 4 A; 6 C; 7 G; 7 T; 0 U; 0 Other;
Query Match 1.4%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
296 CTTGGCAATGTCCTTTGGGCGAG 319
1 CTTGGCAATGTCCTTTGGGCGAG 24
Db

RESULT 16
ABS61086
ID ABS61086 standard; DNA; 27 BP.
XX
XX ABS61086;
AC
XX
DT 05-NOV-2002 (first entry)
XX

Human automated genomic bit analysis (GBA) PCR primer #63.
XX
XX Human; ss; aminopeptidase P; XPNP2; bradykinin receptor B1; primer;
KW BDKRB1; tachykinin receptor B1; TACR1; Cl esterase inhibitor; C1NH;
KW kallikrein 1; KUK1; bradykinin receptor B1; BDKRB2; gene therapy;
KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;
KW polymorphisms; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
KW cardiovascular disease; angina pectoris; hypertension; heart failure;
KW myocardial infarction; ventricular hypertrophy; vascular disease;
KW aneurysm; embolism; thrombosis; coronary artery disease; angiodaema;
KW arteriosclerosis; atherosclerosis; hypersensitivity; sepsis; PCR;
KW autoimmune disease; inflammatory arthritis; cancer; wound; genotyping;
KW viral infection; bacterial infection; fungal infection; COPD; GBA;
KW Chronic obstructive pulmonary disease; enterocolitis;
KW automated genetic bit analysis.
XX
XX Homo sapiens.
OS
XX
XX W0200261131-A2.
PN
XX
XX 08-AUG-2002.
PD
XX
XX 03-DEC-2001; 2001WO-US047235.
PF
XX
XX 04-DEC-2000; 2000US-0251015P.
PR
XX
XX 23-JAN-2001; 2001US-0263678P.
PR
XX
XX 02-MAR-2001; 2001US-0273037P.
PR
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
PA
XX
XX (TSUC/) TSUCHIHASHI Z.
PA
XX
XX (HUIL/) HUI L.
PI
XX
XX Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;
PI Swanson BN, Powell JR,
XX
XX WPI; 2002-619265/66.
DR

New isolated nucleic acid with at least one polymorphic position, useful
PT for detecting, diagnosing and treating disorders such as angioedema,
PT cancer, viral, bacterial or fungal infection, cardiovascular and
PT autoimmune diseases.
XX
XX Example 3; Page 932; 977bp; English.
XX

The invention relates to an isolated nucleic acid from a human gene
CC encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDKRB1),

CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein
 CC 1 (KAL1), bradykinin receptor B2 (BKR2), angiotensin converting enzyme
 CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one
 CC polymorphic position. Also included are (1) a probe that hybridizes to a
 CC polymorphic position as provided in the detailed summary of single
 CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
 CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising
 CC obtaining the sample from one or more individuals and determining the
 CC nucleic acid sequence at one or more polymorphic positions in a gene
 CC encoding a protein selected from the group above; (3) constructing (M2)
 CC haplotypes using the genes comprising grouping at least two nucleic acids
 CC ; (4) identifying (M3) an individual at risk of developing a disorder
 CC upon administration of an ACE inhibitor and/or vasopeptidase inhibitor
 CC using the polymorphic data; (5) a library of nucleic acids, each of which
 CC comprises one or more polymorphic positions within a gene encoding a
 CC human protein selected from the group above; and (6) genotyping (M4) an
 CC individual comprising obtaining a nucleic acid sample, determining the
 CC nucleotide present in at least one polymorphic position, and comparing at
 CC least one position with a known data set. The genes, (M1, M2, M3 and M4)
 CC and compositions are useful for detecting, diagnosing, treating,
 CC preventing various disorders such as angioedema and diseases which
 CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's
 CC disease, trachomas, and cardiovascular diseases like angina pectoris,
 CC hypertension, heart failure, myocardial infarction, ventricular
 CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
 CC artery disease, arteriosclerosis and/or atherosclerosis, and
 CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory
 CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic
 CC obstructive pulmonary disease (COPD) and enterocolitis (many other
 CC diseases and disorders are listed in the specification). The
 CC polynucleotides are also useful for chromosome identification. Antibodies
 CC against the proteins may be utilised for immunophenotyping of cell lines
 CC and biological samples. The present sequence is a genotyping PCR primer
 CC for the gene encoding one of the proteins listed above, using the method
 CC of automated genetic bit analysis, GBA

XX SQ Sequence 27 BP; 3 A; 8 C; 3 G; 10 T; 0 U; 3 Other;

Query Match 1.4%; Score 24; DB 1; Length 27;
 Best Local Similarity 88.9%; Pred. No. 24;
 Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1608 TCCCATCTTTGCCACCCCTGATGCTGT 1634
 DB 1 TCCCATCTTTGCCACCCCTGATGCTGT 27

RESULT 17
 AAT36738/c
 ID AAT36738 standard; DNA; 29 BP.

XX AAT36738;
 XX
 DT 15-OCT-1996 (first entry)

DE G-protein conjugate receptor protein cDNA degenerate PCR primer.

XX G-protein; conjugate receptor; drug; development; antibody;
 KW ligand determination; antiserum; production; construction;
 KW expression system; screening; receptor binding assay system;
 KW drug candidate screening; drug design; probe; primer; preparation;
 KW genetic analysis; gene therapy; PCR; polymerase chain reaction;
 KW degenerate; ss.

XX Synthetic.

XX JP08154682-A.

XX 18-JUN-1996.

XX 02-DEC-1994; 94JP-00299792.

XX 02-DEC-1994; 94JP-00299792.

XX (TAKE) TAKEDA CHEM IND LTD.
 PA WPI; 1996-336572/34.
 XX
 DR
 XX G protein conjugate receptor protein - useful in ligand determination,
 PT antibody prodn., drug screening and design and receptor binding assay
 PT system development.

XX Example 1; Page 22; 23pp; Japanese.

XX The present sequence is a degenerate PCR primer for a G-protein conjugate
 CC receptor (GPCR) protein, cDNA, structure elucidation of which may lead to
 CC the development of unique drugs. The GPCR protein and its cDNA can be
 CC used in ligand determination, antibody and antiserum prodn., recombinant
 CC receptor protein expression system construction (which can be used in
 CC receptor binding assay system development), drug candidate screening,
 CC drug design based on comparisons among structurally similar ligand
 CC receptors and probe and PCR primer prepn., for use in genetic analysis
 CC and gene therapy

XX SQ Sequence 29 BP; 9 A; 4 C; 9 G; 0 T; 0 U; 7 Other;

Query Match 1.4%; Score 24; DB 1; Length 29;
 Best Local Similarity 72.4%; Pred. No. 29;
 Matches 21; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 979 TTGGCCATCTGCTGCGCTGCCCTTCCACAT 1007
 DB 29 TTGCRSMTCTGCTGCTGCCCTTCCACAT 1

RESULT 18
 AAV02408/c
 ID AAV02408 standard; DNA; 29 BP.

XX AAV02408;

XX 06-APR-1998 (first entry)

DE Mouse MINE-derived G protein-coupled receptor PCR primer 2.

KW G-protein-coupled receptor; ligand binding; pharmaceutical; modulator;
 KW pituitary; central nervous system; pancreas; prophylactic;
 KW therapeutic agent; PCR primer; ss.

XX Synthetic.

XX Mus sp.

OS Location/Qualifiers

FT Key modified_base 23
 FT /tag= a
 FT /mod_base= i
 FT /note= "inositol"

PN WO9724436-A2.

XX 10-JUL-1997.

XX 26-DEC-1996; 96WO-JP003821.

XX 28-DEC-1995; 95JP-00343371.

XX 15-MAR-1996; 96JP-00059419.

XX 12-AUG-1996; 96JP-00211805.

XX 18-SEP-1996; 96JP-00246573.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Hinuma S, Habata Y, Kawamata Y, Hosoya M, Fujii R, Fukusumi S;
 PI Kitada C;
 XX WPI; 1997-363672/33.

PT Ligand peptide for G protein-coupled receptor - acts by modulating
PT function in the central nervous system, pancreas and pituitary gland.
XX
PS Example 4, Page 104, 258pp; English.
XX
CC AAV02408 and AAV02407 are PCR primers used to amplify a region of the G
CC protein-coupled receptor from mouse pancreatic beta-cell strain MIN6. The
CC resulting fragment is used in an assay to monitor ligand binding to
CC receptor proteins. Pharmaceutical compositions containing such ligands
CC may be used as a pituitary function modulator, a central nervous system
CC modulator or a pancreatic function modulator. These ligands could have
CC specific applications as a prophylactic or therapeutic agent for
CC dementia, depression, hyperkinetic syndrome, disturbance of
CC consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone
CC secretory disease, hyper- and polyphagia, hypercholesterolemia,
CC hyperglycemia, hyperlipidaemia, hyperprolactinemia, diabetes,
CC cancer, pancreatitis, renal disease, Turner's syndrome, neurosis,
CC rheumatoid arthritis, spinal injury, transient brain ischaemia, asthma,
CC amyotrophic lateral sclerosis, acute myocardial infarction, epilepsy,
CC spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis,
CC osteoporosis, infertility and/or oligogalactia. Assays can also be
CC developed to screen compounds which are capable of altering the binding
CC activity of the ligand thus affecting activation of the G protein-coupled
CC receptor protein
XX
SQ Sequence 29 BP; 9 A; 4 C; 9 G; 0 T; 0 U; 7 Other;
XX
Query Match 1.4%; Score 24; DB 1; Length 29;
Best Local Similarity 72.4%; Pred. No. 29;
Matches 21; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
Qy 979 TTGGCCATCTGCTGCTGCCCTTCCACAT 1007
Db 29 TTCTRYSNCTGCTGCTGCCCTTCCACAT 1
||||:|||||||:|||||:|:|
RESULT 19
AAV81238/c
ID AAV81238 standard; DNA; 29 BP.
XX
AC AAV81238;
XX
DT 10-MAR-1999 (first entry)
XX
DE Mouse MIN6-derived G-protein coupled receptor cDNA amplifying primer.
XX
KM Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor;
KM GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas;
KM tissue; screen; therapeutic; binding; senile dementia; ligand; murine;
KM Alzheimer's disease; Parkinson's disease; Huntington's disease; drug;
KM Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone;
KM secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor;
KM gene therapy; transgenic animal; mouse; PCR primer; ss.
XX
OS Synthetic.
OS Mus sp.
XX
PN WO9849295-A1.
XX
PD 05-NOV-1998.
XX
PE 27-APR-1998; 98WO-JP001923.
XX
PR 28-APR-1997; 97JP-00109974.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Hinuma S, Fukusumi S;
XX
DR WPI; 1999-009423/01.
XX
PT New polypeptide ligand for orphan G protein coupled receptors - used for
PT treating disorders of central nervous system, pituitary and pancreas, and

PT for drug screening.
XX
PS Example 4, Page 98, 206pp; English.
XX
CC The invention relates to a murine pituitary-derived ligand polypeptide
CC which is a ligand for the G-protein coupled orphan receptor designated
CC GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing
CC the ligand polypeptide encoding DNA are used to produce a recombinant
CC ligand polypeptide. The ligand polypeptide, and its fragments, modulate
CC function of the pituitary, central nervous system, pancreas and other
CC tissues and can be used to screen for agents that modulate binding of the
CC polypeptide to the receptor to quantify the amount of receptor in a
CC sample and to raise antibodies. They may also be used therapeutically,
CC e.g. to treat senile dementia, Alzheimer's, Parkinson's or Huntington's
CC diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs;
CC diabetes; schizophrenia; disorders of growth hormone secretion; cancer;
CC rheumatoid arthritis, epilepsy and many others, also to improve post-
CC operative nutritional status and as vasopressor. Transgenic animals
CC carrying the ligand polypeptide encoding DNA or its mutin are used to
CC study the function of the polypeptide-expressing genes, as models of
CC disease, for drug screening and as source of cell lines. The ligand
CC polypeptide DNA is used as a source of probes and primers; to identify
CC related sequences; in receptor-binding assays; for production of Ab and
CC antisera; in drug development; for gene therapy and to develop transgenic
CC animals. Primers AAV81237-238 are used for the PCR amplification of the
CC cDNA encoding a mouse MIN6-derived G-protein coupled receptor protein
XX
SQ Sequence 29 BP; 9 A; 4 C; 9 G; 0 T; 0 U; 7 Other;
XX
Query Match 1.4%; Score 24; DB 1; Length 29;
Best Local Similarity 72.4%; Pred. No. 29;
Matches 21; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
Qy 979 TTGGCCATCTGCTGCTGCCCTTCCACAT 1007
Db 29 TTCTRYSNCTGCTGCTGCCCTTCCACAT 1
||||:|||||||:|||||:|:|
RESULT 20
AAV15513/c
ID AAV15513 standard; DNA; 29 BP.
XX
AC AAV15513;
XX
DT 06-MAY-1999 (first entry)
XX
DE PCR primer used to amplify cDNA encoding a G protein-coupled receptor.
XX
KM G protein-coupled receptor; GPCR; hypovarianism; gonocyte carcinoma;
KM menopause syndrome; euthyroid; hypometabolism; lactation; modulation;
KM pituitary adenomatosis; brain tumour; emmenopathy; autoimmune disease;
KM prolactinoma; infertility; impotence; amenorrhea; galactorrhea;
KM acromegaly; Chiari-Frommel syndrome; Argonaz-del Castillo syndrome;
KM Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia;
KM contraceptive; placental function; chorioncarcinoma; hydatid mole;
KM abortion; unthrifty fetus; abnormal saccharometabolism;
KM abnormal lipidmetabolism; oxytocia; prolactin secretion; PCR primer; ss.
XX
OS Synthetic.
OS Mus sp.
XX
PN WO9858962-A1.
XX
PD 30-DEC-1998.
XX
PE 22-JUN-1998; 98WO-JP002765.
XX
PT

KM angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;
 KM polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
 KM cardiovascular disease; angina pectoris; hypertension; heart failure;
 KM myocardial infarction; ventricular hypertrophy; vascular disease;
 KM aneurysm; embolism; thrombosis; coronary artery disease; angioedema;
 KM arteriosclerosis; atherosclerosis; hypersensitivity; sepsis; PCR;
 KM autoimmune disease; inflammatory arthritis; cancer; wound; genotyping;
 KM viral infection; bacterial infection; fungal infection; COPD;
 KM Chronic obstructive pulmonary disease; enterocolitis.
 OS Homo sapiens.
 XX W0200261131-A2.
 PN 08-AUG-2002.
 XX 03-DEC-2001; 2001WO-US047235.
 PF 04-DEC-2000; 2000US-0251015P.
 XX 23-JAN-2001; 2001US-0263678P.
 PR 02-MAR-2001; 2001US-0273037P.
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 PA (TSUC/) TSUCHIHASHI Z.
 PA (HUIL/) HUI L.
 XX Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;
 PI Swanson BN, Powell JR;
 DR WPI; 2002-619265/66.
 XX New isolated nucleic acid with at least one polymorphic position, useful
 PT for detecting, diagnosing and treating disorders such as angioedema,
 PT cancer, viral, bacterial or fungal infection, cardiovascular and
 PT autoimmune diseases.
 PT Example 3; Page 899; 977bp; English.
 CC The invention relates to an isolated nucleic acid from a human gene
 CC encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDRB1),
 CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein
 CC 1 (KLK1), bradykinin receptor B2 (BDRB2), angiotensin converting enzyme
 CC 2 (ACE2), or protease inhibitor 4 (PI4), comprising at least one
 CC polymorphic position. Also included are (1) a probe that hybridises to a
 CC polymorphic position as provided in the detailed summary of single
 CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
 CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising
 CC obtaining the sample from one or more individuals and determining the
 CC nucleic acid sequence at one or more polymorphic positions in a gene
 CC encoding a protein selected from the group above; (3) constructing (M2)
 CC haplotypes using the genes comprising grouping at least two nucleic acids
 CC ; (4) identifying (M3) an individual at risk of developing a disorder
 CC upon administration of an ACE inhibitor and/or vasopeptidase inhibitor
 CC using the polymorphic data; (5) a library of nucleic acids, each of which
 CC comprises one or more polymorphic positions within a gene encoding a
 CC human protein selected from the group above; and (6) genotyping (M4) an
 CC individual comprising obtaining a nucleic acid sample, determining the
 CC nucleotide present in at least one polymorphic position, and comparing at
 CC least one position with a known data set. The genes, (M1, M2, M3 and M4)
 CC and compositions are useful for detecting, diagnosing, treating,
 CC preventing various disorders such as angioedema and diseases which
 CC involve angioedema, like haemangiomas, tumours, sarcomas, Crohn's
 CC disease, trachoma, and cardiovascular diseases like angina pectoris,
 CC hypertension, heart failure, myocardial infarction, ventricular
 CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
 CC artery disease, arteriosclerosis and/or atherosclerosis, and
 CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory
 CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic
 CC obstructive pulmonary disease (COPD) and enterocolitis (many other
 CC diseases and disorders are listed in the specification). The
 CC polynucleotides are also useful for chromosome identification. Antibodies
 CC against the proteins may be utilised for immunophenotyping of cell lines
 CC and biological samples. The present sequence is a genotyping PCR primer

CC for the gene encoding one of the proteins listed above
 XX Sequence 23 BP; 6 A; 5 C; 4 G; 8 T; 0 U; 0 Other;
 SQ Query Match 1.3%; Score 23; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1675 AATAAAGGTGCGACCACTTTT 1697
 Db 23 AATAAAGGTGCGACCACTTTT 1
 RESULT 25
 AAQ30776/c
 ID AAQ30776 standard; DNA; 24 BP.
 XX
 AC AAQ30776;
 XX
 DT 25-MAR-2003 (revised)
 DT 22-MAR-1993 (first entry)
 XX
 DE PCR primer rspr7a2 to amplify human NK1R 5' core region.
 XX
 XX Neurokinin-1 receptor short form; arthritis; Substance P;
 KM polymerase chain reaction; rat NK1R; ss.
 XX
 OS Synthetic.
 XX
 PN EP514207-A2.
 XX
 PD 19-NOV-1992.
 XX
 PF 15-MAY-1992; 92EP-00304432.
 XX
 XX 17-MAY-1991; 91US-00701930.
 PR 17-MAY-1991; 91US-00701935.
 PR 17-MAY-1991; 91US-00701937.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PL Strader CD, Fong TM;
 PL WPI; 1992-384034/47.
 DR
 XX New human neurokinin-1 receptor short form protein - useful for
 PT identifying and determining substance P antagonists in arthritic
 PT patients.
 PT Example 1; Page 8; 36bp; English.
 PS
 XX Human mRNA was prepared from 3 glioblastoma cell lines T98G, CCF-SSTG1
 CC and U87MG. First strand cDNA was synthesised and used as template with
 CC rat primers rspr254, rspr254h and rspr7a2 (AAQ30774-6) in first round PCR
 CC amplification. Secondary PCR was performed on the amplified product using
 CC the same 3 primers prior to a third round of amplification, this time
 CC using the primers rspr254, rspr254h, rspr7a1 (AAQ30777) and rspr7a1h
 CC (AAQ30778). The tertiary PCR product was sequenced and was found to have
 CC 90% identity at the nucleotide level with the central core region of the
 CC rat NK1R from amino acid 91 to 280. Primer rspr7a2 is an antisense primer
 CC based on the rat NK1R sequence 918-894 (numbering as in J.Biol.Chem. 264:
 CC 17649-17652, 1989). (Updated on 25-MAR-2003 to correct PN field.)
 CC
 SQ Sequence 24 BP; 7 A; 2 C; 8 G; 7 T; 0 U; 0 Other;
 QY Query Match 1.3%; Score 23; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1105 ATGTACAAACCCATCATCTACTG 1127
 24 ATGTACAAACCCATCATCTACTG 2

RESULT 26
ID ABEK63862/c
ABK63862 standard; DNA; 24 BP.
XX
AC ABEK63862;
XX
DT 18-JUN-2002 (first entry)
XX
DE Neurokinin 1 receptor (NK-1) sense oligonucleotide #13.
XX
KM Human; neurokinin receptor-1; NK-1; dermatological disorder;
KM immune disorder; autoimmune disorder; cardiovascular disorder;
KM vascular disorder; airway disorder; neuropathic disorder; pain;
KM psychiatric disorder; central nervous system disorder; inflammation;
KM respiratory condition; ophthalmic condition; intestinal condition;
KM demyelinating disease; small cell lung cancer; depression;
KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
KM neuro-pathological disorder; stress; antisense; primer; ss.
XX
OS Homo sapiens.
XX
XX WO200213799-A2.
XX
XX 21-FEB-2002.
XX
XX 17-AUG-2001; 2001WO-IB001510.
XX
XX 18-AUG-2000; 2000US-0226086P.
XX
XX (UYMC-) UNIV MCGILL.
XX
PI Henry JL, Cahill CM, Yaehpal K;
XX
XX WPI; 2002-241835/29.
XX
XX Treating pathological condition involving neurokinin receptor-1, e.g.
XX pain or inflammation, by administering oligonucleotide or a non-
XX nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
XX pathway.
XX
XX
XX Claim 24; Page 20; 100pp; English.
XX
XX The invention relates to a method of treating a pathological condition
XX characterised partially by involvement of neurokinin receptor-1 (NK-1)
XX receptor, especially treating, attenuating or preventing pain or
XX inflammatory condition. The method comprises administering to a mammal, a
XX compound chosen from an oligonucleotide, its analogue, and a disruptor
XX which interferes with function or production of NK-1 receptors. The
XX method is useful for treating a pathological condition characterised by
XX involvement of NK-1 receptor such as dermatological, immune, autoimmune,
XX cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,
XX psychiatric and central nervous system disorders (e.g. anxiety,
XX psychosis, schizophrenia), gut inflammation, arthritis, and central or
XX peripheral aspects of chronic or acute pain, and for treating,
XX attenuating or preventing pain or inflammation such as peripheral,
XX chronic, acute pain or inflammation, neuropathic pain, inflammation or
XX pain relating to psychiatric disorders and central nervous system
XX disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
XX in a mammal, in particular human. NK-1 receptor related disorders,
XX diseases, or pathological conditions treatable by this method include
XX respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
XX conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
XX (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and
XX Crohn's disease), cardiovascular conditions (e.g. chronic
XX gastrointestinal tract inflammation, and inflammatory diseases such as
XX inflammatory bowel diseases. Other disorders and diseases include
XX cardiovascular pathologies including stroke, chronic inflammatory
XX diseases such as rheumatoid arthritis, demyelinating diseases such as
XX multiple sclerosis, small cell lung cancer, depression, hypersensitivity
XX disorders such as allergies and poison ivy, vasospastic diseases such as
XX angina, addiction disorders such as alcoholism, neurodegenerative

disorders such as acquired immune deficiency syndrome (AIDS) related
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
CC disorders such as peripheral neuropathy, oedema, stress related and
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
CC effectively treat chronic conditions and other pathological states
CC without the co-administration of substance P, and reduce the number of
CC activated receptors while not reducing the number of quiescent NK-1
CC receptors. Receptors not chronically stimulated are less affected,
CC reducing side effects of treatment. ABEK63814-ABK63906 represent NK-1
CC receptor coding sequences and oligonucleotides of the invention
XX
SQ Sequence 24 BP; 7 A; 2 C; 8 G; 7 T; 0 U; 0 Other;
XX
Query Match 1.3%; Score 23; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1105 ATGTACAAACCCCATCTACTGTG 1127
DB 24 ATGTACAAACCCCATCTACTGTG 2
XX
RESULT 27
AAQ30777/c
ID AAQ30777 standard; DNA; 24 BP.
XX
XX AAQ30777;
XX
XX 25-MAR-2003 (revised)
XX 22-MAR-1993 (first entry)
XX
XX PCR primer rspr7a1 to amplify human NK1R 5' core region.
XX
XX Neurokinin-1 receptor short form; arthritis; Substance P;
XX KM polymerase chain reaction; rat NK1R; ss.
XX
XX Synthetic.
XX
XX BP514207-A2.
XX
XX 19-NOV-1992.
XX
XX 15-MAY-1992; 92EP-00304432.
XX
XX 17-MAY-1991; 91US-00701930.
XX 17-MAY-1991; 91US-00701935.
XX 17-MAY-1991; 91US-00701937.
XX
XX (MERI) MERCK & CO INC.
XX
XX Strader CD, Fong TM;
XX
XX WPI; 1992-384034/47.
XX
XX New human neurokinin-1 receptor short form protein - useful for
XX identifying and determining substance P antagonists in arthritic
XX patients.
XX
XX Example 1; Page 8; 36pp; English.
XX
XX Human mRNA was prepared from 3 glioblastoma cell lines T98G, CCF-SSTG1
XX and U87MG. First strand cDNA was synthesised and used as template with
XX rat primers rspr284, rspr284h and rspr7a2 (AAQ30774-6) in first round PCR
XX amplification. Secondary PCR was performed on the amplified product using
XX the same 3 primers prior to a third round of amplification, this time
XX using the primers rspr284, rspr284h, rspr7a1 (AAQ30777) and rspr7a1h
XX (AAQ30778). The tertiary PCR product was sequenced and was found to have
XX 90% identity at the nucleotide level with the central core region of the
XX rat NK1R from amino acid 91 to 280. Primer rspr7a1 is an antisense primer
XX based on the rat NK1R sequence 864-841 (numbering as in J.Biol.Chem. 264:
XX 17649-17652, 1989). (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 24 BP; 6 A; 5 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 22.4; DB 1; Length 24;
 Best Local Similarity 95.8%; Pred. No. 32;
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1051 AAGTTATCCAGCAGGTCTACTG 1074
 24 AAGTTATCCAGCAGGTCTACTG 1

RESULT 28
 ABS60912/C
 ID ABS60912 standard; DNA; 22 BP.
 XX
 AC ABS60912;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Human genotyping PCR primer #65.
 XX
 KW Human; ss; aminopeptidase P; XPNP2; bradykinin receptor B1; primer;
 KW BDKRB1; tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH;
 KW kallikrein 1; KKL1; bradykinin receptor B2; BDKRB2; gene therapy;
 KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;
 KW polymorphisms; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
 KW cardiovascular disease; angina pectoris; hypertension; heart failure;
 KW myocardial infarction; ventricular hypertrophy; vascular disease;
 KW aneurysm; embolism; thrombosis; coronary artery disease; angioedema;
 KW arteriosclerosis; atherosclerosis; hypersensitivity; sepsis; PCR;
 KW autoimmune disease; inflammatory arthritis; cancer; wound; genotyping;
 KW viral infection; bacterial infection; fungal infection; COPD;
 KW Chronic obstructive pulmonary disease; enterocolitis.
 XX
 XX Homo sapiens.
 OS
 FN WO200261131-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 03-DEC-2001; 2001WO-US047235.
 XX
 PR 04-DEC-2000; 2000US-0251015P.
 PR 23-JAN-2001; 2001US-0263678P.
 PR 02-MAR-2001; 2001US-0273037P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 PA (TSUC/) TSUCHIHASHI Z.
 PA (HUI/) HUI L.
 PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonde M, Perrone MH;
 PI Swanson BN, Powell JR;
 PI
 DR WPI; 2002-619265/66.
 XX
 PT New isolated nucleic acid with at least one polymorphic position, useful
 PT for detecting, diagnosing and treating disorders such as angioedema,
 PT cancer, viral, bacterial or fungal infection, cardiovascular and
 PT autoimmune diseases.
 XX
 PS Example 3; Page 899; 977pp; English.
 XX
 CC The invention relates to an isolated nucleic acid from a human gene
 CC encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDKRB1),
 CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein
 CC 1 (KKL1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme
 CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one
 CC polymorphic position. Also included are (1) a probe that hybridizes to a
 CC polymorphic position as provided in the detailed summary of single
 CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
 CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising
 CC obtaining the sample from one or more individuals and determining the
 CC nucleic acid sequence at one or more polymorphic positions in a gene
 CC encoding a protein selected from the group above; (3) constructing (M2)

CC haplotypes using the genes comprising grouping at least two nucleic acids
 CC ; (4) identifying (M3) an individual at risk of developing a disorder
 CC upon administration of an ACE inhibitor and/or vasopressin inhibitor
 CC using the polymorphic data; (5) a library of nucleic acids, each of which
 CC comprises one or more polymorphic positions within a gene encoding a
 CC human protein selected from the group above; and (6) genotyping (M4) an
 CC individual comprising obtaining a nucleic acid sample, determining the
 CC nucleotide present in at least one polymorphic position, and comparing at
 CC least one position with a known data set. The genes, (M1, M2, M3 and M4)
 CC and compositions are useful for detecting, diagnosing, treating,
 CC preventing various disorders such as angioedema and diseases which
 CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's
 CC disease, trachomas, and cardiovascular diseases like angina pectoris,
 CC hypertension, heart failure, myocardial infarction, ventricular
 CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
 CC artery disease, arteriosclerosis and/or atherosclerosis, and
 CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory
 CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic
 CC obstructive pulmonary disease (COPD) and enterocolitis (many other
 CC diseases and disorders are listed in the specification). The
 CC polynucleotides are also useful for chromosome identification. Antibodies
 CC against the proteins may be utilised for immunohenotyping of cell lines
 CC and biological samples. The present sequence is a genotyping PCR primer
 CC for the gene encoding one of the proteins listed above

SO Sequence 22 BP; 3 A; 4 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 1.2%; Score 22; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1373 CACGAAGTGACTCCAGACCAT 1394
 22 CACGAAGTGACTCCAGACCAT 1

Db

RESULT 29
 ABS61083/C
 ID ABS61083 standard; DNA; 22 BP.
 XX
 AC ABS61083;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Human automated genomic bit analysis (GBA) PCR primer #60.
 XX
 KW Human; ss; aminopeptidase P; XPNP2; bradykinin receptor B1; primer;
 KW BDKRB1; tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH;
 KW kallikrein 1; KKL1; bradykinin receptor B2; BDKRB2; gene therapy;
 KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;
 KW polymorphisms; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
 KW cardiovascular disease; angina pectoris; hypertension; heart failure;
 KW myocardial infarction; ventricular hypertrophy; vascular disease;
 KW aneurysm; embolism; thrombosis; coronary artery disease; angioedema;
 KW arteriosclerosis; atherosclerosis; hypersensitivity; sepsis; PCR;
 KW autoimmune disease; inflammatory arthritis; cancer; wound; genotyping;
 KW viral infection; bacterial infection; fungal infection; COPD; GBA;
 KW Chronic obstructive pulmonary disease; enterocolitis;
 KW automated genetic bit analysis.
 XX
 OS Homo sapiens.
 XX
 FN WO200261131-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 03-DEC-2001; 2001WO-US047235.
 XX
 PR 04-DEC-2000; 2000US-0251015P.
 PR 23-JAN-2001; 2001US-0263678P.
 PR 02-MAR-2001; 2001US-0273037P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.

PA (TSUC/) TSUCHIHASHI Z.
 PA (HUI/) HUI L.
 XX
 PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;
 PI Swanson BN, Powell JR;
 XX
 DR WPI: 2002-619265/66.
 XX
 PT New isolated nucleic acid with at least one polymorphic position, useful
 PT for detecting, diagnosing and treating disorders such as angioedema,
 PT cancer, viral, bacterial or fungal infection, cardiovascular and
 PT autoimmune diseases.
 XX
 PS Example 3: Page 931, 977pp; English.
 XX
 CC The invention relates to an isolated nucleic acid from a human gene
 CC encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDRB1),
 CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein
 CC 1 (KLK1), bradykinin receptor B2 (BDRB2), angiotensin converting enzyme
 CC 2 (ACE2), or protease inhibitor 4 (PI4), comprising at least one
 CC polymorphic position. Also included are (1) a probe that hybridizes to a
 CC polymorphic position as provided in the detailed summary of single
 CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
 CC sequence; (2) analyzing (M1) at least one nucleic acid sample comprising
 CC obtaining the sample from one or more individuals and determining the
 CC nucleic acid sequence at one or more polymorphic positions in a gene
 CC encoding a protein selected from the group above; (3) constructing (M2)
 CC haplotypes using the genes comprising grouping at least two nucleic acids
 CC ; (4) identifying (M3) an individual at risk of developing a disorder
 CC upon administration of an ACE inhibitor and/or vasopressinase inhibitor
 CC using the polymorphic data; (5) a library of nucleic acids, each of which
 CC comprises one or more polymorphic positions within a gene encoding a
 CC human protein selected from the group above; and (6) genotyping (M4) an
 CC individual comprising obtaining a nucleic acid sample, determining the
 CC nucleotide present in at least one polymorphic position, and comparing at
 CC least one position with a known data set. The genes, (M1, M2, M3 and M4)
 CC and compositions are useful for detecting, diagnosing, treating,
 CC preventing various disorders such as angioedema and diseases which
 CC involve angiotensin II like haemangiomatosis, tumours, sarcoidosis, Crohn's
 CC disease, trachomas, and cardiovascular diseases like angina pectoris,
 CC hypertension, heart failure, myocardial infarction, ventricular
 CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
 CC artery disease, arteriosclerosis and/or atherosclerosis, and
 CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory
 CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic
 CC obstructive pulmonary disease (COPD) and enterocolitis (many other
 CC diseases and disorders are listed in the specification). The
 CC polymorphisms are also useful for chromosome identification. Antibodies
 CC against the proteins may be utilized for immunophenotyping of cell lines
 CC and biological samples. The present sequence is a genotyping PCR primer
 CC for the gene encoding one of the proteins listed above, using the method
 CC of automated genetic bit analysis, GBA
 XX
 SQ Sequence 22 BP; 7 A; 8 C; 7 G; 0 T; 0 U; 0 Other;
 XX
 Query Match 1.2%; Score 22; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 673 TGGGCTGGCTGCTGCTGCTG 694
 DB 22 TGGGCTGGCTGCTGCTGCTG 1
 XX
 RESULT 30
 AAT18348/c
 ID AAT18348 standard; DNA; 27 BP.
 XX
 AC AAT18348;
 XX
 DT 26-AUG-1996 (first entry)
 XX
 XX G-protein coupled receptor protein DNA primer HS-2.

XX
 KM G-protein coupled receptor protein; G-PCR; agonist; antagonist;
 KM cystic fibrosis; incontinence; diabetes; diagnosis; gene therapy;
 KM transgenic animal; polymerase chain reaction; PCR; primer; ss.
 XX
 OS Synthetic.
 XX
 PN W09605302-A1.
 XX
 PD 22-FEB-1996.
 XX
 PF 10-AUG-1995; 95WO-JP001599.
 XX
 PR 11-AUG-1994; 94JP-00189272.
 PR 11-AUG-1994; 94JP-00189273.
 PR 11-AUG-1994; 94JP-00189274.
 PR 30-SEP-1994; 94JP-00236356.
 PR 30-SEP-1994; 94JP-00236357.
 PR 02-NOV-1994; 94JP-00270017.
 PR 28-DEC-1994; 94JP-00326611.
 PR 20-JAN-1995; 95JP-00007177.
 PR 16-MAR-1995; 95JP-00057186.
 PR 19-APR-1995; 95JP-00093989.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 XX Hinuma S, Hosoya M, Fujii R, Ohtaki T, Fukusumi S, Ohgi K;
 PI WPI: 1996-139698/14.
 DR
 XX
 PT G-protein coupled receptor protein DNA and protein - also methods for
 PT isolating (ant)agonists for treatment of cystic fibrosis, incontinence
 PT and diabetes.
 XX
 PS Claim 1; Page 238; 360pp; English.
 XX
 CC PCR primer HS-2 (AAT18348) is complementary to DNA coding for a region
 CC corresponding to, or near, the sixth transmembrane domain of known G-
 CC protein coupled receptor proteins (G-PCRs). HS-2 and other primers (see
 CC also AAT18347 and AAT18349-65) based on G-PCR transmembrane domains are
 CC used for the PCR amplification of mammalian DNAs to obtain G-PCR-
 CC encoding sequences (see also AAT18366-73 and AAT13901-09)
 CC
 XX
 SQ Sequence 27 BP; 7 A; 5 C; 8 G; 1 T; 0 U; 6 Other;
 XX
 Query Match 1.2%; Score 21.8; DB 1; Length 27;
 Best Local Similarity 74.1%; Pred. No. 54;
 Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 OY 979 TTGGCCATGCTGCTGCTGCTGCTTCCAC 1005
 DB 27 TTGGCCATGCTGCTGCTGCTGCTTCCAC 1
 XX
 RESULT 31
 AAT27220/c
 ID AAT27220 standard; cDNA; 27 BP.
 XX
 AC AAT27220;
 XX
 DT 29-OCT-1996 (first entry)
 XX
 DE Degenerate primer for G protein coupled receptor protein sequence.
 XX
 KM G protein coupled receptor protein; GCR; identification; detection;
 KM ligands; physiological response; arachidonic acid; acetylcholine;
 KM calcium; cyclic adenosine monophosphate; cAMP; inositol;
 KM membrane potential; phosphorylation; c-fos; antibodies;
 KM transgenic animals; ss.
 XX
 OS Synthetic.
 XX
 PN EP711831-A2.

```

XX 15-MAY-1996.
PD 11-NOV-1995; 95EP-00117786.
XX 14-NOV-1994; 94JP-00279545.
PR 24-AUG-1995; 95JP-00215798.
XX (TAKE ) TAKEDA CHEM IND LTD.
XX Hinuma S, Fujii R, Kawamata Y;
PI WPI; 1996-232096/24.
XX New isolated rabbit G protein receptor protein - used partic. to identify
PT agonists or antagonists which can promote or inhibit physiological
PT responses.
PS Disclosure; Page 27; 40pp; English.
XX G protein coupled receptor (GCR) proteins can be used to identify ligands
CC which act as antagonists of GCR/ligand binding. Such ligands can be used
CC for promoting or inhibiting physiological responses such as liberation of
CC arachidonic acid, acetylcholine and endocellular calcium, endocellular
CC cyclic AMP production, production of inositol, changes in cell membrane
CC potential, phosphorylation of endocellular proteins, activation of c-fos,
CC lowering of pH, activation of G protein and cell promulgation. The GCR
CC product can also be used for the detection of ligands and in the
CC production of antibodies and transgenic animals. Two degenerate primers
CC (AA727219, AA727220) were synthesized based on other receptor protein
CC coding sequences in an attempt to amplify the G protein coupled receptor.
CC The resulting amplified fragment was amplified from both sides by the
CC single primer described in AA727219
XX Sequence 27 BP; 7 A; 5 C; 8 G; 1 T; 0 U; 6 Other;
SQ
Query Match 1.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 54;
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 979 TTGGCATTCTGCTGCTGCTGCTTCAC 1005
DB 27 TTGGCATTCTGCTGCTGCTTCAC 1
RESULT 32
AA729438/C
ID AA729438 standard; cDNA; 27 BP.
XX AA729438;
AC
XX 27-OCT-1996 (first entry)
DT
XX Galanin receptor DNA primer.
DE
XX Galanin receptor; stomach ulcer; antiulcer; diabetes; antidiabetic;
XX dementia; neuropeptide; sedative; Alzheimer's disease; obesity;
XX DNA primer; oligonucleotide; polymerase chain reaction; PCR; ss.
XX Synthetic.
XX OS
XX EP711830-A2.
XX 15-MAY-1996.
PD
XX 11-OCT-1995; 95EP-00115996.
PF
XX 13-OCT-1994; 94JP-00247599.
PR 28-DEC-1994; 94JP-00326610.
PR 31-MAY-1995; 95JP-00134412.
XX (TAKE ) TAKEDA CHEM IND LTD.
XX

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PI Hinuma S, Fujii R, Fukusumi S, Ohtaki T, Hosoya M, Ohgi K;
PI Onda H;
XX WPI; 1996-232095/24.
DR
XX Isolated galanin receptor proteins - used partic. to identify agonists or
PT antagonists, which can be used to treat, e.g. ulcers, diabetes or
PT dementia.
XX Disclosure; Page 35; 71pp; English.
XX This DNA primer is used for amplifying DNA coding for G protein coupled
CC receptor protein
CC
XX Sequence 27 BP; 7 A; 5 C; 8 G; 1 T; 0 U; 6 Other;
SQ
Query Match 1.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 54;
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 979 TTGGCATTCTGCTGCTGCTTCAC 1005
DB 27 TTGGCATTCTGCTGCTTCAC 1
RESULT 33
AA798800/C
ID AA798800 standard; cDNA; 27 BP.
XX AA798800;
AC
XX 19-MAR-1998 (first entry)
DT
XX Primer #2 for G protein coupled receptor coding sequence.
DE
XX G protein coupled receptor; amygdaloid nucleus-derived protein; amplify;
XX agonist identification; antagonist; human; PCR primer; gene therapy; ss.
XX Homo sapiens.
XX EP789076-A2.
XX 13-AUG-1997.
PD
XX 05-FEB-1997; 97EP-00101767.
PF
XX 07-FEB-1996; 96JP-00021562.
PR
XX (TAKE ) TAKEDA CHEM IND LTD.
XX Hinuma S, Sakamoto J, Hosoya M;
PI WPI; 1997-395571/37.
XX Human amygdaloid nucleus-derived G protein coupled receptor - useful for
PT identifying (ant)agonists used in the treatment of, e.g., Alzheimer's
PT disease, dementia, angina or epilepsy.
XX Example 1; Page 33; 58pp; English.
XX This sequence represents a primer for the coding sequence for the human
CC amygdaloid nucleus-derived G protein coupled receptor (see AA794512) of
CC the invention. The protein and peptide can be used to identify agonists
CC or antagonists useful for creating spinal injury, Alzheimer's disease,
CC asthma, hyperphagia, neuropathy, dementia, pain, cerebral thrombosis,
CC encephalitis, cerebral infarction, cerebrovascular spasm, spodylitis,
CC angina, neurosis, drug dependence, drug and alcohol withdrawal symptoms,
CC schizophrenia, phobia, stroke, anxiety, depression, respiratory distress
CC syndrome, emesis, epilepsy, etc. The DNA encoding it can be used to
CC produce the recombinant protein or peptide, to construct diagnostic
CC probes and primers, and for gene therapy. An antibody directed against
CC the G protein coupled receptor can be used in immunoassays for the
CC protein

```



```
XX SQ Sequence 27 BP; 7 A; 5 C; 8 G; 1 T; 0 U; 6 Other;
Query Match 1.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 54;
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Oy 979 TTGGCATTGCTGCTGCTGCTTCCAC 1005
Db 27 TTGGCMTCTGCTGCTGCTGCTTCCAC 1

RESULT 34
AAV02406/c
ID AAV02406 standard; DNA; 27 BP.
XX
XX AAV02406;
XX
XX 06-APR-1998 (first entry)
XX
XX Receptor protein degenerate PCR primer 2.
XX
XX G protein-coupled receptor; ligand binding; pharmaceutical; modulator;
XX pituitary; central nervous system; pancreas; prophylactic;
XX therapeutic agent; PCR primer; ss.
XX
XX Synthetic.
XX
XX MO9724436-A2.
XX
XX 10-JUL-1997.
XX
XX 26-DEC-1996; 96WO-JP003821.
XX
XX 28-DEC-1995; 95JP-00343371.
XX PR 15-MAR-1996; 96JP-00059419.
XX PR 12-AUG-1996; 96JP-00211805.
XX PR 18-SEP-1996; 96JP-00246573.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Hinuma S, Habata Y, Kawamata Y, Hosoya M, Fujii R, Fukusumi S;
XX Kitada C;
XX
XX WPI; 1997-363672/33.
XX
XX Ligand peptide for G protein-coupled receptor - acts by modulating
XX function in the central nervous system, pancreas and pituitary gland.
XX
XX Example 1; Page 101; 258pp; English.
XX
XX AAV02406 and AAV02405 are degenerate PCR primers designed to amplify a
XX large number of G protein-coupled receptor protein sequences for
XX comparative sequence study. Such sequences are used in ligand assays to
XX monitor ligand binding to receptor proteins. Pharmaceutical compositions
XX containing such ligands may be used as a pituitary functional modulator, a
XX central nervous system modulator or a pancreatic function modulator.
XX These ligands could have specific applications as a prophylactic or
XX therapeutic agent for dementia, depression, hyperkinetic syndrome,
XX disturbance of consciousness, anxiety syndrome, schizophrenia, trauma,
XX growth hormone secretory disease, hyper- and polyphagia, diabetes,
XX hypercholesterolemia, hyperglycemia, hyperlipidemia, renal disease
XX hyperprolactinemia, pancreatitis, cancer, Turner's syndrome, neurosis,
XX rheumatoid arthritis, spinal injury, transient brain ischemia, epilepsy,
XX amyotrophic lateral sclerosis, acute myocardial infarction, infertility,
XX spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis,
XX osteoporosis, asthma, and/or oligosaccharia. Assays can also be developed
XX to screen compounds which are capable of altering the binding activity of
XX the ligand thus affecting activation of the G protein-coupled receptor
XX protein
XX
XX Sequence 27 BP; 7 A; 5 C; 8 G; 1 T; 0 U; 6 Other;
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```
Oy 979 TTGGCATTGCTGCTGCTGCTTCCAC 1005
Db 27 TTGGCMTCTGCTGCTGCTGCTTCCAC 1

Query Match 1.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 54;
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Oy 979 TTGGCATTGCTGCTGCTGCTTCCAC 1005
Db 27 TTGGCMTCTGCTGCTGCTGCTTCCAC 1

RESULT 35
AAV81236/c
ID AAV81236 standard; DNA; 27 BP.
XX
XX AAV81236;
XX
XX 10-MAR-1999 (first entry)
XX
XX Human G-protein coupled receptor cDNA amplifying primer.
XX
XX Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor;
XX GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas;
XX tissue; screen; therapeutic; binding; senile dementia; ligand; murine;
XX Alzheimer's disease; Parkinson's disease; Huntington's disease; drug;
XX Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone;
XX secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor;
XX gene therapy; transgenic animal; human; PCR primer; ss.
XX
XX Synthetic.
XX
XX Homo sapiens.
XX
XX MO9849295-A1.
XX
XX 05-NOV-1998.
XX
XX 27-APR-1998; 98WO-JP001923.
XX
XX 28-APR-1997; 97JP-00109974.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Hinuma S, Fukusumi S;
XX
XX WPI; 1999-009423/01.
XX
XX New polypeptide ligand for orphan G protein coupled receptors - used for
XX treating disorders of central nervous system, pituitary and pancreas, and
XX for drug screening.
XX
XX Example 1; Page 95; 206pp; English.
XX
XX The invention relates to a murine pituitary-derived ligand polypeptide
XX which is a ligand for the G-protein coupled orphan receptor designated
XX GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing
XX the ligand polypeptide encoding DNA are used to produce a recombinant
XX ligand polypeptide. The ligand polypeptide, and its fragments, modulate
XX function of the pituitary, central nervous system, pancreas and other
XX tissues and can be used to screen for agents that modulate binding of the
XX polypeptide to the receptor; to quantify the amount of receptor in a
XX sample and to raise antibodies. They may also be used therapeutically,
XX e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's
XX diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs;
XX diabetes; schizophrenia; disorders of growth hormone secretion; cancer;
XX rheumatoid arthritis, epilepsy and many others, also to improve post-
XX operative nutritional status and as vasopressor. Transgenic animals
XX carrying the ligand polypeptide encoding DNA or its mutin are used to
XX study the function of the polypeptide-expressing genes, as models of
XX disease, for drug screening and as source of cell lines. The ligand
XX polypeptide DNA is used as a source of probes and primers; to identify
XX related sequences; in receptor-binding assays; for production of Ab and
XX antisera. Primers AAV81235-236 are used for the PCR amplification of the
XX cDNA encoding a human pituitary-derived G-protein coupled receptor
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XX
DT 25-MAR-2003 (revised)
DT 22-MAR-1993 (first entry)
XX
DE PCR primer hsp341 to amplify human NK1R sf N-terminal region.
XX
KM Neurokinin-1 receptor short form; arthritis; Substance P;
KM polymerase chain reaction; rat NK1R; ss.
XX
OS Synthetic.
XX
PN EP514207-A2.
XX
PD 19-NOV-1992.
XX
PF 15-MAY-1992; 92EP-00304432.
XX
PR 17-MAY-1991; 91US-00701930.
PR 17-MAY-1991; 91US-00701935.
PR 17-MAY-1991; 91US-00701937.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Strader CD, Fong TM;
XX
PS WPI; 1992-384034/47.
XX
PT New human neurokinin-1 receptor short form protein - useful for
PT identifying and determining substance P antagonists in arthritic
PT patients.
XX
PS Example 1; Page 8; 36pp; English.
XX
CC The core region of human NK1R sf was isolated by PCR and sequenced (see
CC AAQ30774-Q30778). The antisense primers hsp345, hsp341, hsp342,
CC hsp341 and hsp342 (AAQ30784-Q30788) were synthesised based on the human
CC core sequence. Human glioblastoma mRNA and each of these primers were
CC used in first strand cDNA synthesis to produce the template for a primary
CC PCR amplification. Primer hsp345 was used with 2 rat sense primers r3p1n
CC and r3p1n (AAQ30779 and AAQ30780) for the primary amplification. The PCR
CC product was then used as template for secondary PCR with the same rat
CC primers and the human antisense primer hsp344 (AAQ30783). The secondary
CC PCR product was the template for tertiary PCR amplification, again using
CC the same rat sense primers but with human antisense primer hsp341
CC (AAQ30782). The amplified DNA fragment hybridised to hsp342 (AAQ30781),
CC indicating it is not a non-specific by-product. The DNA was sequenced and
CC found to encode the human NK1R sf N-terminal region and also contains a
CC 5' UTR. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 21 BP; 7 A; 3 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 559 TTGCGCAGTACTACTCCATG 579
DB 21 TTGCGCAGTACTACTCCATG 1
RESULT 39
AAQ30790
ID AAQ30790 standard; DNA; 21 BP.
XX
AC AAQ30790;
XX
DT 25-MAR-2003 (revised)
DT 22-MAR-1993 (first entry)
XX
DE PCR primer hsp342 to amplify human NK1R sf C-terminal region.
XX
KM Neurokinin-1 receptor short form; arthritis; Substance P;
KM anchored polymerase chain reaction; rat NK1R; ss.
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```
XX
OS Synthetic.
XX
PN EP514207-A2.
XX
PD 19-NOV-1992.
XX
PF 15-MAY-1992; 92EP-00304432.
XX
PR 17-MAY-1991; 91US-00701930.
PR 17-MAY-1991; 91US-00701935.
PR 17-MAY-1991; 91US-00701937.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Strader CD, Fong TM;
XX
PS WPI; 1992-384034/47.
XX
PT New human neurokinin-1 receptor short form protein - useful for
PT identifying and determining substance P antagonists in arthritic
PT patients.
XX
PS Example 1; Page 8; 36pp; English.
XX
CC Double-stranded cDNA was prepared from human glioblastoma mRNA and large-
CC size cDNA was ligated to EcoRI linkers. Linker-ligated cDNA was then
CC ligated to the calf intestinal phosphatase-treated EcoRI site of the
CC vector Bluescript SK+. The ligated plasmid DNA was used as template in a
CC primary PCR amplification with human primers hsp341 and hsp342
CC (AAQ30789 and AAQ30790) and the vector-specific primer t3 (from
CC "Stratagene"). The primary PCR product was used as template for secondary
CC PCR with the human primer hsp343 (AAQ30791) and t3. The product of this
CC reaction was amplified in a tertiary PCR amplification with hsp344
CC (AAQ30792) and vector-specific primer SK (also from "Stratagene"). A
CC 400bp DNA fragment was detected which hybridised to human oligoprobe
CC hsp345 (AAQ30793). This fragment was subcloned and sequenced. It was
CC found to encode the C-terminal region of human NK1R sf and also contains
CC 3' UTR. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 21 BP; 3 A; 2 C; 8 G; 8 T; 0 U; 0 Other;
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 956 TGATGATTGTCGTGTCGCA 976
DB 1 TGATGATTGTCGTGTCGCA 21
RESULT 40
AAQ30785/C
ID AAQ30785 standard; DNA; 21 BP.
XX
AC AAQ30785;
XX
DT 25-MAR-2003 (revised)
DT 22-MAR-1993 (first entry)
XX
DE PCR primer hsp341 to amplify human NK1R sf N-terminal region.
XX
KM Neurokinin-1 receptor short form; arthritis; Substance P;
KM polymerase chain reaction; rat NK1R; ss.
XX
OS Synthetic.
XX
PN EP514207-A2.
XX
PD 19-NOV-1992.
XX
PF 15-MAY-1992; 92EP-00304432.
```

PR 17-MAY-1991; 91US-00701930.
 PR 17-MAY-1991; 91US-00701935.
 PR 17-MAY-1991; 91US-00701937.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Strader CD, Fong TM;
 XX
 DR WPI; 1992-384034/47.
 XX
 PT New human neurokinin-1 receptor short form protein - useful for
 PT identifying and determining substance P antagonists in arthritic
 PT patients.
 PS
 PS Example 1; Page 8; 36pp; English.
 XX
 CC The core region of human NK1R sf was isolated by PCR and sequenced (see
 CC AAQ30774-Q30778). The antisense primers hsp3a5, hsp3a1, hsp3a2,
 CC hsp3a4 and hsp3a2 (AAQ30784-Q30788) were synthesised based on the human
 CC core sequence. Human glioblastoma mRNA and each of these primers were
 CC used in first strand cDNA synthesis to produce the template for a primary
 CC PCR amplification. Primer hsp3a5 was used with 2 rat sense primers reprim
 CC and rsp3rn (AAQ30779 and AAQ30780) for the primary amplification. The PCR
 CC product was then used as template for secondary PCR with the same rat
 CC primers and the human antisense primer hsp3a4 (AAQ30783). The secondary
 CC PCR product was the template for tertiary PCR amplification, again using
 CC the same rat sense primers but with human antisense primer hsp3a1
 CC (AAQ30782). The amplified DNA fragment hybridised to hsp3a2 (AAQ30781),
 CC indicating it is not a non-specific by-product. The DNA was sequenced and
 CC found to encode the human NK1R sf N-terminal region and also contains a
 CC 5' UTR. (Updated on 25-MAR-2003 to correct FN field.)
 XX
 SQ Sequence 21 BP; 8 A; 7 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 836 TGCTGGTGAATGCTATGCAT 856
 |||||
 Db 21 TGCTGGTGAATGCTATGCAT 1

RESULT 41
 AAQ30789
 ID AAQ30789 standard; DNA; 21 BP.
 XX
 AC AAQ30789;
 XX
 DT 25-MAR-2003 (revised)
 DT 22-MAR-1993 (first entry)
 XX
 DE PCR primer hsp3a1 to amplify human NK1R sf C-terminal region.
 XX
 KM Neurokinin-1 receptor short form; arthritis; Substance P;
 KM anchored polymerase chain reaction; rat NK1R; ss.
 XX
 OS Synthetic.
 OS
 XX EP514207-A2.
 XX
 PD 19-NOV-1992.
 PD
 PF 15-MAY-1992; 92EP-00304432.
 PF
 XX 17-MAY-1991; 91US-00701930.
 PR 17-MAY-1991; 91US-00701935.
 PR 17-MAY-1991; 91US-00701937.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PS Strader CD, Fong TM;
 XX

DR WPI; 1992-384034/47.
 XX
 XX New human neurokinin-1 receptor short form protein - useful for
 PT identifying and determining substance P antagonists in arthritic
 PT patients.
 PT
 PS
 PS Example 1; Page 8; 36pp; English.
 XX
 CC Double-stranded cDNA was prepared from human glioblastoma mRNA and large-
 CC size cDNA was ligated to EcoRI linkers. Linker-ligated cDNA was then
 CC ligated to the calf intestinal phosphatase-treated EcoRI site of the
 CC vector Bluescript SK+. The ligated plasmid DNA was used as template in a
 CC primary PCR amplification with human primers hsp3a1 and hsp3a2
 CC (AAQ30789 and AAQ30790) and the vector-specific primer t3 (from
 CC "Stratagene"). The primary PCR product was used as template for secondary
 CC PCR with the human primer hsp3a3 (AAQ30791) and t3. The product of this
 CC reaction was amplified in a tertiary PCR amplification with hsp3a4
 CC (AAQ30792) and vector-specific primer SK (also from "Stratagene"). A
 CC 400bp DNA fragment was detected which hybridised to human Oligoprobe
 CC hsp3a5 (AAQ30793). This fragment was subcloned and sequenced. It was
 CC found to encode the C-terminal region of human NK1R sf and also contains
 CC 3'UTR. (Updated on 25-MAR-2003 to correct FN field.)
 XX
 SQ Sequence 21 BP; 6 A; 7 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 924 GCAAGTCTGCGAAGCGCAA 944
 |||||
 Db 1 GCAAGTCTGCGAAGCGCAA 21

RESULT 42
 AAQ30787/c
 ID AAQ30787 standard; DNA; 21 BP.
 XX
 AC AAQ30787;
 XX
 DT 25-MAR-2003 (revised)
 DT 22-MAR-1993 (first entry)
 XX
 DE PCR primer hsp3a1 to amplify human NK1R sf N-terminal region.
 XX
 KM Neurokinin-1 receptor short form; arthritis; Substance P;
 KM polymerase chain reaction; rat NK1R; ss.
 XX
 OS Synthetic.
 OS
 XX EP514207-A2.
 XX
 PD 19-NOV-1992.
 PD
 PF 15-MAY-1992; 92EP-00304432.
 PF
 XX 17-MAY-1991; 91US-00701930.
 PR 17-MAY-1991; 91US-00701935.
 PR 17-MAY-1991; 91US-00701937.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PS Strader CD, Fong TM;
 XX
 DR WPI; 1992-384034/47.
 XX
 PT New human neurokinin-1 receptor short form protein - useful for
 PT identifying and determining substance P antagonists in arthritic
 PT patients.
 PS
 PS Example 1; Page 8; 36pp; English.
 XX
 CC The core region of human NK1R sf was isolated by PCR and sequenced (see

CC AAQ030774-Q30778). The antisense primers hsp3a5, hsp5a1, hsp5a2, hsp6a1 and hsp6a2 (AAQ030784-Q30788) were synthesised based on the human CC core sequence. Human glioblastoma mRNA and each of these primers were CC used in first strand cDNA synthesis to produce the template for a primary CC PCR amplification. Primer hsp3a5 was used with 2 rat sense primers reprim CC and reprim (AAQ030779 and AAQ030780) for the primary amplification. The PCR CC product was then used as template for secondary PCR with the same rat CC primers and the human antisense primer hsp3a4 (AAQ030783). The secondary CC PCR product was the template for tertiary PCR amplification, again using CC the same rat sense primers but with human antisense primer hsp3a1 (AAQ030782). The amplified DNA fragment hybridised to hsp3a2 (AAQ030781), CC indicating it is not a non-specific by-product. The DNA was sequenced and CC found to encode the human NKIR sF N-terminal region and also contains a CC 5' UTR. (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 21 BP; 8 A; 8 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 956 TGATGATTGTCGTGTGCA 976
21 TGATGATTGTCGTGTGCA 1

Db

RESULT 43
AAQ29783/c
ID AAQ29783 standard; DNA; 21 BP.
XX
XX AAQ29783;
XX
XX 25-MAR-2003 (revised)
DT 15-MAR-1993 (first entry)
XX
XX hsp3a5 primer 1499-1479.
DE
XX
XX Human, neurokinin-1 receptor; NKIR; membrane receptor; substance P;
KW neurotransmitter; polymerase chain reaction; PCR; rat NKIR; primer;
amplify; probe; ss.
XX
XX Homo sapiens.
OS
XX
XX EP510878-A1.
PN
XX 28-OCT-1992.
PD
XX
XX 16-APR-1992; 92EP-00303457.
PF
XX 25-APR-1991; 91US-00691197.
PR 25-APR-1991; 91US-00691198.
PR 25-APR-1991; 91US-00691200.
XX
XX (MERI) MERCK & CO INC.
PA
XX Fong TM, Strader CD;
PI
XX WPI; 1992-359073/44.
DR
XX
XX New recombinant human neurokinin-1 receptor - used to detect and evaluate
PT substances that bind to substance P receptor, and to determine substance
PT P in body fluid of arthritis patients.
XX
XX Disclosure; Page 8; 35pp; English.

CC The sequences given in AAQ29670-82, AAQ29783 and AAQ29746-48 are primers
CC which were used in the isolation of fragments of the human neurokinin-1
CC receptor (NKIR) cDNA. Human NKIR is a membrane receptor for the
CC neurotransmitter substance P. The primers were designed using regions of
CC the human NKIR cDNA and also regions of the rat NKIR which were thought
CC to be similar to human regions. Part of the human cDNA sequence was
CC derived by amplification using these primers. The remaining part of human
CC NKIR cDNA was obtained from a human cDNA library utilising portions of

CC PCR generated fragments as probes. See also AAQ29749. (Updated on 25-MAR-
CC 2003 to correct PN field.)

SQ Sequence 21 BP; 5 A; 4 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1567 AGGAAAACATTCATCTTG 1587
21 AGGAAAACATTCATCTTG 1

Db

RESULT 44
AAQ29679
ID AAQ29679 standard; DNA; 21 BP.
XX
XX AAQ29679;
AC
XX 25-MAR-2003 (revised)
DT 15-MAR-1993 (first entry)
XX
XX hsp6a2 primer 868-888.
DE
XX
XX Human, neurokinin-1 receptor; NKIR; membrane receptor; substance P;
KW neurotransmitter; polymerase chain reaction; PCR; rat NKIR; primer;
amplify; probe; ss.
XX
XX Homo sapiens.
OS
XX
XX EP510878-A1.
PN
XX 28-OCT-1992.
PD
XX
XX 16-APR-1992; 92EP-00303457.
PF
XX 25-APR-1991; 91US-00691197.
PR 25-APR-1991; 91US-00691198.
PR 25-APR-1991; 91US-00691200.
XX
XX (MERI) MERCK & CO INC.
PA
XX Fong TM, Strader CD;
PI
XX WPI; 1992-359073/44.
DR
XX
XX New recombinant human neurokinin-1 receptor - used to detect and evaluate
PT substances that bind to substance P receptor, and to determine substance
PT P in body fluid of arthritis patients.
XX
XX Disclosure; Page 8; 35pp; English.

CC The sequences given in AAQ29670-82, AAQ29783 and AAQ29746-48 are primers
CC which were used in the isolation of fragments of the human neurokinin-1
CC receptor (NKIR) cDNA. Human NKIR is a membrane receptor for the
CC neurotransmitter substance P. The primers were designed using regions of
CC the human NKIR cDNA and also regions of the rat NKIR which were thought
CC to be similar to human regions. Part of the human cDNA sequence was
CC derived by amplification using these primers. The remaining part of human
CC NKIR cDNA was obtained from a human cDNA library utilising portions of
CC PCR generated fragments as probes. See also AAQ29749. (Updated on 25-MAR-
CC 2003 to correct PN field.)

SQ Sequence 21 BP; 3 A; 2 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 956 TGATGATTGTCGTGTGCA 976
1 TGATGATTGTCGTGTGCA 21

Db

RESULT 45
AAQ29674/C
ID AAQ29674 standard; DNA; 21 BP.
XX
AC AAQ29674;
XX
DT 25-MAR-2003 (revised)
DT 15-MAR-1993 (first entry)
XX
DE hsp95a1 primer 768-748.
XX
KW Human; neurokinin-1 receptor; NKIR; membrane receptor; substance P;
KW neurotransmitter; polymerase chain reaction; PCR; rat NKIR; primer;
KW amplify; probe; ss.
XX
OS Homo sapiens.
XX
PN EP510878-A1.
XX
PD 28-OCT-1992.
XX
PF 16-APR-1992; 92EP-00303457.
XX
PR 25-APR-1991; 91US-00691197.
PR 25-APR-1991; 91US-00691198.
PR 25-APR-1991; 91US-00691200.
XX
PA (MERI) MERCK & CO INC.
XX
PI Fong TM, Strader CD;
XX
DR WPI; 1992-359073/44.
XX
PT New recombinant human neurokinin-1 receptor - used to detect and evaluate
PT substances that bind to substance P receptor, and to determine substance
PT P in body fluid of arthritis patients.
XX
PS Disclosure; Page 8; 35pp; English.
XX
CC The sequences given in AAQ29670-82, AAQ29783 and AAQ29746-48 are primers
CC which were used in the isolation of fragments of the human neurokinin-1
CC receptor (NKIR) cDNA. Human NKIR is a membrane receptor for the
CC neurotransmitter substance P. The primers were designed using regions of
CC the human NKIR cDNA and also regions of the rat NKIR which were thought
CC to be similar to human regions. Part of the human cDNA sequence was
CC derived by amplification using these primers. The remaining part of human
CC NKIR cDNA was obtained from a human cDNA library utilising portions of
CC PCR generated fragments as probes. See also AAQ29749. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 21 BP; 8 A; 7 C; 3 G; 3 T; 0 U; 0 Other;
XX
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 836 TCTGTGATGCTATGCA 856
DB 21 TGTGTGATGCTATGCA 1
XX
RESULT 46
AAQ29676/C
ID AAQ29676 standard; DNA; 21 BP.
XX
AC AAQ29676;
XX
DT 25-MAR-2003 (revised)
DT 15-MAR-1993 (first entry)
XX
DE hsp95a1 primer 888-868.
XX

XX
KW Human; neurokinin-1 receptor; NKIR; membrane receptor; substance P;
KW neurotransmitter; polymerase chain reaction; PCR; rat NKIR; primer;
KW amplify; probe; ss.
XX
OS Homo sapiens.
XX
PN EP510878-A1.
XX
PD 28-OCT-1992.
XX
PF 16-APR-1992; 92EP-00303457.
XX
PR 25-APR-1991; 91US-00691197.
PR 25-APR-1991; 91US-00691198.
PR 25-APR-1991; 91US-00691200.
XX
PA (MERI) MERCK & CO INC.
XX
PI Fong TM, Strader CD;
XX
DR WPI; 1992-359073/44.
XX
PF New recombinant human neurokinin-1 receptor - used to detect and evaluate
PT substances that bind to substance P receptor, and to determine substance
PT P in body fluid of arthritis patients.
XX
PS Disclosure; Page 8; 35pp; English.
XX
CC The sequences given in AAQ29670-82, AAQ29783 and AAQ29746-48 are primers
CC which were used in the isolation of fragments of the human neurokinin-1
CC receptor (NKIR) cDNA. Human NKIR is a membrane receptor for the
CC neurotransmitter substance P. The primers were designed using regions of
CC the human NKIR cDNA and also regions of the rat NKIR which were thought
CC to be similar to human regions. Part of the human cDNA sequence was
CC derived by amplification using these primers. The remaining part of human
CC NKIR cDNA was obtained from a human cDNA library utilising portions of
CC PCR generated fragments as probes. See also AAQ29749. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 21 BP; 8 A; 8 C; 2 G; 3 T; 0 U; 0 Other;
XX
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 956 TGATGATTTGCTGTGCA 976
DB 21 TGATGATTTGCTGTGCA 1
XX
RESULT 47
AAQ29677/C
ID AAQ29677 standard; DNA; 21 BP.
XX
AC AAQ29677;
XX
DT 25-MAR-2003 (revised)
DT 15-MAR-1993 (first entry)
XX
DE hsp95a1 primer 491-471.
XX
KW Human; neurokinin-1 receptor; NKIR; membrane receptor; substance P;
KW neurotransmitter; polymerase chain reaction; PCR; rat NKIR; primer;
KW amplify; probe; ss.
XX
OS Homo sapiens.
XX
PN EP510878-A1.
XX
PD 28-OCT-1992.
XX
PF 16-APR-1992; 92EP-00303457.
XX

```
XX 25-APR-1991; 91US-00691197.
PR 25-APR-1991; 91US-00691198.
PR 25-APR-1991; 91US-00691200.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Fong TM, Strader CD;
XX
DR WPI; 1992-359073/44.
XX
PT New recombinant human neurokinin-1 receptor - used to detect and evaluate
PT substances that bind to substance P receptor, and to determine substance
PT P in body fluid of arthritis patients.
XX
PS Disclosure; Page 8; 35pp; English.
XX
CC The sequences given in AAQ29670-82, AAQ29783 and AAQ29746-48 are primers
CC which were used in the isolation of fragments of the human neurokinin-1
CC receptor (NK1R) cDNA. Human NK1R is a membrane receptor for the
CC neurotransmitter substance P. The primers were designed using regions of
CC the human NK1R cDNA and also regions of the rat NK1R which were thought
CC to be similar to human regions. Part of the human cDNA sequence was
CC derived by amplification using these primers. The remaining part of human
CC NK1R cDNA was obtained from a human cDNA library utilising portions of
CC PCR generated fragments as probes. See also AAQ29749. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 21 BP; 7 A; 3 C; 7 G; 4 T; 0 U; 0 Other;
XX
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 559 TTCCGCGATCTACTCCATG 579
DB 21 TTCCGCGATCTACTCCATG 1
XX
RESULT 48
AAQ29678
ID AAQ29678 standard; DNA; 21 BP.
XX
AC AAQ29678;
XX
DT 25-MAR-2003 (revised)
DT 15-MAR-1993 (first entry)
XX
DE hepr661 primer 836-856.
XX
XX Human; neurokinin-1 receptor; NK1R; membrane receptor; substance P;
KW neurotransmitter; polymerase chain reaction; PCR; rat NK1R; primer;
KW amplify; probe; ss.
XX
OS Homo sapiens.
XX
PN EP510878-A1.
XX
PD 28-OCT-1992.
XX
PF 16-APR-1992; 92EP-00303457.
XX
PR 25-APR-1991; 91US-00691197.
PR 25-APR-1991; 91US-00691198.
PR 25-APR-1991; 91US-00691200.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Fong TM, Strader CD;
XX
DR WPI; 1992-359073/44.
XX
PT New recombinant human neurokinin-1 receptor - used to detect and evaluate
```

```
PT substances that bind to substance P receptor, and to determine substance
PT P in body fluid of arthritis patients.
XX
PS Disclosure; Page 8; 35pp; English.
XX
CC The sequences given in AAQ29670-82, AAQ29783 and AAQ29746-48 are primers
CC which were used in the isolation of fragments of the human neurokinin-1
CC receptor (NK1R) cDNA. Human NK1R is a membrane receptor for the
CC neurotransmitter substance P. The primers were designed using regions of
CC the human NK1R cDNA and also regions of the rat NK1R which were thought
CC to be similar to human regions. Part of the human cDNA sequence was
CC derived by amplification using these primers. The remaining part of human
CC NK1R cDNA was obtained from a human cDNA library utilising portions of
CC PCR generated fragments as probes. See also AAQ29749. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 21 BP; 6 A; 7 C; 5 G; 3 T; 0 U; 0 Other;
XX
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 924 GCAAGTCTGCGCAGCGCAA 944
DB 1 GCAAGTCTGCGCAGCGCAA 21
XX
RESULT 49
ABS60219
ID ABS60219 standard; DNA; 21 BP.
XX
AC ABS60219;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human polymorphism associated DNA sequence #113.
XX
KW Aminopeptidase P; XPNP2; bradykinin receptor B1; de; BDKRB1;
KW tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH; kallikrein 1;
KW KKT1; bradykinin receptor B2; BDKRB2; gene therapy;
KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;
KW polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
KW cardiovascular disease; angina pectoris; hypertension; heart failure;
KW myocardial infarction; ventricular hypertrophy; vascular disease;
KW aneurysm; embolism; chondrosis; coronary artery disease; angiodaema;
KW arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;
KW autoimmune disease; inflammatory arthritis; cancer; wound;
KW viral infection; bacterial infection; fungal infection; COPD;
KW Chronic obstructive pulmonary disease; enterocolitis.
XX
XX Homo sapiens.
XX
OS
XX
PN WO200261131-A2.
XX
PD 08-AUG-2002.
XX
PF 03-DEC-2001; 2001WO-US047235.
XX
PR 04-DEC-2000; 2000US-0251015P.
PR 23-JAN-2001; 2001US-0263678P.
PR 02-MAR-2001; 2001US-0273037P.
XX
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
PA (TSUC/) TSUCHIHASHI Z.
PA (HUI/L) HUI L.
XX
PI Tsuchihashi Z, Hui L, Zerba KB, Ma-Edmonds M, Perrone MH;
PI Swanson BN, Powell JR.
XX
DR WPI; 2002-619265/66.
XX
PT New isolated nucleic acid with at least one polymorphic position, useful
PT for detecting, diagnosing and treating disorders such as angiodema,
```

PT cancer, viral, bacterial or fungal infection, cardiovascular and
PT autoimmune diseases.
PS Disclosure; Page 717; 977bp; English.
XX
XX The invention relates to an isolated nucleic acid from a human gene
XX encoding aminopeptidase P (XPNPE2), bradykinin receptor B1 (BDKRB1),
XX tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein
XX 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme
XX 2 (ACE2), or protease inhibitor 4 (PI4), comprising at least one
XX polymorphic position. Also included are (1) a probe that hybridises to a
XX polymorphic position as provided in the detailed summary of single
XX nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
XX sequence; (2) analysing (M1) at least one nucleic acid sample comprising
XX the sample from one or more individuals and determining the
XX nucleic acid sequence at one or more polymorphic positions in a gene
XX encoding a protein selected from the group above; (3) constructing (M2)
XX haplotypes using the genes comprising grouping at least two nucleic acids
XX (4) identifying (M3) an individual at risk of developing a disorder
XX upon administration of an ACE inhibitor and/or vasopeptidase inhibitor
XX using the polymorphic data; (5) a library of nucleic acids, each of which
XX comprises one or more polymorphic positions within a gene encoding a
XX human protein selected from the group above; and (6) genotyping (M4) an
XX individual comprising obtaining a nucleic acid sample, determining the
XX nucleotide present in at least one polymorphic position, and comparing at
XX least one position with a known data set. The genes, (M1, M2, M3 and M4)
XX and compositions are useful for detecting, diagnosing, treating,
XX preventing various disorders such as angioedema and diseases which
XX involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's
XX disease, trachomas, and cardiovascular diseases like angina pectoris,
XX hypertension, heart failure, myocardial infarction, ventricular
XX hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
XX artery disease, arteriosclerosis and/or atherosclerosis, and
XX hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory
XX arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic
XX obstructive pulmonary disease (COPD) and enterocolitis (many other
XX diseases and disorders are listed in the specification). The
XX polynucleotides are also useful for chromosome identification. Antibodies
XX against the proteins may be utilised for immunophenotyping of cell lines
XX and biological samples. The present sequence is included in the sequence
XX listing but is not referred to anywhere else in the specification
SQ Sequence 21 BP; 5 A; 7 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1360 TCCAACTGCTCTTCGCAAGT 1380
DB 1 TCCAACTGCTCTTCGCAAGT 21

RESULT 50
ABS60157/c
ID ABS60157 standard; DNA; 21 BP.
XX
XX ABS60157;
XX
XX 05-NOV-2002 (first entry)
XX
XX Human polymorphism associated DNA sequence #51.
DE
XX Aminopeptidase P; XPNPE2; bradykinin receptor B1; de; BDKRB1;
XX tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH; kallikrein 1;
XX KLK1; bradykinin receptor B2; BDKRB2; gene therapy;
XX angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;
XX polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
XX cardiovascular disease; angina pectoris; hypertension; heart failure;
XX myocardial infarction; ventricular hypertrophy; vascular disease;
XX aneurysm; embolism; thrombosis; coronary artery disease; angioedema;
XX arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;
XX autoimmune disease; inflammatory arthritis; cancer; wound;

KW viral infection; bacterial infection; fungal infection; COPD;
KW Chronic obstructive pulmonary disease; enterocolitis.
XX
XX Homo sapiens.
XX
XX WO200261131-A2.
XX
XX 08-AUG-2002.
XX
XX 03-DEC-2001; 2001WO-US047235.
XX
XX 04-DEC-2000; 2000US-0251015P.
XX 23-JAN-2001; 2001US-0263678P.
XX 02-MAR-2001; 2001US-0273037P.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX (TSUC/) TSUCHIHASHI Z.
XX (HUI/) HUI L.
PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MR;
PI Swanson BN, Powell JR;
XX
XX WPI; 2002-619265/66.
XX
XX New isolated nucleic acid with at least one polymorphic position, useful
XX for detecting, diagnosing and treating disorders such as angioedema,
XX cancer, viral, bacterial or fungal infection, cardiovascular and
XX autoimmune diseases.
XX
XX Disclosure; Page 707; 977bp; English.
XX
XX The invention relates to an isolated nucleic acid from a human gene
XX encoding aminopeptidase P (XPNPE2), bradykinin receptor B1 (BDKRB1),
XX tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein
XX 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme
XX 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one
XX polymorphic position. Also included are (1) a probe that hybridises to a
XX polymorphic position as provided in the detailed summary of single
XX nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
XX sequence; (2) analysing (M1) at least one nucleic acid sample comprising
XX the sample from one or more individuals and determining the
XX nucleic acid sequence at one or more polymorphic positions in a gene
XX encoding a protein selected from the group above; (3) constructing (M2)
XX haplotypes using the genes comprising grouping at least two nucleic acids
XX (4) identifying (M3) an individual at risk of developing a disorder
XX upon administration of an ACE inhibitor and/or vasopeptidase inhibitor
XX using the polymorphic data; (5) a library of nucleic acids, each of which
XX comprises one or more polymorphic positions within a gene encoding a
XX human protein selected from the group above; and (6) genotyping (M4) an
XX individual comprising obtaining a nucleic acid sample, determining the
XX nucleotide present in at least one polymorphic position, and comparing at
XX least one position with a known data set. The genes, (M1, M2, M3 and M4)
XX and compositions are useful for detecting, diagnosing, treating,
XX preventing various disorders such as angioedema and diseases which
XX involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's
XX disease, trachomas, and cardiovascular diseases like angina pectoris,
XX hypertension, heart failure, myocardial infarction, ventricular
XX hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
XX artery disease, arteriosclerosis and/or atherosclerosis, and
XX hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory
XX arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic
XX obstructive pulmonary disease (COPD) and enterocolitis (many other
XX diseases and disorders are listed in the specification). The
XX polynucleotides are also useful for chromosome identification. Antibodies
XX against the proteins may be utilised for immunophenotyping of cell lines
XX and biological samples. The present sequence is included in the sequence
XX listing but is not referred to anywhere else in the specification
SQ Sequence 21 BP; 4 A; 8 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX
XX WPI; 2002-619265/66.
XX
XX New isolated nucleic acid with at least one polymorphic position, useful
PT for detecting, diagnosing and treating disorders such as angioedema,
PT cancer, viral, bacterial or fungal infection, cardiovascular and
PT autoimmune diseases.
XX
XX
PS Disclosure; Page 726; 977bp; English.
XX
XX The invention relates to an isolated nucleic acid from a human gene
CC encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDKRB1),
CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein
CC 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme
CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one
CC polymorphic position. Also included are (1) a probe that hybridises to a
CC polymorphic position as provided in the detailed summary of single
CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising
CC obtaining the sample from one or more individuals and determining the
CC nucleic acid sequence at one or more polymorphic positions in a gene
CC encoding a protein selected from the group above; (3) constructing (M2)
CC haplotypes using the genes comprising grouping at least two nucleic acids
CC ; (4) identifying (M3) an individual at risk of developing a disorder
CC upon administration of an ACE inhibitor and/or vasopeptidase inhibitor
CC using the polymorphic data; (5) a library of nucleic acids, each of which
CC comprises one or more polymorphic positions within a gene encoding a
CC human protein selected from the group above; and (6) genotyping (M4) an
CC individual comprising obtaining a nucleic acid sample, determining the
CC nucleotide present in at least one polymorphic position, and comparing at
CC least one position with a known data set. The genes, (M1, M2, M3 and M4)
CC and compositions are useful for detecting, diagnosing, treating,
CC preventing various disorders such as angioedema and diseases which
CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's
CC disease, trachomas, and cardiovascular diseases like angina pectoris,
CC hypertension, heart failure, myocardial infarction, ventricular
CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
CC artery disease, arteriosclerosis and/or atherosclerosis, and
CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory
CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic
CC obstructive pulmonary disease (COPD) and enterocolitis (many other
CC diseases and disorders are listed in the specification). The
CC polynucleotides are also useful for chromosome identification. Antibodies
CC against the proteins may be utilised for immunophenotyping of cell lines
CC and biological samples. The present sequence is included in the sequence
CC listing but is not referred to anywhere else in the specification
XX
XX
SQ Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Fred. NO. 37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 372 GTGGATCATCTTAGCCACAA 392
|||
Db 21 GTGGATCATCTTAGCCACAA 1

RESULT 53
AB60343
ID AB60343 standard; DNA; 21 BP.
XX
XX
AC AB60343;
XX
XX
DT 05-NOV-2002 (first entry)
XX
XX
DB Human polymorphism associated DNA sequence #237.
XX
XX Aminopeptidase P; XPNP2; bradykinin receptor B1; ds; BDKRB1;
KM tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH; kallikrein 1;
KM KLK1; bradykinin receptor B2; BDKRB2; gene therapy;
KM angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;
KM polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;

KM cardiovascular disease; angina pectoris; hypertension; heart failure;
KM myocardial infarction; ventricular hypertrophy; vascular disease;
KM aneurysm; embolism; thrombosis; coronary artery disease; angioedema;
KM arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;
KM autoimmune disease; inflammatory arthritis; cancer; wound;
KM viral infection; bacterial infection; fungal infection; COPD;
KM Chronic obstructive pulmonary disease; enterocolitis.
XX
XX Homo sapiens.
OS
XX
XX WO200261131-A2.
XX
XX
XX 08-AUG-2002.
XX
XX 03-DEC-2001; 2001WO-US047235.
XX
XX 04-DEC-2000; 2000US-0251015P.
PR 23-JAN-2001; 2001US-0263678P.
PR 02-MAR-2001; 2001US-0273037P.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
PA (TSUC/) TSUCHIHASHI Z.
PA (HUI/L/) HUI L.
PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;
PI Swanson BN, Powell JR;
XX
XX WPI; 2002-619265/66.
XX
XX New isolated nucleic acid with at least one polymorphic position, useful
PT for detecting, diagnosing and treating disorders such as angioedema,
PT cancer, viral, bacterial or fungal infection, cardiovascular and
PT autoimmune diseases.
XX
XX
PS Disclosure; Page 736; 977bp; English.
XX
XX The invention relates to an isolated nucleic acid from a human gene
CC encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDKRB1),
CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein
CC 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme
CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one
CC polymorphic position. Also included are (1) a probe that hybridises to a
CC polymorphic position as provided in the detailed summary of single
CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising
CC obtaining the sample from one or more individuals and determining the
CC nucleic acid sequence at one or more polymorphic positions in a gene
CC encoding a protein selected from the group above; (3) constructing (M2)
CC haplotypes using the genes comprising grouping at least two nucleic acids
CC ; (4) identifying (M3) an individual at risk of developing a disorder
CC upon administration of an ACE inhibitor and/or vasopeptidase inhibitor
CC using the polymorphic data; (5) a library of nucleic acids, each of which
CC comprises one or more polymorphic positions within a gene encoding a
CC human protein selected from the group above; and (6) genotyping (M4) an
CC individual comprising obtaining a nucleic acid sample, determining the
CC nucleotide present in at least one polymorphic position, and comparing at
CC least one position with a known data set. The genes, (M1, M2, M3 and M4)
CC and compositions are useful for detecting, diagnosing, treating,
CC preventing various disorders such as angioedema and diseases which
CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's
CC disease, trachomas, and cardiovascular diseases like angina pectoris,
CC hypertension, heart failure, myocardial infarction, ventricular
CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
CC artery disease, arteriosclerosis and/or atherosclerosis, and
CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory
CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic
CC obstructive pulmonary disease (COPD) and enterocolitis (many other
CC diseases and disorders are listed in the specification). The
CC polynucleotides are also useful for chromosome identification. Antibodies
CC against the proteins may be utilised for immunophenotyping of cell lines
CC and biological samples. The present sequence is included in the sequence
CC listing but is not referred to anywhere else in the specification
XX

SQ Sequence 21 BP; 3 A; 8 C; 4 G; 6 T; 0 U; 0 Other;
 Query Match 1.2%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 GY 1399 GAGAGCTTCAGCTTCTCTCC 1419
 Db 1 GAGAGCTTCAGCTTCTCTCC 21
 RESULT 54
 ABS60999
 ID ABS60999 standard; DNA; 21 BP.
 AC ABS60999;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Human genotyping PCR primer #152.
 XX
 KW Human; ss; aminopeptidase P; XPNBP2; bradykinin receptor B1; primer;
 KW BDKRB1; tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH;
 KW kallikrein 1; K1K1; bradykinin receptor B2; BDKRB2; gene therapy;
 KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;
 KW polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
 KW cardiovascular disease; angina pectoris; hypertension; heart failure;
 KW myocardial infarction; ventricular hypertrophy; vascular disease;
 KW aneurysm; embolism; thrombosis; coronary artery disease; angioedema;
 KW arteriosclerosis; atherosclerosis; hypersensitivity; sepsis; PCR;
 KW autoimmune disease; inflammatory arthritis; cancer; wound; genotyping;
 KW viral infection; bacterial infection; fungal infection; COPD;
 KW Chronic obstructive pulmonary disease; enterocolitis.
 KW
 XX
 OS Homo sapiens.
 XX
 PN WO200261131-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 03-DEC-2001; 2001WO-US047235.
 XX
 PR 04-DEC-2000; 2000US-0251015P.
 PR 23-JAN-2001; 2001US-0263678P.
 PR 02-MAR-2001; 2001US-0273037P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 PA (TSUC/) TSUCHIHASHI Z.
 PA (HUIL/) HUI L.
 XX
 PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;
 PI Swanson BN, Powell JR;
 XX
 DR WPI; 2002-619265/66.
 XX
 PT New isolated nucleic acid with at least one polymorphic position, useful
 PT for detecting, diagnosing and treating disorders such as angioedema,
 PT cancer, viral, bacterial or fungal infection, cardiovascular and
 PT autoimmune diseases.
 XX
 PS Example 3; Page 913; 977pp; English.
 XX
 CC The invention relates to an isolated nucleic acid from a human gene
 CC encoding aminopeptidase P (XPNBP2), bradykinin receptor B1 (BDKRB1),
 CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein
 CC 1 (K1K1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme
 CC 2 (ACE2) or protease inhibitor 4 (P14), comprising at least one
 CC polymorphic position. Also included are (1) a probe that hybridises to a
 CC polymorphic position as provided in the detailed summary of single
 CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
 CC sequence; (2) analysing (M) at least one nucleic acid sample comprising
 CC obtaining the sample from one or more individuals and determining the
 CC nucleic acid sequence at one or more polymorphic positions in a gene

CC encoding a protein selected from the group above; (3) constructing (M2)
 CC haplotypes using the genes comprising grouping at least two nucleic acids
 CC ; (4) identifying (M3) an individual at risk of developing a disorder
 CC upon administration of an ACE inhibitor and/or vasopressinase inhibitor
 CC using the polymorphic data; (5) a library of nucleic acids, each of which
 CC comprises one or more polymorphic positions within a gene encoding a
 CC human protein selected from the group above; and (6) genotyping (M4) an
 CC individual comprising obtaining a nucleic acid sample, determining the
 CC nucleotide present in at least one polymorphic position, and comparing at
 CC least one position with a known data set. The genes, (M1, M2, M3 and M4)
 CC and compositions are useful for detecting, diagnosing, treating,
 CC preventing various disorders such as angioedema and diseases which
 CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's
 CC disease, trachomas, and cardiovascular diseases like angina pectoris,
 CC hypertension, heart failure, myocardial infarction, ventricular
 CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
 CC artery disease, arteriosclerosis and/or atherosclerosis, and
 CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory
 CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic
 CC obstructive pulmonary disease (COPD) and enterocolitis (many other
 CC diseases and disorders are listed in the specification). The
 CC polymorphisms are also useful for chromosome identification. Antibodies
 CC against the proteins may be utilised for immunophenotyping of cell lines
 CC and biological samples. The present sequence is a genotyping PCR primer
 CC for the gene encoding one of the proteins listed above
 XX
 SQ Sequence 21 BP; 5 A; 6 C; 3 G; 7 T; 0 U; 0 Other;
 Query Match 1.2%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 GY 1492 CATGGAATTCCTTCATCTG 1512
 Db 1 CATGGAATTCCTTCATCTG 21
 RESULT 55
 ABS60214
 ID ABS60214 standard; DNA; 21 BP.
 XX
 AC ABS60214;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Human polymorphism associated DNA sequence #108.
 XX
 KW Aminopeptidase P; XPNBP2; bradykinin receptor B1; ds; BDKRB1;
 KW tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH; kallikrein 1;
 KW K1K1; bradykinin receptor B2; BDKRB2; gene therapy;
 KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;
 KW polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
 KW cardiovascular disease; angina pectoris; hypertension; heart failure;
 KW myocardial infarction; ventricular hypertrophy; vascular disease;
 KW aneurysm; embolism; thrombosis; coronary artery disease; angioedema;
 KW arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;
 KW autoimmune disease; inflammatory arthritis; cancer; wound;
 KW viral infection; bacterial infection; fungal infection; COPD;
 KW Chronic obstructive pulmonary disease; enterocolitis.
 KW
 XX
 OS Homo sapiens.
 XX
 PN WO200261131-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 03-DEC-2001; 2001WO-US047235.
 XX
 PR 04-DEC-2000; 2000US-0251015P.
 PR 23-JAN-2001; 2001US-0263678P.
 PR 02-MAR-2001; 2001US-0273037P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.

PA (TSUC/) TSUCHIHASHI Z.
 PA (HUII/) HUI L.
 XX Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;
 P1 Swanson BN, Powell JR;
 XX WPI; 2002-619265/66.
 DR
 XX New isolated nucleic acid with at least one polymorphic position, useful
 PT for detecting, diagnosing and treating disorders such as angioedema,
 PT cancer, viral, bacterial or fungal infection, cardiovascular and
 PT autoimmune diseases.
 XX
 PS Disclosure; Page 716; 977pp; English.
 XX
 CC The invention relates to an isolated nucleic acid from a human gene
 CC encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDRB1),
 CC tachykinin receptor B1 (TACR1), CI esterase inhibitor (CINH), kallikrein
 CC 1 (KLK1), bradykinin receptor B2 (BDRB2), angiotensin converting enzyme
 CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one
 CC polymorphic position. Also included are (1) a probe that hybridises to a
 CC nucleotide polymorphism comprising additional 5' and 3' flanking genomic
 CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising
 CC the sample from one or more individuals and determining the
 CC nucleic acid sequence at one or more polymorphic positions in a gene
 CC encoding a protein selected from the group above; (3) constructing (M2)
 CC haplotypes using the genes comprising grouping at least two nucleic acids
 CC ; (4) identifying (M3) an individual at risk of developing a disorder
 CC upon administration of an ACE inhibitor and/or vasopeptidase inhibitor
 CC using the polymorphic data; (5) a library of nucleic acids, each of which
 CC comprises one or more polymorphic positions within a gene encoding a
 CC human protein selected from the group above; and (6) genotyping (M4) an
 CC individual comprising obtaining a nucleic acid sample, determining the
 CC nucleotide present in at least one polymorphic position, and comparing at
 CC least one position with a known data set. The genes, (M1, M2, M3 and M4)
 CC and compositions are useful for detecting, diagnosing, treating,
 CC preventing various disorders such as angioedema and diseases which
 CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's
 CC disease, trachomas, and cardiovascular diseases like angina pectoris,
 CC hypertension, heart failure, myocardial infarction, ventricular
 CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
 CC artery disease, arteriosclerosis and/or atherosclerosis, and
 CC hypersensitively reactions, sepsis, autoimmune diseases, inflammatory
 CC arthritis, cancer, wounds, viral, bacterial or fungal infection. Chronic
 CC obstructive pulmonary disease (COPD) and enterocolitis (many other
 CC diseases and disorders are listed in the specification). The
 CC polynucleotides are also useful for chromosome identification. Antibodies
 CC against the proteins may be utilised for immunophenotyping of cell lines
 CC and biological samples. The present sequence is included in the sequence
 CC listing but is not referred to anywhere else in the specification
 XX
 SQ Sequence 21 BP; 6 A; 9 C; 2 G; 4 T; 0 U; 0 Other;
 XX
 Query Match 1.2%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 252 CATCTCCACTACACCTCGGA 272
 Db 1 CATCTCCACTACACCTCGGA 21
 RESULT 56
 ABS60345
 ID ABS60345 standard; DNA; 21 BP.
 XX
 AC ABS60345;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Human polymorphism associated DNA sequence #239.
 XX

KW Aminopeptidase P; XPNP2; bradykinin receptor B1; de; BDRB1;
 KW tachykinin receptor B1; TACR1; CI esterase inhibitor; CINH; kallikrein 1;
 KW KLK1; bradykinin receptor B2; BDRB2; gene therapy; inhibitor 4; PI4;
 KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;
 KW polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
 KW cardiovascular disease; angina pectoris; hypertension; heart failure;
 KW myocardial infarction; ventricular hypertrophy; vascular disease;
 KW aneurysm; embolism; thrombosis; coronary artery disease; angioedema;
 KW arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;
 KW autoimmune disease; inflammatory arthritis; cancer; wound;
 KW viral infection; bacterial infection; fungal infection; COPD;
 KW Chronic obstructive pulmonary disease; enterocolitis.
 XX
 OS Homo sapiens.
 XX
 PN WO200261131-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 03-DEC-2001; 2001WO-US047235.
 XX
 PR 04-DEC-2000; 2000US-0251015P.
 PR 23-JAN-2001; 2001US-0263678P.
 PR 02-MAR-2001; 2001US-0273037P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 PA (TSUC/) TSUCHIHASHI Z.
 PA (HUII/) HUI L.
 P1 Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;
 P1 Swanson BN, Powell JR;
 XX WPI; 2002-619265/66.
 DR
 XX New isolated nucleic acid with at least one polymorphic position, useful
 PT for detecting, diagnosing and treating disorders such as angioedema,
 PT cancer, viral, bacterial or fungal infection, cardiovascular and
 PT autoimmune diseases.
 XX
 PS Disclosure; Page 737; 977pp; English.
 XX
 CC The invention relates to an isolated nucleic acid from a human gene
 CC encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDRB1),
 CC tachykinin receptor B1 (TACR1), CI esterase inhibitor (CINH), kallikrein
 CC 1 (KLK1), bradykinin receptor B2 (BDRB2), angiotensin converting enzyme
 CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one
 CC polymorphic position. Also included are (1) a probe that hybridises to a
 CC nucleotide polymorphism comprising additional 5' and 3' flanking genomic
 CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising
 CC the sample from one or more individuals and determining the
 CC nucleic acid sequence at one or more polymorphic positions in a gene
 CC encoding a protein selected from the group above; (3) constructing (M2)
 CC haplotypes using the genes comprising grouping at least two nucleic acids
 CC upon administration of an ACE inhibitor and/or vasopeptidase inhibitor
 CC using the polymorphic data; (5) a library of nucleic acids, each of which
 CC comprises one or more polymorphic positions within a gene encoding a
 CC human protein selected from the group above; and (6) genotyping (M4) an
 CC individual comprising obtaining a nucleic acid sample, determining the
 CC nucleotide present in at least one polymorphic position, and comparing at
 CC least one position with a known data set. The genes, (M1, M2, M3 and M4)
 CC and compositions are useful for detecting, diagnosing, treating,
 CC preventing various disorders such as angioedema and diseases which
 CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's
 CC disease, trachomas, and cardiovascular diseases like angina pectoris,
 CC hypertension, heart failure, myocardial infarction, ventricular
 CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
 CC artery disease, arteriosclerosis and/or atherosclerosis, and
 CC hypersensitively reactions, sepsis, autoimmune diseases, inflammatory
 CC arthritis, cancer, wounds, viral, bacterial or fungal infection. Chronic
 CC obstructive pulmonary disease (COPD) and enterocolitis (many other
 CC diseases and disorders are listed in the specification). The

CC polynucleotides are also useful for chromosome identification. Antibodies
CC against the proteins may be utilised for immunophenotyping of cell lines
CC and biological samples. The present sequence is included in the sequence
CC listing but is not referred to anywhere else in the specification
XX

SO Sequence 21 BP; 3 A; 8 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 37;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1399 GAGAGCTTCAGCTTCTCTCC 1419

Db 1 GAGAGCTTCAGCTTCTCTCC 21

RESULT 57
ABS60217
ID ABS60217 standard; DNA; 21 BP.

XX ABS60217;

XX 05-NOV-2002 (first entry)

XX Human polymorphism associated DNA sequence #111.

DE Amino-peptidase P; XPNP2; bradykinin receptor B1; ds; BDKRB1;

XX tachykinin receptor B1; TACR1; CI esterase inhibitor; C1NH; kallikrein 1;

XX KKL1; bradykinin receptor B2; BDKRB2; gene therapy;

XX angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;

XX polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;

XX cardiovascular disease; angina pectoris; hypertension; heart failure;

XX myocardial infarction; ventricular hypertrophy; vascular disease;

XX aneurysm; embolism; thrombosis; coronary artery disease; angiodaema;

XX arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;

XX autoimmune disease; inflammatory arthritis; cancer; wound;

XX viral infection; bacterial infection; fungal infection; COPD;

XX Chronic obstructive pulmonary disease; enterocolitis.

XX Homo sapiens.

XX WO200261131-A2.

XX 08-AUG-2002.

XX 03-DEC-2001; 2001WO-US047235.

XX 04-DEC-2000; 2000US-0251015P.

XX 23-JAN-2001; 2001US-0263678P.

XX 02-MAR-2001; 2001US-0273037P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX PA (TSUC/) TSUCHIHASHI Z.

XX PA (HUI/L) HUI L.

XX Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;

XX Swanson BW, Powell JR;

XX WPI; 2002-619265/66.

XX New isolated nucleic acid with at least one polymorphic position, useful
XX for detecting, diagnosing and treating disorders such as angioedema,
XX cancer, viral, bacterial or fungal infection, cardiovascular and
XX autoimmune diseases.

XX Disclosure; Page 716; 977p; English.

XX The invention relates to an isolated nucleic acid from a human gene
XX encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDKRB1),
XX tachykinin receptor B1 (TACR1), CI esterase inhibitor (C1NH), kallikrein
XX 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme
XX 2 (ACE2) or protease inhibitor 4 (P14), comprising at least one
XX polymorphic position. Also included are (1) a probe that hybridises to a

CC polymorphic position as provided in the detailed summary of single

CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic

CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising

CC obtaining the sample from one or more individuals and determining the

CC nucleic acid sequence at one or more polymorphic positions in a gene

CC encoding a protein selected from the group above; (3) constructing (M2)

CC haplotypes using the genes comprising grouping at least two nucleic acids

CC; (4) identifying (M3) an individual at risk of developing a disorder

CC upon administration of an ACE inhibitor and/or vasopressinase inhibitor

CC using the polymorphic data; (5) a library of nucleic acids, each of which

CC comprises one or more polymorphic positions within a gene encoding a

CC human protein selected from the group above; and (6) genotyping (M4) an

CC individual comprising obtaining a nucleic acid sample, determining the

CC nucleotide present in at least one polymorphic position, and comparing at

CC least one position with a known data set. The genes, (M1, M2, M3 and M4)

CC and compositions are useful for detecting, diagnosing, treating,

CC preventing various disorders such as angioedema and diseases which

CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's

CC disease, trachomas, and cardiovascular diseases like angina pectoris,

CC hypertension, heart failure, myocardial infarction, ventricular

CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary

CC artery disease, arteriosclerosis and/or atherosclerosis, and

CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory

CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic

CC obstructive pulmonary disease (COPD) and enterocolitis (many other

CC diseases and disorders are listed in the specification). The

CC polynucleotides are also useful for chromosome identification. Antibodies

CC against the proteins may be utilised for immunophenotyping of cell lines

CC and biological samples. The present sequence is included in the sequence

CC listing but is not referred to anywhere else in the specification

XX Sequence 21 BP; 5 A; 7 C; 3 G; 6 T; 0 U; 0 Other;

SO Query Match 1.2%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 37;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1360 TCCACATGCTCTTCACGAGT 1380

Db 1 TCCACATGCTCTTCACGAGT 21

RESULT 58
ABS60283/C
ID ABS60283 standard; DNA; 21 BP.

XX ABS60283;

XX 05-NOV-2002 (first entry)

XX Human polymorphism associated DNA sequence #177.

DE Amino-peptidase P; XPNP2; bradykinin receptor B1; ds; BDKRB1;

XX tachykinin receptor B1; TACR1; CI esterase inhibitor; C1NH; kallikrein 1;

XX KKL1; bradykinin receptor B2; BDKRB2; gene therapy;

XX angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;

XX polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;

XX cardiovascular disease; angina pectoris; hypertension; heart failure;

XX myocardial infarction; ventricular hypertrophy; vascular disease;

XX aneurysm; embolism; thrombosis; coronary artery disease; angiodaema;

XX arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;

XX autoimmune disease; inflammatory arthritis; cancer; wound;

XX viral infection; bacterial infection; fungal infection; COPD;

XX Chronic obstructive pulmonary disease; enterocolitis.

XX Homo sapiens.

XX WO200261131-A2.

XX 08-AUG-2002.

XX 03-DEC-2001; 2001WO-US047235.

CC artery disease, arteriosclerosis and/or atherosclerosis, and
CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory
CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic
CC obstructive pulmonary disease (COPD) and enterocolitis (many other
CC diseases and disorders are listed in the specification). The
CC polynucleotides are also useful for chromosome identification. Antibodies
CC against the proteins may be utilized for immunophenotyping of cell lines
CC and biological samples. The present sequence is included in the sequence
CC listing but is not referred to anywhere else in the specification
XX
SQ Sequence 21 BP; 3 A; 8 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1399 GAGAGCTTCAGCTTCTCTCC 1419
Db 1 GAGAGCTTCAGCTTCTCTCC 21
RESULT 60
ABS60994
ID ABS60994 standard; DNA; 21 BP.
AC ABS60994;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human genotyping PCR primer #147.
XX
KW Human; ss; antipeptidase P; XPNR2; bradykinin receptor B1; primer;
KW BDKRB1; bradykinin receptor B1; TACRL; C1 esterase inhibitor; C1NH;
KW kallikrein 1; KKL1; bradykinin receptor B2; BDKRB2; gene therapy;
KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;
KW polymorphisms; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
KW cardiovascular disease; angina pectoris; hypertension; heart failure;
KW myocardial infarction; ventricular hypertrophy; vascular disease;
KW aneurysm; embolism; thrombosis; coronary artery disease; angiodaema;
KW arteriosclerosis; atherosclerosis; hypersensitivity; sepsis; PCR;
KW autoimmune disease; inflammatory arthritis; cancer; wound; genotyping;
KW viral infection; bacterial infection; fungal infection; COPD;
KW Chronic obstructive pulmonary disease; enterocolitis.
XX
OS Homo sapiens.
XX
PN WO200261131-A2.
XX
PD 08-AUG-2002.
XX
PF 03-DEC-2001; 2001WO-US047235.
XX
PR 04-DEC-2000; 2000US-0251015P.
PR 23-JAN-2001; 2001US-0263678P.
PR 02-MAR-2001; 2001US-0273037P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
PA (TSUC/) TSUCHIHASHI Z.
PA (HUI/) HUI L.
PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;
PI Swanson BN, Powell JR;
XX WPI; 2002-619265/66.
XX
XX New isolated nucleic acid with at least one polymorphic position, useful
XX for detecting, diagnosing and treating disorders such as angiodaema,
XX cancer, viral, bacterial or fungal infection, cardiovascular and
XX autoimmune diseases.
XX
XX Example 3; Page 912; 977pp; English.
XX
XX The invention relates to an isolated nucleic acid from a human gene

CC encoding aminopeptidase P (XPNR2), bradykinin receptor B1 (BDKRB1),
CC tachykinin receptor B1 (TACRL), C1 esterase inhibitor (C1NH), kallikrein
CC 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme
CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one
CC polymorphic position. Also included are (1) a probe that hybridises to a
CC polymorphic position as provided in the detailed summary of single
CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising
CC obtaining the sample from one or more individuals and determining the
CC nucleic acid sequence at one or more polymorphic positions in a gene
CC encoding a protein selected from the group above; (3) constructing (M2)
CC haplotypes using the genes comprising grouping at least two nucleic acids
CC; (4) identifying (M3) an individual at risk of developing a disorder
CC upon administration of an ACE inhibitor and/or vasopressin inhibitor
CC using the polymorphic data; (5) a library of nucleic acids, each of which
CC comprises one or more polymorphic positions within a gene encoding a
CC human protein selected from the group above; and (6) genotyping (M4) an
CC individual comprising obtaining a nucleic acid sample, determining the
CC nucleotide present in at least one polymorphic position, and comparing at
CC least one position with a known data set. The genes, (M1, M2, M3 and M4)
CC and compositions are useful for detecting, diagnosing, treating,
CC preventing various disorders such as angiodaema and diseases which
CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's
CC disease, trachomas, and cardiovascular diseases like angina pectoris,
CC hypertension, heart failure, myocardial infarction, ventricular
CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
CC artery disease, arteriosclerosis and/or atherosclerosis, and
CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory
CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic
CC obstructive pulmonary disease (COPD) and enterocolitis (many other
CC diseases and disorders are listed in the specification). The
CC polynucleotides are also useful for chromosome identification. Antibodies
CC against the proteins may be utilised for immunophenotyping of cell lines
CC and biological samples. The present sequence is a genotyping PCR primer
XX for the gene encoding one of the proteins listed above
XX
SQ Sequence 21 BP; 7 A; 6 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 493 CACAACGAATGCTACTACGGC 513
Db 1 CACAACGAATGCTACTACGGC 21
RESULT 61
ABK63856/c
ID ABK63856 standard; DNA; 21 BP.
XX
XX ABK63856;
XX
XX 18-JUN-2002 (first entry)
XX
DE Neurokinin 1 receptor (NK-1) sense oligonucleotide #7.
XX
XX
KW Human; neurokinin receptor-1; NK-1; dermatological disorder;
KW immune disorder; autoimmune disorder; cardiovascular disorder;
KW vascular disorder; airway disorder; neuropathic disorder; pain;
KW psychiatric disorder; central nervous system disorder; inflammation;
KW respiratory condition; ophthalmic condition; intestinal condition;
KW demyelinating disease; small cell lung cancer; depression;
KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
KW neuro-pathological disorder; stress; antisense; primer; ss.
XX
OS Homo sapiens.
XX
XX WO200213799-A2.
XX
XX 21-FEB-2002.
XX
XX

PF 17-AUG-2001; 2001WO-IB001510.
 XX
 PR 18-AUG-2000; 2000US-0226086P.
 XX
 PA (UYMC-) UNIV MCGILL.
 XX
 PI Henry JL, Cahill CM, Yashpal K;
 DR WPI; 2002-241835/29.
 XX
 PT Treating pathological condition involving neurokinin receptor-1, e.g.
 PT pain or inflammation, by administering oligonucleotide or a non-
 PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
 PT pathway.
 XX
 PS Claim 24; Page 20; 100pp; English.
 XX
 CC The invention relates to a method of treating a pathological condition
 CC characterised partially by involvement of neurokinin receptor-1 (NK-1)
 CC receptor, especially treating, attenuating or preventing pain or
 CC inflammatory condition. The method comprises administering to a mammal, a
 CC compound chosen from an oligonucleotide, its analogue, and a disruptor
 CC which interferes with function or production of NK-1 receptors. The
 CC method is useful for treating a pathological condition characterised by
 CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,
 CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,
 CC psychiatric and central nervous system disorders (e.g. anxiety,
 CC psychosis, schizophrenia), gut inflammation, arthritis, and central or
 CC peripheral aspects of chronic or acute pain, and for treating,
 CC attenuating or preventing pain or inflammation, neuropathic pain, inflammation or
 CC chronic, acute pain or inflammation, central nervous system
 CC pain relating to psychiatric disorders and central nervous system
 CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
 CC in a mammal, in particular human. NK-1 receptor related disorders,
 CC diseases, or pathological conditions treatable by this method include
 CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
 CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
 CC (allergic dermatitis), intestinal conditions (stroke), chronic
 CC Crohn's disease), cardiovascular conditions (stroke), chronic
 CC gastrointestinal tract inflammation, and inflammatory diseases such as
 CC inflammatory bowel diseases. Other disorders and diseases include
 CC cardiovascular pathologies including stroke, chronic inflammatory
 CC diseases such as rheumatoid arthritis, demyelinating diseases such as
 CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
 CC disorders such as allergies and poison ivy, vasospastic diseases such as
 CC angina, addiction disorders such as alcoholism, neurodegenerative
 CC disorders such as acquired immune deficiency syndrome (AIDS) related
 CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
 CC disorders such as peripheral neuropathy, oedema, stress related and
 CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
 CC effectively treat chronic conditions and other pathological states
 CC without the co-administration of substance P, and reduce the number of
 CC activated receptors while not reducing the number of quiescent NK-1
 CC receptors. Receptors not chronically stimulated are less affected,
 CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1
 CC receptor coding sequences and oligonucleotides of the invention
 XX
 SQ Sequence 21 BP; 8 A; 7 C; 3 G; 3 T; 0 U; 0 Other;
 XX
 QY
 Best Match 1.2%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 836 TGCTGGTGGATTGGCTATGCAT 856
 21 TGCTGGTGGATTGGCTATGCAT 1
 RESULT 62
 ABK63871/c
 ID ABK63871 standard; DNA; 21 BP.
 XX
 XX ABK63871;

XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #16.
 XX
 KW Human; neurokinin receptor-1; NK-1; dermatological disorder;
 KW immune disorder; autoimmune disorder; cardiovascular disorder;
 KW vascular disorder; airway disorder; neuropathic disorder; pain;
 KW psychiatric disorder; central nervous system disorder; inflammation;
 KW respiratory condition; ophthalmic condition; intestinal condition;
 KW demyelinating disease; small cell lung cancer; depression;
 KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
 KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
 KW neuro-pathological disorder; stress; antisense; primer; ss.
 KM
 XX Homo sapiens.
 OS
 XX WO200213799-A2.
 XX
 PN 21-FEB-2002.
 XX
 PD 17-AUG-2001; 2001WO-IB001510.
 XX
 PE 18-AUG-2000; 2000US-0226086P.
 XX
 PR (UYMC-) UNIV MCGILL.
 XX
 PA Henry JL, Cahill CM, Yashpal K;
 XX
 PI WPI; 2002-241835/29.
 XX
 DR Treating pathological condition involving neurokinin receptor-1, e.g.
 XX pain or inflammation, by administering oligonucleotide or a non-
 PT pain or inflammation, by administering oligonucleotide or a non-
 PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
 PT pathway.
 XX
 PS Claim 24; Page 65; 100pp; English.
 XX
 CC The invention relates to a method of treating a pathological condition
 CC characterised partially by involvement of neurokinin receptor-1 (NK-1)
 CC receptor, especially treating, attenuating or preventing pain or
 CC inflammatory condition. The method comprises administering to a mammal, a
 CC compound chosen from an oligonucleotide, its analogue, and a disruptor
 CC which interferes with function or production of NK-1 receptors. The
 CC method is useful for treating a pathological condition characterised by
 CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,
 CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,
 CC psychiatric and central nervous system disorders (e.g. anxiety,
 CC psychosis, schizophrenia), gut inflammation, arthritis, and central or
 CC peripheral aspects of chronic or acute pain, and for treating,
 CC attenuating or preventing pain or inflammation, neuropathic pain, inflammation or
 CC chronic, acute pain or inflammation, central nervous system
 CC pain relating to psychiatric disorders and central nervous system
 CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
 CC in a mammal, in particular human. NK-1 receptor related disorders,
 CC diseases, or pathological conditions treatable by this method include
 CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
 CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
 CC (allergic dermatitis), intestinal conditions (stroke), chronic
 CC Crohn's disease), cardiovascular conditions (stroke), chronic
 CC gastrointestinal tract inflammation, and inflammatory diseases such as
 CC inflammatory bowel diseases. Other disorders and diseases include
 CC cardiovascular pathologies including stroke, chronic inflammatory
 CC diseases such as rheumatoid arthritis, demyelinating diseases such as
 CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
 CC disorders such as allergies and poison ivy, vasospastic diseases such as
 CC angina, addiction disorders such as alcoholism, neurodegenerative
 CC disorders such as acquired immune deficiency syndrome (AIDS) related
 CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
 CC disorders such as peripheral neuropathy, oedema, stress related and
 CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
 CC effectively treat chronic conditions and other pathological states
 CC without the co-administration of substance P, and reduce the number of

CC activated receptors while not reducing the number of quiescent NK-1
CC receptors. Receptors not chronically stimulated are less affected,
CC reducing side effects of treatment. ABR63834-ABR63906 represent NK-1
CC receptor coding sequences and oligonucleotides of the invention
XX
SQ Sequence 21 BP; 3 A; 5 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 924 GCAAGTCTCTGCCAAGCCAA 944
DB 21 GCAAGTCTCTGCCAAGCCAA 1
|||||
RESULT 63
ABR63894
ID ABR63894 standard; DNA; 21 BP.
XX
AC ABR63894;
XX
DT 18-JUN-2002 (first entry)
XX
DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #39.
XX
KM Human; neurokinin receptor-1; NK-1; dermatological disorder;
KM immune disorder; autoimmune disorder; cardiovascular disorder;
KM vascular disorder; airway disorder; neuropathic disorder; pain;
KM psychiatric disorder; central nervous system disorder; inflammation;
KM respiratory condition; ophthalmic condition; intestinal condition;
KM demyelinating disease; small cell lung cancer; depression;
KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
KM neuro-pathological disorder; stress; antisense; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200213799-A2.
XX
PD 21-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-IB001510.
XX
PR 18-AUG-2000; 2000US-0226086P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Henry JL, Cahill CM, Yashpal K;
XX
DR WPI; 2002-241835/29.
XX
PT Treating pathological condition involving neurokinin receptor-1, e.g.
PT pain or inflammation, by administering oligonucleotide or a non-
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
PT pathway.
XX
PS Example 18; Page 65; 100pp; English.
XX
CC The invention relates to a method of treating a pathological condition
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)
CC receptor, especially treating, attenuating or preventing pain or
CC inflammatory condition. The method comprises administering to a mammal, a
CC compound chosen from an oligonucleotide, its analogue, and a disruptor
CC which interferes with function or production of NK-1 receptors. The
CC method is useful for treating a pathological condition characterised by
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,
CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,
CC psychiatric and central nervous system disorders (e.g. anxiety,
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or
CC peripheral aspects of chronic or acute pain, and for treating,
CC attenuating or preventing pain or inflammation such as peripheral,
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or

CC pain relating to psychiatric disorders and central nervous system
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
CC in a mammal, in particular human. NK-1 receptor related disorders,
CC diseases, or pathological conditions treatable by this method include
CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and
CC Crohn's disease), cardiovascular conditions (stroke), chronic
CC gastrointestinal tract inflammation, and inflammatory diseases such as
CC inflammatory bowel diseases. Other disorders and diseases include
CC cardiovascular pathologies including stroke, chronic inflammatory
CC diseases such as rheumatoid arthritis, demyelinating diseases such as
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
CC disorders such as allergies and poison ivy, vasospastic diseases such as
CC angina, addiction disorders such as alcoholism, neurodegenerative
CC disorders such as acquired immune deficiency syndrome (AIDS) related
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
CC disorders such as peripheral neuropathy, oedema, stress related and
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
CC effectively treat chronic conditions and other pathological states
CC without the co-administration of substance P, and reduce the number of
CC activated receptors while not reducing the number of quiescent NK-1
CC receptors. Receptors not chronically stimulated are less affected,
CC reducing side effects of treatment. ABR63834-ABR63906 represent NK-1
CC receptor coding sequences and oligonucleotides of the invention
XX
SQ Sequence 21 BP; 3 A; 3 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 836 TGCTGTGATGGCTATGCAT 856
DB 1 TGCTGTGATGGCTATGCAT 21
|||||
RESULT 64
ABR63875
ID ABR63875 standard; DNA; 21 BP.
XX
AC ABR63875;
XX
DT 18-JUN-2002 (first entry)
XX
DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #20.
XX
KM Human; neurokinin receptor-1; NK-1; dermatological disorder;
KM immune disorder; autoimmune disorder; cardiovascular disorder;
KM vascular disorder; airway disorder; neuropathic disorder; pain;
KM psychiatric disorder; central nervous system disorder; inflammation;
KM respiratory condition; ophthalmic condition; intestinal condition;
KM demyelinating disease; small cell lung cancer; depression;
KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
KM neuro-pathological disorder; stress; antisense; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200213799-A2.
XX
PD 21-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-IB001510.
XX
PR 18-AUG-2000; 2000US-0226086P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Henry JL, Cahill CM, Yashpal K;
XX
DR WPI; 2002-241835/29.
XX

PT Treating pathological condition involving neurokinin receptor-1, e.g.
PT pain or inflammation, by administering oligonucleotide or a non-
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
PT pathway.

PS Claim 24; Page 65; 100pp; English.

XX The invention relates to a method of treating a pathological condition
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)
CC receptor, especially treating, attenuating or preventing pain or
CC inflammatory condition. The method comprises administering to a mammal, a
CC compound chosen from an oligonucleotide, its analogue, and a disruptor
CC which interferes with function or production of NK-1 receptors. The
CC method is useful for treating a pathological condition characterised by
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,
CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,
CC psychiatric and central nervous system disorders (e.g. anxiety,
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or
CC peripheral aspects of chronic or acute pain, and for treating,
CC attenuating or preventing pain or inflammation such as peripheral,
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or
CC pain relating to psychiatric disorders and central nervous system
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
CC in a mammal, in particular human. NK-1 receptor related disorders,
CC diseases, or pathological conditions treatable by this method include
CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and
CC Crohn's disease), cardiovascular conditions (stroke), chronic
CC gastrointestinal tract inflammation, and inflammatory diseases such as
CC inflammatory bowel diseases. Other disorders and diseases include
CC cardiovascular pathologies including stroke, chronic inflammatory
CC diseases such as rheumatoid arthritis, demyelinating diseases such as
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
CC disorders such as allergies and poison ivy, vasospastic diseases such as
CC angina, addiction disorders such as alcoholism, neurodegenerative
CC disorders such as acquired immune deficiency syndrome (AIDS) related
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
CC disorders such as peripheral neuropathy, oedema, stress related and
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
CC effectively treat chronic conditions and other pathological states
CC without the co-administration of substance P, and reduce the number of
CC activated receptors while not reducing the number of quiescent NK-1
CC receptors. Receptors not chronically stimulated are less affected,
CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1
CC receptor coding sequences and oligonucleotides of the invention
XX

SO Sequence 21 BP; 3 A; 3 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 836 TCGTGTGATGTGCTATGCAT 856
|||||
Db 1 TCGTGTGATGTGCTATGCAT 21

RESULT 65
ABK63890/c
ID ABK63890 standard; DNA; 21 BP.

XX ABK63890;
XX 18-JUN-2002 (first entry)
XX
XX Neurokinin 1 receptor (NK-1) antisense oligonucleotide #35.
XX

KW Human; neurokinin receptor-1; NK-1; dermatological disorder;
KW immune disorder; autoimmune disorder; cardiovascular disorder;
KW vascular disorder; airway disorder; neuropathic disorder; pain;
KW psychiatric disorder; central nervous system disorder; inflammation;
KW respiratory condition; ophthalmic condition; intestinal condition;

KW demyelinating disease; small cell lung cancer; depression;
KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
KW neuro-pathological disorder; stress; antisense; primer; ss.

XX Homo sapiens.

XX W0200213799-A2.

XX 21-FEB-2002.

PF 17-AUG-2001; 2001WO-1B001510.

XX 18-AUG-2000; 2000US-0226086P.

PA (UVMC-) UNIV MCGILL.

PI Henry JL, Cahill CM, Yashpal K;

DR WPI; 2002-241835/29.

XX Treating pathological condition involving neurokinin receptor-1, e.g.
PT pain or inflammation, by administering oligonucleotide or a non-
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
PT pathway.

PS Example 18; Page 65; 100pp; English.

XX The invention relates to a method of treating a pathological condition
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)
CC receptor, especially treating, attenuating or preventing pain or
CC inflammatory condition. The method comprises administering to a mammal, a
CC compound chosen from an oligonucleotide, its analogue, and a disruptor
CC which interferes with function or production of NK-1 receptors. The
CC method is useful for treating a pathological condition characterised by
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,
CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,
CC psychiatric and central nervous system disorders (e.g. anxiety,
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or
CC peripheral aspects of chronic or acute pain, and for treating,
CC attenuating or preventing pain or inflammation such as peripheral,
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or
CC pain relating to psychiatric disorders and central nervous system
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
CC in a mammal, in particular human. NK-1 receptor related disorders,
CC diseases, or pathological conditions treatable by this method include
CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and
CC Crohn's disease), cardiovascular conditions (stroke), chronic
CC gastrointestinal tract inflammation, and inflammatory diseases such as
CC inflammatory bowel diseases. Other disorders and diseases include
CC cardiovascular pathologies including stroke, chronic inflammatory
CC diseases such as rheumatoid arthritis, demyelinating diseases such as
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
CC disorders such as allergies and poison ivy, vasospastic diseases such as
CC angina, addiction disorders such as alcoholism, neurodegenerative
CC disorders such as acquired immune deficiency syndrome (AIDS) related
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
CC disorders such as peripheral neuropathy, oedema, stress related and
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
CC effectively treat chronic conditions and other pathological states
CC without the co-administration of substance P, and reduce the number of
CC activated receptors while not reducing the number of quiescent NK-1
CC receptors. Receptors not chronically stimulated are less affected,
CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1
CC receptor coding sequences and oligonucleotides of the invention
XX

SO Sequence 21 BP; 3 A; 5 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 924 GCAAGTCTTCGCAAGCCAA 944
Db 21 GCAAGTCTTCGCAAGCCAA 1

RESULT 66
ABK63904
ID ABK63904 standard; DNA, 21 BP.
AC
XX ABK63904;
XX 18-JUN-2002 (first entry)
XX
DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #9.
XX
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;
KM immune disorder; autoimmune disorder; cardiovascular disorder;
KM vascular disorder; airway disorder; neuropathic disorder; pain;
KM psychiatric disorder; central nervous system disorder; inflammation;
KM respiratory condition; ophthalmic condition; intestinal condition;
KM demyelinating disease; small cell lung cancer; depression;
KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
KM neuro-pathological disorder; stress; antisense; primer; ss.
XX
OS Homo sapiens.
XX
XX WO200213799-A2.
XX
XX 21-FEB-2002.
XX
XX 17-AUG-2001; 2001WO-IB001510.
XX
XX 18-AUG-2000; 2000US-0226086P.
XX
XX (UYMC-) UNIV MCGILL.
XX
XX Henry JL, Cahill CM, Yashpal K;
XX
XX WPI; 2002-241835/29.
XX

Treating pathological condition involving neurokinin receptor-1, e.g.
PT pain or inflammation, by administering oligonucleotide or a non-
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
PT pathway.
XX
XX
XX Example 18; Page 66; 100pp; English.

The invention relates to a method of treating a pathological condition
characterised partially by involvement of neurokinin receptor-1 (NK-1)
receptor, especially treating, attenuating or preventing pain or
inflammatory condition. The method comprises administering to a mammal, a
compound chosen from an oligonucleotide, its analogue, and a disruptor
which interferes with function or production of NK-1 receptors. The
method is useful for treating a pathological condition characterised by
involvement of NK-1 receptor such as dermatological, immune, autoimmune,
cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,
psychiatric and central nervous system disorders (e.g. anxiety,
psychosis, schizophrenia), gut inflammation, arthritis, and central or
peripheral aspects of chronic or acute pain, and for treating,
attenuating or preventing pain or inflammation such as peripheral,
chronic, acute pain or inflammation, neuropathic pain, inflammation or
pain relating to psychiatric disorders and central nervous system
disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
in a mammal, in particular human. NK-1 receptor related disorders,
diseases, or pathological conditions treatable by this method include
respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
(allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and
Crohn's disease), cardiovascular conditions (stroke), chronic
gastrointestinal tract inflammation, and inflammatory diseases such as
inflammatory bowel diseases. Other disorders and diseases include

CC cardiovascular pathologies including stroke, chronic inflammatory
CC diseases such as rheumatoid arthritis, demyelinating diseases such as
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
CC disorders such as allergies and poison ivy, vasospastic diseases such as
CC angina, addiction disorders such as alcoholism, neurodegenerative
CC disorders such as acquired immune deficiency syndrome (AIDS) related
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
CC disorders such as peripheral neuropathy, oedema, stress related and
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
CC effectively treat chronic conditions and other pathological states
CC without the co-administration of substance P, and reduce the number of
CC activated receptors while not reducing the number of quiescent NK-1
CC receptors. Receptors not chronically stimulated are less affected
CC reducing side effects of treatment. ABK63851-ABK63906 represent NK-1
CC receptor coding sequences and oligonucleotides of the invention
XX

SQ Sequence 21 BP; 7 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1567 AGGAAACATTCATCCTTG 1587
Db 1 AGGAAACATTCATCCTTG 21

RESULT 67
ABK63851
ID ABK63851 standard; DNA, 21 BP.
AC
XX ABK63851;
XX
XX 18-JUN-2002 (first entry)
XX
XX Neurokinin 1 receptor (NK-1) sense oligonucleotide #2.
XX
XX
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;
KM immune disorder; autoimmune disorder; cardiovascular disorder;
KM vascular disorder; airway disorder; neuropathic disorder; pain;
KM psychiatric disorder; central nervous system disorder; inflammation;
KM respiratory condition; ophthalmic condition; intestinal condition;
KM demyelinating disease; small cell lung cancer; depression;
KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
KM neuro-pathological disorder; stress; antisense; primer; ss.
XX
XX
XX Homo sapiens.
XX
XX WO200213799-A2.
XX
XX 21-FEB-2002.
XX
XX 17-AUG-2001; 2001WO-IB001510.
XX
XX 18-AUG-2000; 2000US-0226086P.
XX
XX (UYMC-) UNIV MCGILL.
XX
XX Henry JL, Cahill CM, Yashpal K;
XX
XX WPI; 2002-241835/29.
XX

Treating pathological condition involving neurokinin receptor-1, e.g.
PT pain or inflammation, by administering oligonucleotide or a non-
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
PT pathway.
XX
XX
XX Claim 24; Page 20; 100pp; English.

The invention relates to a method of treating a pathological condition
characterised partially by involvement of neurokinin receptor-1 (NK-1)
receptor, especially treating, attenuating or preventing pain or

CC inflammatory condition. The method comprises administering to a mammal, a
CC compound chosen from an oligonucleotide, its analogue, and a disruptor
CC which interferes with function or production of NK-1 receptors. The
CC method is useful for treating a pathological condition characterised by
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,
CC cardiovascular, vascular disorders (e.g. migraine), allergy, neuropathic,
CC psychiatric and central nervous system disorders (e.g. anxiety,
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or
CC peripheral aspects of chronic or acute pain, and for treating,
CC attenuating or preventing pain or inflammation such as peripheral,
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or
CC pain relating to psychiatric disorders and central nervous system
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
CC in a mammal, in particular human. NK-1 receptor related disorders,
CC diseases, or pathological conditions treatable by this method include
CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and
CC Crohn's disease), cardiovascular conditions (stroke), chronic
CC gastrointestinal tract inflammation, and inflammatory diseases such as
CC inflammatory bowel diseases. Other disorders and diseases include
CC cardiovascular pathologies including stroke, chronic inflammatory
CC diseases such as rheumatoid arthritis, demyelinating diseases such as
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
CC disorders such as allergies and poison ivy, vasospastic diseases such as
CC angina, addiction disorders such as alcoholism, neurodegenerative
CC disorders such as acquired immune deficiency syndrome (AIDS) related
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
CC disorders such as peripheral neuropathy, oedema, stress related and
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
CC effectively treat chronic conditions and other pathological states
CC without the co-administration of substance P, and reduce the number of
CC activated receptors while not reducing the number of quiescent NK-1
CC receptors. Receptors not chronically stimulated are less affected,
CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1
CC receptor coding sequences and oligonucleotides of the invention

XX Sequence 21 BP; 3 A; 2 C; 8 G; 8 T; 0 U; 0 Other;

XX Query Match 1.2%; Score 21; DB 1; Length 21;

XX Best Local Similarity 100.0%; Pred. No. 37;

XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 956 TGAATGATGTCGTGCTGCA 976

DB 1 TGAATGATGTCGTGCTGCA 21

RESULT 68

ABK63885

ID ABK63885 standard; DNA; 21 BP.

XX ABK63885;

DT 18-JUN-2002 (first entry)

XX Neurokinin 1 receptor (NK-1) antisense oligonucleotide #30.

XX Human; neurokinin receptor-1; NK-1; dermatological disorder;
KW immune disorder; autoimmune disorder; cardiovascular disorder;
KW vascular disorder; airway disorder; neuropathic disorder; pain;
KW psychiatric disorder; central nervous system disorder; inflammation;
KW respiratory condition; ophthalmic condition; intestinal condition;
KW demyelinating disease; small cell lung cancer; depression;
KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
KW neuro-pathological disorder; stress; antisense; primer; ss.

XX Homo sapiens.

XX WO200213799-A2.

XX 21-FEB-2002.

XX 17-AUG-2001; 2001WO-IB001510.
XX 18-AUG-2000; 2000US-0226086P.
XX (UYMC-) UNIV MCGILL.
XX Henry JL, Cahill CM, Yashpal K;
PI WPI; 2002-241835/29.
XX
XX Treating pathological condition involving neurokinin receptor-1, e.g.
PT pain or inflammation, by administering oligonucleotide or a non-
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
PT pathway.

XX Claim 24; Page 65; 100pp; English.

XX The invention relates to a method of treating a pathological condition
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)
CC receptor, especially treating, attenuating or preventing pain or
CC inflammatory condition. The method comprises administering to a mammal, a
CC compound chosen from an oligonucleotide, its analogue, and a disruptor
CC which interferes with function or production of NK-1 receptors. The
CC method is useful for treating a pathological condition characterised by
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,
CC cardiovascular, vascular disorders (e.g. migraine), allergy, neuropathic,
CC psychiatric and central nervous system disorders (e.g. anxiety,
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or
CC peripheral aspects of chronic or acute pain, and for treating,
CC attenuating or preventing pain or inflammation, neuropathic pain, inflammation or
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or
CC pain relating to psychiatric disorders and central nervous system
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
CC in a mammal, in particular human. NK-1 receptor related disorders,
CC diseases, or pathological conditions treatable by this method include
CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and
CC Crohn's disease), cardiovascular conditions (stroke), chronic
CC gastrointestinal tract inflammation, and inflammatory diseases such as
CC inflammatory bowel diseases. Other disorders and diseases include
CC cardiovascular pathologies including stroke, chronic inflammatory
CC diseases such as rheumatoid arthritis, demyelinating diseases such as
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
CC disorders such as allergies and poison ivy, vasospastic diseases such as
CC angina, addiction disorders such as alcoholism, neurodegenerative
CC disorders such as acquired immune deficiency syndrome (AIDS) related
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
CC disorders such as peripheral neuropathy, oedema, stress related and
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
CC effectively treat chronic conditions and other pathological states
CC without the co-administration of substance P, and reduce the number of
CC activated receptors while not reducing the number of quiescent NK-1
CC receptors. Receptors not chronically stimulated are less affected,
CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1
CC receptor coding sequences and oligonucleotides of the invention

XX Sequence 21 BP; 7 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

XX Query Match 1.2%; Score 21; DB 1; Length 21;

XX Best Local Similarity 100.0%; Pred. No. 37;

XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1567 AGGAAACATTCATCCTTG 1587

DB 1 AGGAAACATTCATCCTTG 21

RESULT 69

ABK63889/C

ID ABK63889 standard; DNA; 21 BP.

XX

AC ABR63889;
XX
XX 18-JUN-2002 (first entry)
XX
XX Neurokinin 1 receptor (NK-1) antisense oligonucleotide #14.
XX
KM Human; neurokinin receptor-1; NK-1; dermatological disorder;
KM immune disorder; autoimmune disorder; cardiovascular disorder;
KM vascular disorder; airway disorder; neuropathic disorder; pain;
KM psychiatric disorder; central nervous system disorder; inflammation;
KM respiratory condition; ophthalmic condition; intestinal condition;
KM demyelinating disease; small cell lung cancer; depression;
KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
KM hyperdegenerative disorder; acquired immune deficiency syndrome; AIDS;
KM neuro-pathological disorder; stress; antisense; primer; ss.
XX
OS Homo sapiens.
XX
XX WO200213799-A2.
XX
XX 21-FEB-2002.
XX
XX 17-AUG-2001; 2001WO-IB001510.
XX
XX 18-AUG-2000; 2000US-0226086P.
XX
XX (UYMC-) UNIV MCGILL.
XX
XX Henry JL, Cahill CM, Yaehpal K;
XX
XX WPI; 2002-241835/29.
XX
XX
XX Treating pathological condition involving neurokinin receptor-1, e.g.
XX pain or inflammation, by administering oligonucleotide or a non-
XX nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
XX pathway.
XX
XX Example 18; Page 65; 100pp; English.
XX
XX The invention relates to a method of treating a pathological condition
XX characterised partially by involvement of neurokinin receptor-1 (NK-1)
XX receptor, especially treating, attenuating or preventing pain or
XX inflammatory condition. The method comprises administering to a mammal, a
XX compound chosen from an oligonucleotide, its analogue, and a disruptor
XX which interferes with function or production of NK-1 receptors. The
XX method is useful for treating a pathological condition characterised by
XX involvement of NK-1 receptor such as dermatological, immune, autoimmune,
XX cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,
XX psychiatric and central nervous system disorders (e.g. anxiety,
XX psychosis, schizophrenia), gut inflammation, arthritis, and central or
XX peripheral aspects of chronic or acute pain, and for treating,
XX attenuating or preventing pain or inflammation such as peripheral,
XX chronic, acute pain or inflammation, neuropathic pain, inflammation or
XX pain relating to psychiatric disorders and central nervous system
XX disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
XX in a mammal, in particular human. NK-1 receptor related disorders,
XX diseases, or pathological conditions treatable by this method include
XX respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
XX conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
XX (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and
XX Crohn's disease), cardiovascular conditions (stroke), chronic
XX gastrointestinal tract inflammation, and inflammatory diseases such as
XX inflammatory bowel diseases. Other disorders and diseases include
XX cardiovascular pathologies including stroke, chronic inflammatory
XX diseases such as rheumatoid arthritis, demyelinating diseases such as
XX multiple sclerosis, small cell lung cancer, depression, hypersensitivity
XX disorders such as allergies and poison ivy, vasospastic diseases such as
XX angina, addiction disorders such as alcoholism, neurodegenerative
XX disorders such as acquired immune deficiency syndrome (AIDS) related
XX dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
XX disorders such as peripheral neuropathy, oedema, stress related and
XX somatic disorders, and osteoarthritis. Antisense oligonucleotides
XX effectively treat chronic conditions and other pathological states

CC without the co-administration of substance P, and reduce the number of
CC activated receptors while not reducing the number of quiescent NK-1
CC receptors. Receptors not chronically stimulated are less affected,
CC reducing side effects of treatment. ABR63894-ABR63906 represent NK-1
CC receptor coding sequences and oligonucleotides of the invention
XX
XX Sequence 21 BP; 8 A; 8 C; 2 G; 3 T; 0 U; 0 Other;
XX
XX
XX Query Match 1.2%; Score 21; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 37;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 956 TGAATTCGTCGTCGTGCA 976
XX Db 21 TGAATTCGTCGTCGTGCA 1
XX
XX
XX RESULT 70
XX ABR63870/c
XX ID ABR63870 standard; DNA; 21 BP.
XX
XX ABR63870;
XX
XX 18-JUN-2002 (first entry)
XX
XX Neurokinin 1 receptor (NK-1) antisense oligonucleotide #15.
XX
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;
XX immune disorder; autoimmune disorder; cardiovascular disorder;
XX vascular disorder; airway disorder; neuropathic disorder; pain;
XX psychiatric disorder; central nervous system disorder; inflammation;
XX respiratory condition; ophthalmic condition; intestinal condition;
XX demyelinating disease; small cell lung cancer; depression;
XX hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
XX hyperdegenerative disorder; acquired immune deficiency syndrome; AIDS;
XX neuro-pathological disorder; stress; antisense; primer; ss.
XX
XX Homo sapiens.
XX
XX WO200213799-A2.
XX
XX 21-FEB-2002.
XX
XX 17-AUG-2001; 2001WO-IB001510.
XX
XX 18-AUG-2000; 2000US-0226086P.
XX
XX (UYMC-) UNIV MCGILL.
XX
XX Henry JL, Cahill CM, Yaehpal K;
XX
XX WPI; 2002-241835/29.
XX
XX Treating pathological condition involving neurokinin receptor-1, e.g.
XX pain or inflammation, by administering oligonucleotide or a non-
XX nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
XX pathway.
XX
XX Claim 24; Page 65; 100pp; English.
XX
XX The invention relates to a method of treating a pathological condition
XX characterised partially by involvement of neurokinin receptor-1 (NK-1)
XX receptor, especially treating, attenuating or preventing pain or
XX inflammatory condition. The method comprises administering to a mammal, a
XX compound chosen from an oligonucleotide, its analogue, and a disruptor
XX which interferes with function or production of NK-1 receptors. The
XX method is useful for treating a pathological condition characterised by
XX involvement of NK-1 receptor such as dermatological, immune, autoimmune,
XX cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,
XX psychiatric and central nervous system disorders (e.g. anxiety,
XX psychosis, schizophrenia), gut inflammation, arthritis, and central or
XX peripheral aspects of chronic or acute pain, and for treating,
XX attenuating or preventing pain or inflammation such as peripheral,

CC chronic, acute pain or inflammation, neuropathic pain, inflammation or
 CC pain relating to psychiatric disorders and central nervous system
 CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
 CC in a mammal, in particular human. NK-1 receptor related disorders,
 CC diseases, or pathological conditions treatable by this method include
 CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
 CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
 CC (allergic dermatitis), intestinal conditions (stroke), chronic
 CC gastrintestinal tract inflammation, and inflammatory diseases such as
 CC inflammatory bowel diseases. Other disorders and diseases include
 CC cardiovascular pathologies including stroke, chronic inflammatory
 CC diseases such as rheumatoid arthritis, demyelinating diseases such as
 CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
 CC disorders such as allergies and poison ivy, vasospastic diseases such as
 CC angina, addiction disorders such as alcoholism, neurodegenerative
 CC disorders such as acquired immune deficiency syndrome (AIDS) related
 CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
 CC disorders such as peripheral neuropathy, oedema, stress related and
 CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
 CC effectively treat chronic conditions and other pathological states
 CC without the co-administration of substance P, and reduce the number of
 CC activated receptors while not reducing the number of quiescent NK-1
 CC receptors. Receptors not chronically stimulated are less affected.
 CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1
 CC receptor coding sequences and oligonucleotides of the invention
 CC

XX Sequence 21 BP; 8 A; 8 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 956 TGAATGTCGTGTCGTCGA 976
 21 TGAATGTCGTGTCGTCGA 1

RESULT 71
 ABK63878
 ID ABK63878 strand; DNA; 21 BP.

XX AC ABK63878;

XX DT 18-JUN-2002 (first entry)

XX DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #23.

XX KM Human; neurokinin receptor-1; NK-1; dermatological disorder;
 KM immune disorder; autoimmune disorder; cardiovascular disorder;
 KM vascular disorder; airway disorder; neuropathic disorder; pain;
 KM psychiatric disorder; central nervous system disorder; inflammation;
 KM respiratory condition; ophthalmic condition; intestinal condition;
 KM demyelinating disease; small cell lung cancer; depression;
 KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
 KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
 KM neuro-pathological disorder; stress; antisense; primer; ss.

XX OS Homo sapiens.

XX PN WO200213799-A2.

XX PD 21-FEB-2002.

XX PF 17-AUG-2001; 2001WO-1B001510.

XX PR 18-AUG-2000; 2000US-0226086P.

XX PA (UWMC-) UNIV MCGILL.

XX PI Henry JL, Cahill CM, Yashpal K;

XX DR WPI; 2002-241835/29.

XX Treating pathological condition involving neurokinin receptor-1, e.g.
 PT pain or inflammation, by administering oligonucleotide or a non-
 PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
 PT pathway.

XX Claim 24; Page 65; 100pp; English.

XX The invention relates to a method of treating a pathological condition
 CC characterised partially by involvement of neurokinin receptor-1 (NK-1)
 CC receptor, especially treating, attenuating or preventing pain or
 CC inflammatory condition. The method comprises administering to a mammal, a
 CC compound chosen from an oligonucleotide, its analogue, and a disruptor
 CC which interferes with function or production of NK-1 receptors. The
 CC method is useful for treating a pathological condition characterised by
 CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,
 CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,
 CC psychiatric and central nervous system disorders (e.g. anxiety,
 CC psychosis, schizophrenia), gut inflammation, arthritis, and central or
 CC peripheral aspects of chronic or acute pain, and for treating,
 CC attenuating or preventing pain or inflammation such as peripheral,
 CC chronic, acute pain or inflammation, neuropathic pain, inflammation or
 CC pain relating to psychiatric disorders and central nervous system
 CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
 CC in a mammal, in particular human. NK-1 receptor related disorders,
 CC diseases, or pathological conditions treatable by this method include
 CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
 CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
 CC (allergic dermatitis), intestinal conditions (stroke), chronic
 CC gastrintestinal tract inflammation, and inflammatory diseases such as
 CC inflammatory bowel diseases. Other disorders and diseases include
 CC cardiovascular pathologies including stroke, chronic inflammatory
 CC diseases such as rheumatoid arthritis, demyelinating diseases such as
 CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
 CC disorders such as allergies and poison ivy, vasospastic diseases such as
 CC angina, addiction disorders such as alcoholism, neurodegenerative
 CC disorders such as acquired immune deficiency syndrome (AIDS) related
 CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
 CC disorders such as peripheral neuropathy, oedema, stress related and
 CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
 CC effectively treat chronic conditions and other pathological states
 CC without the co-administration of substance P, and reduce the number of
 CC activated receptors while not reducing the number of quiescent NK-1
 CC receptors. Receptors not chronically stimulated are less affected.
 CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1
 CC receptor coding sequences and oligonucleotides of the invention
 CC

XX Sequence 21 BP; 4 A; 7 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 559 TTCGCCAGTATCTACTCCATG 579
 1 TTCGCCAGTATCTACTCCATG 21

RESULT 72
 ABK63866/c
 ID ABK63866 strand; DNA; 21 BP.

XX AC ABK63866;

XX DT 18-JUN-2002 (first entry)

XX DE Neurokinin 1 receptor (NK-1) sense oligonucleotide #17.

XX KM Human; neurokinin receptor-1; NK-1; dermatological disorder;
 KM immune disorder; autoimmune disorder; cardiovascular disorder;
 KM vascular disorder; airway disorder; neuropathic disorder; pain;
 KM psychiatric disorder; central nervous system disorder; inflammation;

KM respiratory condition; ophthalmic condition; intestinal condition;
 KM demyelinating disease; small cell lung cancer; depression;
 KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
 KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
 KM neuro-pathological disorder; stress; antisense; primer; ss.
 OS Homo sapiens.
 XX
 XX WO200213799-A2.
 XX
 XX 21-FEB-2002.
 XX
 XX 17-AUG-2001; 2001WO-IB001510.
 XX
 XX 18-AUG-2000; 2000US-0226086P.
 XX
 XX (UYMC-) UNIV MCGILL.
 PA Henry JL, Cahill CM, Yaehpal K;
 PI WPI; 2002-241835/29.
 DR
 XX
 XX Treating pathological condition involving neurokinin receptor-1, e.g.
 PT pain or inflammation, by administering oligonucleotide or a non-
 PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
 PT pathway.
 PS
 XX Claim 24; Page 20; 100pp; English.
 XX
 CC The invention relates to a method of treating a pathological condition
 CC characterised partially by involvement of neurokinin receptor-1 (NK-1)
 CC receptor, especially treating, attenuating or preventing pain or
 CC inflammatory condition. The method comprises administering to a mammal, a
 CC compound chosen from an oligonucleotide, its analogue, and a disruptor
 CC which interferes with function or production of NK-1 receptors. The
 CC method is useful for treating a pathological condition characterised by
 CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,
 CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,
 CC psychiatric and central nervous system disorders (e.g. anxiety,
 CC psychosis, schizophrenia), gut inflammation, arthritis, and central or
 CC peripheral aspects of chronic or acute pain, and for treating,
 CC attenuating or preventing pain or inflammation such as peripheral,
 CC chronic, acute pain or inflammation, neuropathic pain, inflammation or
 CC pain relating to psychiatric disorders and central nervous system
 CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
 CC in a mammal, in particular human. NK-1 receptor related disorders,
 CC diseases, or pathological conditions treatable by this method include
 CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
 CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
 CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and
 CC Crohn's disease), cardiovascular conditions (stroke), chronic
 CC gastrointestinal tract inflammation, and inflammatory diseases such as
 CC inflammatory bowel diseases. Other disorders and diseases include
 CC cardiovascular pathologies including stroke, chronic inflammatory
 CC diseases such as rheumatoid arthritis, demyelinating diseases such as
 CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
 CC disorders such as allergies and poison ivy, vasospastic diseases such as
 CC angina, addition disorders such as alcoholism, neurodegenerative
 CC disorders such as acquired immune deficiency syndrome (AIDS) related
 CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
 CC disorders such as peripheral neuropathy, oedema, stress related and
 CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
 CC effectively treat chronic conditions and other pathological states
 CC without the co-administration of substance P, and reduce the number of
 CC activated receptors while not reducing the number of quiescent NK-1
 CC receptors. Receptors not chronically stimulated are less affected,
 CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1
 CC receptor coding sequences and oligonucleotides of the invention
 XX
 XX Sequence 21 BP; 5 A; 4 C; 5 G; 7 T; 0 U; 0 Other;
 SQ
 Query Match 1.2%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 37;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1567 AGGGAACATTCATCCTTG 1587
 Db 21 AGGGAACATTCATCCTTG 1
 RESULT 73
 ABK63880
 ID ABK63880 standard; DNA; 21 BP.
 XX
 XX
 AC ABK63880;
 XX
 XX 18-JUN-2002 (first entry)
 DT
 XX
 XX Neurokinin 1 receptor (NK-1) antisense oligonucleotide #25.
 DE
 XX
 XX Human; neurokinin receptor-1; NK-1; dermatological disorder;
 KM immune disorder; autoimmune disorder; cardiovascular disorder;
 KM vascular disorder; airway disorder; neuropathic disorder; pain;
 KM psychiatric disorder; central nervous system disorder; inflammation;
 KM respiratory condition; ophthalmic condition; intestinal condition;
 KM demyelinating disease; small cell lung cancer; depression;
 KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
 KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
 KM neuro-pathological disorder; stress; antisense; primer; ss.
 KM
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO200213799-A2.
 XX
 XX 21-FEB-2002.
 XX
 XX 17-AUG-2001; 2001WO-IB001510.
 XX
 XX 18-AUG-2000; 2000US-0226086P.
 XX
 XX (UYMC-) UNIV MCGILL.
 PA Henry JL, Cahill CM, Yaehpal K;
 PI WPI; 2002-241835/29.
 DR
 XX
 XX Treating pathological condition involving neurokinin receptor-1, e.g.
 PT pain or inflammation, by administering oligonucleotide or a non-
 PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
 PT pathway.
 PS
 XX Claim 24; Page 65; 100pp; English.
 XX
 CC The invention relates to a method of treating a pathological condition
 CC characterised partially by involvement of neurokinin receptor-1 (NK-1)
 CC receptor, especially treating, attenuating or preventing pain or
 CC inflammatory condition. The method comprises administering to a mammal, a
 CC compound chosen from an oligonucleotide, its analogue, and a disruptor
 CC which interferes with function or production of NK-1 receptors. The
 CC method is useful for treating a pathological condition characterised by
 CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,
 CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,
 CC psychiatric and central nervous system disorders (e.g. anxiety,
 CC psychosis, schizophrenia), gut inflammation, arthritis, and central or
 CC peripheral aspects of chronic or acute pain, and for treating,
 CC attenuating or preventing pain or inflammation such as peripheral,
 CC chronic, acute pain or inflammation, neuropathic pain, inflammation or
 CC pain relating to psychiatric disorders and central nervous system
 CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
 CC in a mammal, in particular human. NK-1 receptor related disorders,
 CC diseases, or pathological conditions treatable by this method include
 CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
 CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
 CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and
 CC Crohn's disease), cardiovascular conditions (stroke), chronic
 CC gastrointestinal tract inflammation, and inflammatory diseases such as

CC inflammatory bowel diseases. Other disorders and diseases include
CC cardiovascular pathologies including stroke, chronic inflammatory
CC diseases such as rheumatoid arthritis, demyelinating diseases such as
CC multiple sclerosis, small cell lung cancer, depression, hypertension
CC disorders such as allergies and poison ivy, vasospastic diseases such as
CC angina, addiction disorders such as alcoholism, neurodegenerative
CC disorders such as acquired immune deficiency syndrome (AIDS) related
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
CC disorders such as peripheral neuropathy, edema, stress related and
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
CC effectively treat chronic conditions and other pathological states
CC without the co-administration of substance P, and reduce the number of
CC activated receptors while not reducing the number of quiescent NK-1
CC receptors. Receptors not chronically stimulated are less affected,
CC reducing side effects of treatment. ABR63834-ABR63906 represent NK-1
CC receptor coding sequences and oligonucleotides of the invention
CC
CC
CC Sequence 21 BP; 6 A; 5 C; 4 G; 6 T; 0 U; 0 Other;
CC
CC
CC

Query Match	1.2%	Score 21,	DB 1;	Length 21;
Best local Similarity	100.0%	Pred. No. 37,		
Matches 21; Conservative	0;	Mismatches	0;	Indels 0;
				Gaps 0;

QY 1051 AAGTTATCCAGCAGGTCTAC 1071
|||||
Db 1 AAGTTATCCAGCAGGTCTAC 21

RESULT 74
ABK63887/c
ID ABK63887 standard; DNA: 21 BP.

AC ABK63887;
XX
DT 18-JUN-2002 (first entry)

XX Neurokinin 1 receptor (NK-1) antisense oligonucleotide #32.
DE

XX Human; neurokinin receptor-1; NK-1; dermatological disorder;
 XX immune disorder; autoimmune disorder; cardiovascular disorder;
 KM vascular disorder; airway disorder; neuropathic disorder; pain;
 KM psychiatric disorder; central nervous system disorder; inflammation;
 KM respiratory condition; ophthalmic condition; intestinal condition;
 KM hypersensitivity disorder; small cell lung cancer; depression;
 KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
 KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
 KM neuro-rheological disorder; stress; antinease; primer; ss.

OS Homo sapiens.

PN WO200213799-A2.

PD 21-FEB-2002.

17-AUG-2001; 2001WO-IB001510.

18-AUG-2000; 2000US-0226086P.

PA (UYMC-) UNIV MCGILL.

Henry JL, Cahill CM, Yashpal K;

WPI: 2002-241835/29.

Treating pathological condition involving neurokinin receptor-1, e.g.

PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic

Paliway.

F1 XX

PS Claim 24; page 63; 100pp; English
XX

CC characterised partially by involvement of neurokinin receptor-1 (NK-1)

characterised partially by involvement of neurokinin receptor-1 (NK-1)

characterised partially by involvement of neurokinin receptor-1 (NK-1)

receptor, especially treating, attenuating or preventing pain or inflammatory condition. The method comprises administering to a mammal, a compound chosen from an oligonucleotide, its analogue, and a disruptor which interferes with function or production of NK-1 receptors. The method is useful for treating a pathological condition characterised by involvement of NK-1 receptor such as dermatological, immune, autoimmune, cardiovascular, vascular disorders (e.g. migraine), allergy, neuropathic, psychiatric and central nervous system disorders (e.g. anxiety, psychosis, schizophrenia), gut inflammation, arthritis, and central or peripheral aspects of chronic or acute pain, and for treating, attenuating or preventing pain or inflammation such as peripheral, chronic, acute pain or inflammation, neuropathic pain, inflammation or pain relating to psychiatric disorders and central nervous system disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia in a mammal, in particular human. NK-1 receptor related disorders, diseases, or pathological conditions treatable by this method include respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic conditions (e.g. conjunctivitis), cutaneous/dermatological conditions (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and Crohn's disease), cardiovascular conditions (stroke), chronic gastrointestinal tract inflammation, and inflammatory diseases include inflammatory bowel diseases. Other disorders and diseases include cardiovascular pathologies including stroke, chronic inflammatory diseases such as rheumatoid arthritis, demyelinating diseases such as multiple sclerosis, small cell lung cancer, depression, hypersensitivity disorders such as allergies and poison ivy, vasospastic diseases such as angina, addiction disorders such as alcoholism, neurodegenerative disorders such as acquired immune deficiency syndrome (AIDS) related disorders such as peripheral neuropathy, oedema, stress related and dementia, epilepsy, Alzheimer's disease, and other neuro-pathological disorders such as peripheral neuropathy. Antisense oligonucleotides and somatic disorders, and osteoarthritis. Antisense oligonucleotides effectively treat chronic conditions and other pathological states without the co-administration of substance P, and reduce the number of activated receptors while not reducing the number of quiescent NK-1 receptors. Receptors not chronically stimulated are less affected, reducing side effects of treatment. ABK63834-ABK63906 represent NK-1 receptor coding sequences and oligonucleotides of the invention

Query Match	1.2%;	Score 21;	DB 1;	Length 21;
Best Local Similarity	100.0%;	Pred. No. 37;		
Matches 21; Conservative	0;	Mismatches	0;	Indels 0;
				Gaps 0;

QY 205 TTCGAATGATACTCTC 225
|||||
Db 21 TTCGAATGATACTCTC 1

RESULT 75
ABK63868
ID ABK63868 standard: DNA: 21 BP.

XX
AC
APK63868:

18-JUN-2002 (first entry)

XX
NR Neurokinin 1 receptor (NK-1) sense oligonucleotide #19.

XX Human; neurokinin receptor-1, NK-1; dermatological disorder;
XX immune disorder; autoimmune disorder; cardiovascular disorder;
XX vascular disorder; airway disorder; neuropathic disorder; pain;
XX psychiatric disorder; central nervous system disorder; inflammation;
XX respiratory condition; ophthalmic condition; intestinal condition;
XX demyelinating disease; small cell lung cancer; depression;
XX hypersensitivity disorder; allergy; vasoplastic disease; alcoholism;
XX neurodegenerative disorder; acquired immune deficiency syndrome; AIDS
XX neuroendocrine disorder; stress; arthritis; primer; ss

XX

XX
XX
XXXXXX-XX

XX

 \mathbb{Y}

PD 21-FEB-2002.

XX 17-AUG-2001; 2001WO-IB001510.

PF 18-AUG-2000; 2000US-0226086P.

PR (UWMC-) UNIV MCGILL.

XX Henry JL, Cahill CM, Yashpal K;

XX WI; 2002-241835/29.

XX Treating pathological condition involving neurokinin receptor-1, e.g.

XX pain or inflammation, by administering oligonucleotide or a non-

XX nucleotide disruptor compound which modulate NK-1 receptor biosynthetic

XX pathway.

XX Claim 24; Page 20; 100pp; English.

PS The invention relates to a method of treating a pathological condition

CC characterised partially by involvement of neurokinin receptor-1 (NK-1)

CC receptor, especially treating, attenuating or preventing pain or

CC inflammatory condition. The method comprises administering to a mammal, a

CC compound chosen from an oligonucleotide, its analogue, and a disruptor

CC which interferes with function or production of NK-1 receptors. The

CC method is useful for treating a pathological condition characterised by

CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,

CC cardiovascular, vascular disorders (e.g. migraine), allergy, neuropathic,

CC psychiatric and central nervous system disorders (e.g. anxiety,

CC psychosis, schizophrenia), gut inflammation, arthritis, and central or

CC peripheral aspects of chronic or acute pain, and for treating,

CC attenuating or preventing pain or inflammation such as peripheral,

CC chronic, acute pain or inflammation, neuropathic pain, inflammation or

CC pain relating to psychiatric disorders and central nervous system

CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia

CC in a mammal, in particular human. NK-1 receptor related disorders,

CC diseases, or pathological conditions treatable by this method include

CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic

CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions

CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and

CC Crohn's disease), cardiovascular conditions (stroke), chronic

CC gastrointestinal tract inflammation, and inflammatory diseases such as

CC inflammatory bowel diseases. Other disorders and diseases include

CC cardiovascular pathologies including stroke, chronic inflammatory

CC diseases such as rheumatoid arthritis, demyelinating diseases such as

CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity

CC disorders such as allergies and poison ivy, vasospastic diseases such as

CC angina, addiction disorders such as alcoholism, neurodegenerative

CC disorders such as acquired immune deficiency syndrome (AIDS) related

CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological

CC disorders such as peripheral neuropathy, oedema, stress related and

CC somatic disorders, and osteoarthritis. Antisense oligonucleotides

CC effectively treat chronic conditions and other pathological states

CC without the co-administration of substance P, and reduce the number of

CC activated receptors while not reducing the number of quiescent NK-1

CC receptors. Receptors not chronically stimulated are less affected,

CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1

CC receptor coding sequences and oligonucleotides of the invention

XX

XX Sequence 21 BP; 6 A; 5 C; 4 G; 6 T; 0 U; 0 Other;

XX

Query March 1, 2%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 37;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 205 TTGGAATAAGATACGTCCTC 225

|||||

Db 1 TTGGAATAAGATACGTCCTC 21

RESULT 76

ABK63899

ID ABK63899 standard; DNA; 21 BP.

AC ABK63899;
AD
AE
AF
AG 18-JUN-2002 (first entry)
AH
AI
AJ
AK Neurokinin 1 receptor (NK-1) antisense oligonucleotide #44.
AL
AM
AN
AO
AP
AQ
AR
AS
AT
AU
AV
AW
AX
AY
AZ
BA
BB
BC
BD
BE
BF
BG
BH
BI
BJ
BK
BL
BM
BN
BO
BP
BQ
BR
BS
BT
BU
BV
BW
BX
BY
BZ
CA
CB
CC
CD
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effectively treat chronic conditions and other pathological states without the co-administration of substance P, and reduce the number of activated receptors while not reducing the number of quiescent NK-1 receptors. Receptors not chronically stimulated are less affected, reducing side effects of treatment. ABR63834-ABR63906 represent NK-1 receptor coding sequences and oligonucleotides of the invention

Sequence 21 BP; 6 A; 5 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1051 AAGTTATCCAGCAGGTCTAC 1071
1 AAGTTATCCAGCAGGTCTAC 21

RESULT 77
ABR63897 standard; DNA; 21 BP.

ABR63897;
18-JUN-2002 (first entry)

Neurokinin 1 receptor (NK-1) antisense oligonucleotide #42.

Human; neurokinin receptor-1; NK-1; dermatological disorder; immune disorder; autoimmune disorder; cardiovascular disorder; vascular disorder; airway disorder; neuropathic disorder; pain; psychiatric disorder; central nervous system disorder; inflammation; respiratory condition; small cell lung cancer; depression; demyelinating disease; allergy; vasospastic disease; alcoholism; hypersensitivity disorder; acquired immune deficiency syndrome; AIDS; neurodegenerative disorder; acquired immune deficiency syndrome; AIDS; neuro-pathological disorder; stress; antisense; primer; ss.

Homo sapiens.
WO200213799-A2.
21-FEB-2002.
17-AUG-2001; 2001WO-1B001510.
18-AUG-2000; 2000US-0226086P.
(UYMC-) UNIV MCGILL.
Henry JL, Cahill CM, Yashpal K;
WPI; 2002-241835/29.

Treating pathological condition involving neurokinin receptor-1, e.g. pain or inflammation, by administering oligonucleotide or a non-nucleotide disruptor compound which modulate NK-1 receptor biosynthetic pathway.

Example 18; Page 65; 100pp; English.

The invention relates to a method of treating a pathological condition characterised partially by involvement of neurokinin receptor-1 (NK-1) receptor, especially treating, attenuating or preventing pain or inflammatory condition. The method comprises administering to a mammal, a compound chosen from an oligonucleotide, its analogue, and a disruptor which interferes with function or production of NK-1 receptors. The method is useful for treating a pathological condition characterised by involvement of NK-1 receptor such as dermatological, immune, autoimmune, cardiovascular, vascular disorders (e.g. migraine), allergy, neuropathic, psychiatric and central nervous system disorders (e.g. anxiety, psychosis, schizophrenia), gut inflammation, arthritis, and central or peripheral aspects of chronic or acute pain, and for treating,

attenuating or preventing pain or inflammation such as peripheral, chronic, acute pain or inflammation, neuropathic pain, inflammation or pain relating to psychiatric disorders and central nervous system disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia in a mammal, in particular human. NK-1 receptor related disorders, diseases, or pathological conditions treatable by this method include respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic conditions (e.g. conjunctivitis), cutaneous/dermatological conditions (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and Crohn's disease), cardiovascular conditions (stroke), chronic gastrointestinal tract inflammation, and inflammatory diseases such as inflammatory bowel diseases. Other disorders and diseases include cardiovascular pathologies including stroke, chronic inflammatory diseases such as rheumatoid arthritis, demyelinating diseases such as multiple sclerosis, small cell lung cancer, depression, hypersensitivity disorders such as allergies and poison ivy, vasospastic diseases such as angina, addiction disorders such as alcoholism, neurodegenerative disorders such as acquired immune deficiency syndrome (AIDS) related dementia, epilepsy, Alzheimer's disease, and other neuro-pathological disorders such as peripheral neuropathy, oedema, stress related and somatic disorders, and osteoarthritis. Antisense oligonucleotides effectively treat chronic conditions and other pathological states without the co-administration of substance P, and reduce the number of activated receptors while not reducing the number of quiescent NK-1 receptors. Receptors not chronically stimulated are less affected, reducing side effects of treatment. ABR63834-ABR63906 represent NK-1 receptor coding sequences and oligonucleotides of the invention

Sequence 21 BP; 4 A; 7 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

559 TTGCGCAGATCTACTCCAG 579
1 TTGCGCAGATCTACTCCAG 21

RESULT 78
ABR63852 standard; DNA; 21 BP.

ABR63852;
18-JUN-2002 (first entry)

Neurokinin 1 receptor (NK-1) sense oligonucleotide #3.

Human; neurokinin receptor-1; NK-1; dermatological disorder; immune disorder; autoimmune disorder; cardiovascular disorder; pain; vascular disorder; airway disorder; neuropathic disorder; inflammation; psychiatric disorder; central nervous system disorder; inflammation; respiratory condition; ophthalmic condition; intestinal condition; demyelinating disease; small cell lung cancer; depression; hypersensitivity disorder; allergy; vasospastic disease; alcoholism; neurodegenerative disorder; acquired immune deficiency syndrome; AIDS; neuro-pathological disorder; stress; antisense; primer; ss.

Homo sapiens.
WO200213799-A2.
21-FEB-2002.
17-AUG-2001; 2001WO-1B001510.
18-AUG-2000; 2000US-0226086P.
(UYMC-) UNIV MCGILL.
Henry JL, Cahill CM, Yashpal K;
WPI; 2002-241835/29.

DR WPI; 2002-241835/29.

XX Treating pathological condition involving neurokinin receptor-1, e.g.

PT pain or inflammation, by administering oligonucleotide or a non-

PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic pathway.

XX

PS Claim 24; Page 20; 100pp; English.

XX

CC The invention relates to a method of treating a pathological condition

CC characterised partially by involvement of neurokinin receptor-1 (NK-1)

CC receptor, especially treating, attenuating or preventing pain or

CC inflammatory condition. The method comprises administering to a mammal, a

CC compound chosen from an oligonucleotide, its analogue, and a disruptor

CC which interferes with function or production of NK-1 receptors. The

CC method is useful for treating a pathological condition characterised by

CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,

CC cardiovascular, vascular disorders (e.g. migraine), allergy, neuropathic,

CC psychiatric and central nervous system disorders (e.g. anxiety,

CC psychosis, schizophrenia), gut inflammation, arthritis, and central or

CC peripheral aspects of chronic or acute pain, and for treating,

CC attenuating or preventing pain or inflammation such as peripheral,

CC chronic, acute pain or inflammation, neuropathic pain, inflammation or

CC pain relating to psychiatric disorders and central nervous system

CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia

CC in a mammal, in particular human. NK-1 receptor related disorders,

CC diseases, or pathological conditions treatable by this method include

CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic

CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions

CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and

CC Crohn's disease), cardiovascular conditions (stroke), chronic

CC gastrointestinal tract inflammation, and inflammatory diseases such as

CC inflammatory bowel diseases. Other disorders and diseases include

CC cardiovascular pathologies including stroke, chronic inflammatory

CC diseases such as rheumatoid arthritis, demyelinating diseases such as

CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity

CC disorders such as allergies and poison ivy, vasospastic diseases such as

CC angina, addiction disorders such as alcoholism, neurodegenerative

CC disorders such as acquired immune deficiency syndrome (AIDS) related

CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological

CC disorders such as peripheral neuropathy, oedema, stress related and

CC somatic disorders, and osteoarthritis. Antisense oligonucleotides

CC effectively treat chronic conditions and other pathological states

CC without the co-administration of substance P, and reduce the number of

CC activated receptors while not reducing the number of quiescent NK-1

CC receptors. Receptors not chronically stimulated are less affected,

CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1

CC receptor coding sequences and oligonucleotides of the invention

XX

SQ Sequence 21 BP; 6 A; 7 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 37;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 924 GCAAGTCTCTCCCAAGCCCA 944

Db 1 GCAAGTCTCTCCCAAGCCCA 21

RESULT 79

ABK63906/C

ID ABK63906 standard; DNA; 21 BP.

XX

AC ABK63906;

XX

DT 18-JUN-2002 (first entry)

XX

DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #1.

XX

XX Human; neurokinin receptor-1; NK-1; dermatological disorder;

KW immune disorder; autoimmune disorder; cardiovascular disorder;

KW vascular disorder; allergy disorder; neuropathic disorder; pain;

KW psychiatric disorder; central nervous system disorder; inflammation;

KW respiratory condition; ophthalmic condition; intestinal condition;

KW demyelinating disease; small cell lung cancer; depression;

KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;

KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;

KW neuro-pathological disorder; stress; antisense; primer; ss.

XX

OS Homo sapiens.

XX

PN MO200213799-A2.

XX

PD 21-FEB-2002.

XX

PP 17-AUG-2001; 2001MO-IB001510.

XX

PR 18-AUG-2000; 2000US-0226086P.

XX

PA (UYMC-) UNIV MCGILL.

PI Henry JL, Cahill CM, Yaehpal K;

XX

XX WPI; 2002-241835/29.

DR

XX

XX Treating pathological condition involving neurokinin receptor-1, e.g.

PT pain or inflammation, by administering oligonucleotide or a non-

PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic pathway.

XX

PS Example 18; Page 66; 100pp; English.

XX

CC The invention relates to a method of treating a pathological condition

CC characterised partially by involvement of neurokinin receptor-1 (NK-1)

CC receptor, especially treating, attenuating or preventing pain or

CC inflammatory condition. The method comprises administering to a mammal, a

CC compound chosen from an oligonucleotide, its analogue, and a disruptor

CC which interferes with function or production of NK-1 receptors. The

CC method is useful for treating a pathological condition characterised by

CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,

CC cardiovascular, vascular disorders (e.g. migraine), allergy, neuropathic,

CC psychiatric and central nervous system disorders (e.g. anxiety,

CC psychosis, schizophrenia), gut inflammation, arthritis, and central or

CC peripheral aspects of chronic or acute pain, and for treating,

CC attenuating or preventing pain or inflammation such as peripheral,

CC chronic, acute pain or inflammation, neuropathic pain, inflammation or

CC pain relating to psychiatric disorders and central nervous system

CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia

CC in a mammal, in particular human. NK-1 receptor related disorders,

CC diseases, or pathological conditions treatable by this method include

CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic

CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions

CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and

CC Crohn's disease), cardiovascular conditions (stroke), chronic

CC gastrointestinal tract inflammation, and inflammatory diseases such as

CC inflammatory bowel diseases. Other disorders and diseases include

CC cardiovascular pathologies including stroke, chronic inflammatory

CC diseases such as rheumatoid arthritis, demyelinating diseases such as

CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity

CC disorders such as allergies and poison ivy, vasospastic diseases such as

CC angina, addiction disorders such as alcoholism, neurodegenerative

CC disorders such as acquired immune deficiency syndrome (AIDS) related

CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological

CC disorders such as peripheral neuropathy, oedema, stress related and

CC somatic disorders, and osteoarthritis. Antisense oligonucleotides

CC effectively treat chronic conditions and other pathological states

CC without the co-administration of substance P, and reduce the number of

CC activated receptors while not reducing the number of quiescent NK-1

CC receptors. Receptors not chronically stimulated are less affected,

CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1

CC receptor coding sequences and oligonucleotides of the invention

XX

SQ Sequence 21 BP; 6 A; 4 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 205 TTGGAATGATTAACGCTCC 225
Db 21 TTGGAATGATTAACGCTCC 1

RESULT 80
ABK63854/c
ID ABK63854 standard; DNA; 21 BP.
XX AC ABK63854;
XX DT 18-JUN-2002 (first entry)
XX DE Neurokinin 1 receptor (NK-1) sense oligonucleotide #5.
XX KW Human; neurokinin receptor-1; NK-1; dermatological disorder;
KW immunologic disorder; autoimmune disorder; cardiovascular disorder;
KW immunologic disorder; airway disorder; neuropathic disorder; pain;
KW psychiatric disorder; central nervous system disorder; inflammation;
KW respiratory condition; ophthalmic condition; intestinal condition;
KW demyelinating disease; small cell lung cancer; depression;
KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
KW neuro-pathological disorder; stress; antisense; primer; ss.
XX OS Homo sapiens.
XX PN WO200213799-A2.
XX PD 21-FEB-2002.
XX PF 17-AUG-2001; 2001WO-1B001510.
XX PR 18-AUG-2000; 2000US-0226086P.
XX PA (UYMC-) UNIV MCGILL.
XX PI Henry JL, Cahill CM, Yashpal K;
XX DR WPI; 2002-241835/29.
XX PT Treating pathological condition involving neurokinin receptor-1, e.g.
PT pain or inflammation, by administering oligonucleotide or a non-
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
PT pathway.
XX PS Claim 24; Page 20; 100pp; English.
XX CC The invention relates to a method of treating a pathological condition
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)
CC receptor, especially treating, attenuating or preventing pain or
CC inflammatory condition. The method comprises administering to a mammal, a
CC compound chosen from an oligonucleotide, its analogue, and a disruptor
CC which interferes with function or production of NK-1 receptors. The
CC method is useful for treating a pathological condition characterised by
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,
CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,
CC psychiatric and central nervous system disorders (e.g. anxiety,
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or
CC peripheral aspects of chronic or inflammation such as peripheral,
CC attenuating or preventing pain or inflammation, neuropathic pain, inflammation or
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or
CC pain relating to psychiatric disorders and central nervous system
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
CC in a mammal, in particular human. NK-1 receptor related disorders,
CC diseases, or pathological conditions treatable by this method include
CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and
CC Crohn's disease), cardiovascular conditions (stroke), chronic

CC gastrointestinal tract inflammation, and inflammatory diseases such as
CC inflammatory bowel diseases. Other disorders and diseases include
CC cardiovascular pathologies including stroke, chronic inflammatory
CC diseases such as rheumatoid arthritis, demyelinating diseases such as
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
CC disorders such as allergies and poison ivy, vasospastic diseases such as
CC angina, addiction disorders such as alcoholism, neurodegenerative
CC disorders such as acquired immune deficiency syndrome (AIDS) related
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
CC disorders such as peripheral neuropathy, edema, stress related and
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
CC effectively treat chronic conditions and other pathological states
CC without the co-administration of substance P, and reduce the number of
CC activated receptors while not reducing the number of quiescent NK-1
CC receptors. Receptors not chronically stimulated are less affected,
CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1
CC receptor coding sequences and oligonucleotides of the invention
XX SQ Sequence 21 BP; 8 A; 8 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 956 TGATGATTCGTCGTGTGCA 976
Db 21 TGATGATTCGTCGTGTGCA 1

RESULT 81
ABK63873
ID ABK63873 standard; DNA; 21 BP.
XX AC ABK63873;
XX DT 18-JUN-2002 (first entry)
XX DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #18.
XX KW Human; neurokinin receptor-1; NK-1; dermatological disorder;
KW immunologic disorder; autoimmune disorder; cardiovascular disorder;
KW immunologic disorder; airway disorder; neuropathic disorder; pain;
KW psychiatric disorder; central nervous system disorder; inflammation;
KW respiratory condition; ophthalmic condition; intestinal condition;
KW demyelinating disease; small cell lung cancer; depression;
KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
KW neuro-pathological disorder; stress; antisense; primer; ss.
XX OS Homo sapiens.
XX PN WO200213799-A2.
XX PD 21-FEB-2002.
XX PF 17-AUG-2001; 2001WO-1B001510.
XX PR 18-AUG-2000; 2000US-0226086P.
XX PA (UYMC-) UNIV MCGILL.
XX PI Henry JL, Cahill CM, Yashpal K;
XX DR WPI; 2002-241835/29.
XX PT Treating pathological condition involving neurokinin receptor-1, e.g.
PT pain or inflammation, by administering oligonucleotide or a non-
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
PT pathway.
XX PS Claim 24; Page 65; 100pp; English.
XX CC The invention relates to a method of treating a pathological condition

CC characterised partially by involvement of neurokinin receptor-1 (NK-1),
CC receptor, especially treating, attenuating or preventing pain or
CC inflammatory condition. The method comprises administering to a mammal, a
CC compound chosen from an oligonucleotide, its analogue, and a disruptor
CC which interferes with function or production of NK-1 receptors. The
CC method is useful for treating a pathological condition characterised by
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,
CC cardiovascular, vascular disorders (e.g. migraine), allergy, neuropathic,
CC psychiatric and central nervous system disorders (e.g. anxiety,
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or
CC peripheral aspects of chronic or acute pain, and for treating,
CC attenuating or preventing pain or inflammation such as peripheral,
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or
CC pain relating to psychiatric disorders and central nervous system
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
CC in a mammal, in particular human. NK-1 receptor related disorders,
CC diseases, or pathological conditions treatable by this method include
CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and
CC Crohn's disease), cardiovascular conditions (stroke), chronic
CC gastrointestinal tract inflammation, and inflammatory diseases such as
CC inflammatory bowel diseases. Other disorders and diseases include
CC cardiovascular pathologies including stroke, chronic inflammatory
CC diseases such as rheumatoid arthritis, demyelinating diseases such as
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
CC disorders such as allergies and poison ivy, vasospastic diseases such as
CC angina, addiction disorders such as alcoholism, neurodegenerative
CC diseases such as acquired immune deficiency syndrome (AIDS) related
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
CC disorders such as peripheral neuropathy, oedema, stress related and
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
CC effectively treat chronic conditions and other pathological states
CC without the co-administration of substance P, and reduce the number of
CC activated receptors while not reducing the number of quiescent NK-1
CC receptors. Receptors not chronically stimulated are less affected.
CC reducing side effects of treatment. ABR63834-ABR63906 represent NK-1
CC receptor coding sequences and oligonucleotides of the invention

XX
SQ Sequence 21 BP; 3 A; 2 C; 8 G; 8 T; 0 U; 0 Other;

XX
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 956 TGATGATTGTCGTGTGCA 976
|||
Db 1 TGATGATTGTCGTGTGCA 21

RESULT 82
ABR63861/c
ID ABR63861 standard; DNA; 21 BP.
XX
AC ABR63861;
XX
DT 18-JUN-2002 (first entry)
XX
DE Neurokinin 1 receptor (NK-1) sense oligonucleotide #12.
XX
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;
KM immune disorder; autoimmune disorder; cardiovascular disorder;
KM vascular disorder; airway disorder; neuropathic disorder; pain;
KM psychiatric disorder; central nervous system disorder; inflammation;
KM respiratory condition; ophthalmic condition; intestinal condition;
KM demyelinating disease; small cell lung cancer; depression;
KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
KM neuro-pathological disorder; stress; antisense; primer; 88.
XX
XX Homo sapiens.
OS
XX
PN W0200213799-A2.

XX
PD 21-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-IB001510.
XX
PR 18-AUG-2000; 2000US-0226086P.
XX
XX (UVMC-) UNIV MCGILL.
XX
XX Henry JL, Cahill CM, Yashpal K;
PI WPI; 2002-241835/29.
XX
PT Treating pathological condition involving neurokinin receptor-1, e.g.
PT pain or inflammation, by administering oligonucleotide or a non-
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
PT pathway.

PS Claim 24; Page 20; 100pp; English.

XX
CC The invention relates to a method of treating a pathological condition
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)
CC receptor, especially treating, attenuating or preventing pain or
CC inflammatory condition. The method comprises administering to a mammal, a
CC compound chosen from an oligonucleotide, its analogue, and a disruptor
CC which interferes with function or production of NK-1 receptors. The
CC method is useful for treating a pathological condition characterised by
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,
CC cardiovascular, vascular disorders (e.g. migraine), allergy, neuropathic,
CC psychiatric and central nervous system disorders (e.g. anxiety,
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or
CC peripheral aspects of chronic or acute pain, and for treating,
CC attenuating or preventing pain or inflammation such as peripheral,
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or
CC pain relating to psychiatric disorders and central nervous system
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
CC in a mammal, in particular human. NK-1 receptor related disorders,
CC diseases, or pathological conditions treatable by this method include
CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and
CC Crohn's disease), cardiovascular conditions (stroke), chronic
CC gastrointestinal tract inflammation, and inflammatory diseases such as
CC inflammatory bowel diseases. Other disorders and diseases include
CC cardiovascular pathologies including stroke, chronic inflammatory
CC diseases such as rheumatoid arthritis, demyelinating diseases such as
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
CC disorders such as allergies and poison ivy, vasospastic diseases such as
CC angina, addiction disorders such as alcoholism, neurodegenerative
CC disorders such as acquired immune deficiency syndrome (AIDS) related
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
CC disorders such as peripheral neuropathy, oedema, stress related and
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
CC effectively treat chronic conditions and other pathological states
CC without the co-administration of substance P, and reduce the number of
CC activated receptors while not reducing the number of quiescent NK-1
CC receptors. Receptors not chronically stimulated are less affected.
CC reducing side effects of treatment. ABR63834-ABR63906 represent NK-1
CC receptor coding sequences and oligonucleotides of the invention

XX
SQ Sequence 21 BP; 6 A; 4 C; 5 G; 6 T; 0 U; 0 Other;

XX
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1051 AAGTTATCCAGCAGCTTAC 1071
|||
Db 21 AAGTTATCCAGCAGCTTAC 1

RESULT 83
ABR63881

ID ABK63881 standard; DNA; 21 BP.
XX ABK63881;
AC
XX
XX
XX 18-JUN-2002 (first entry)
XX
XX
XX Neurokinin 1 receptor (NK-1) antisense oligonucleotide #26.
XX
XX
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;
XX immune disorder; autoimmune disorder; cardiovascular disorder;
XX vascular disorder; airway disorder; neuropathic disorder; pain;
XX psychiatric disorder; central nervous system disorder; inflammation;
XX respiratory condition; ophthalmic condition; intestinal condition;
XX demyelinating disease; small cell lung cancer; depression;
XX hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
XX neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
XX neuro-pathological disorder; stress; antisense; primer; ss.
XX
XX Homo sapiens.
XX
XX WO200213799-A2.
XX
XX 21-FEB-2002.
XX
XX 17-AUG-2001; 2001WO-IB001510.
XX
XX 18-AUG-2000; 2000US-0226086P.
XX
XX (UYMC-) UNIV MCGILL.
XX
XX Henry JL, Cahill CM, Yashpal K;
XX
XX WPI; 2002-241835/29.
XX
XX
XX Treating pathological condition involving neurokinin receptor-1, e.g.
XX pain or inflammation, by administering oligonucleotide or a non-
XX nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
XX pathway.
XX
XX
XX Claim 24; Page 65; 100pp; English.
XX
XX
XX The invention relates to a method of treating a pathological condition
XX characterised partially by involvement of neurokinin receptor-1 (NK-1)
XX receptor, especially treating, attenuating or preventing pain or
XX inflammatory condition. The method comprises administering to a mammal, a
XX compound chosen from an oligonucleotide, its analogue, and a disruptor
XX which interferes with function or production of NK-1 receptors. The
XX method is useful for treating a pathological condition characterised by
XX involvement of NK-1 receptor such as dermatological, immune, autoimmune,
XX cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,
XX psychiatric and central nervous system disorders (e.g. anxiety,
XX psychosis, schizophrenia), gut inflammation, arthritis, and central or
XX peripheral aspects of chronic or acute pain, and for treating,
XX attenuating or preventing pain or inflammation such as peripheral,
XX chronic, acute pain or inflammation, neuropathic pain, inflammation or
XX pain relating to psychiatric disorders and central nervous system
XX disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
XX in a mammal, in particular human. NK-1 receptor related disorders,
XX diseases, or pathological conditions treatable by this method include
XX respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
XX conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
XX (allergic dermatitis), intestinal conditions (stroke), chronic
XX Crohn's disease), cardiovascular conditions and inflammatory diseases such as
XX gastrointestinal tract inflammation, and inflammatory diseases include
XX inflammatory bowel diseases. Other disorders and diseases include
XX cardiovascular pathologies including stroke, chronic inflammatory
XX diseases such as rheumatoid arthritis, demyelinating diseases such as
XX multiple sclerosis, small cell lung cancer, depression, hypersensitivity
XX disorders such as allergies and poison ivy, vasospastic diseases such as
XX angina, addiction disorders such as alcoholism, neurodegenerative
XX disorders such as acquired immune deficiency syndrome (AIDS) related
XX dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
XX disorders such as peripheral neuropathy, oedema, stress related and

CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
CC effectively treat chronic conditions and other pathological states
CC without the co-administration of substance P, and reduce the number of
CC activated receptors while not reducing the number of quiescent NK-1
CC receptors. Receptors not chronically stimulated are less affected,
CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1
CC receptor coding sequences and oligonucleotides of the invention
XX
XX
XX Sequence 21 BP; 7 A; 8 C; 1 G; 5 T; 0 U; 0 Other;
XX
XX
XX Query Match 1.2%; Score 21; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 37;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX 1105 ATGTACAAACCCATCATCTAC 1125
XX ||||||||||||||||||||
XX 1 ATGTACAAACCCATCATCTAC 21
XX
XX
XX RESULT 84
XX ABK63859/C
XX ID ABK63859 standard; DNA; 21 BP.
XX
XX
XX ABK63859;
XX
XX 18-JUN-2002 (first entry)
XX
XX
XX Neurokinin 1 receptor (NK-1) sense oligonucleotide #10.
XX
XX
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;
XX immune disorder; autoimmune disorder; cardiovascular disorder;
XX vascular disorder; airway disorder; neuropathic disorder; pain;
XX psychiatric disorder; central nervous system disorder; inflammation;
XX respiratory condition; ophthalmic condition; intestinal condition;
XX demyelinating disease; small cell lung cancer; depression;
XX hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
XX neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
XX neuro-pathological disorder; stress; antisense; primer; ss.
XX
XX
XX Homo sapiens.
XX
XX WO200213799-A2.
XX
XX 21-FEB-2002.
XX
XX 17-AUG-2001; 2001WO-IB001510.
XX
XX 18-AUG-2000; 2000US-0226086P.
XX
XX (UYMC-) UNIV MCGILL.
XX
XX Henry JL, Cahill CM, Yashpal K;
XX
XX WPI; 2002-241835/29.
XX
XX
XX Treating pathological condition involving neurokinin receptor-1, e.g.
XX pain or inflammation, by administering oligonucleotide or a non-
XX nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
XX pathway.
XX
XX
XX Claim 24; Page 20; 100pp; English.
XX
XX
XX The invention relates to a method of treating a pathological condition
XX characterised partially by involvement of neurokinin receptor-1 (NK-1)
XX receptor, especially treating, attenuating or preventing pain or
XX inflammatory condition. The method comprises administering to a mammal, a
XX compound chosen from an oligonucleotide, its analogue, and a disruptor
XX which interferes with function or production of NK-1 receptors. The
XX method is useful for treating a pathological condition characterised by
XX involvement of NK-1 receptor such as dermatological, immune, autoimmune,
XX cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,
XX psychiatric and central nervous system disorders (e.g. anxiety,
XX psychosis, schizophrenia), gut inflammation, arthritis, and central or

peripheral aspects of chronic or acute pain, and for treating, attenuating or preventing pain or inflammation such as peripheral, chronic, acute pain or inflammation, neuropathic pain, inflammation or pain relating to psychiatric disorders and central nervous system disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia in a mammal, in particular human, NK-1 receptor related disorders, diseases, or pathological conditions treatable by this method include respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic conditions (e.g. conjunctivitis), cutaneous/dermatological conditions (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and Crohn's disease), cardiovascular conditions (stroke), chronic gastrointestinal tract inflammation, and inflammatory diseases such as inflammatory bowel diseases. Other disorders and diseases include cardiovascular pathologies including stroke, chronic inflammatory diseases such as rheumatoid arthritis, demyelinating diseases such as multiple sclerosis, small cell lung cancer, depression, hypersensitivity disorders such as allergies and poison ivy, vasospastic diseases such as angina, addiction disorders such as alcoholism, neurodegenerative disorders such as acquired immune deficiency syndrome (AIDS) related dementia, epilepsy, Alzheimer's disease, and other neuro-pathological disorders such as peripheral neuropathy, oedema, stress related and somatic disorders, and osteoarthritis. Antisense oligonucleotides effectively treat chronic conditions and other pathological states without the co-administration of substance P, and reduce the number of activated receptors while not reducing the number of quiescent NK-1 receptors. Receptors not chronically stimulated are less affected, reducing side effects of treatment. ABR63834-ABR63906 represent NK-1 receptor coding sequences and oligonucleotides of the invention

Sequence 21 BP; 7 A; 3 C; 7 G; 4 T; 0 U; 0 Other;

Query Match Best Local Similarity 1.2%; Score 21; DB 1; Length 21;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

559 TTGCGCAGTATCTACTCCATG 579
21 TTGCGCAGTATCTACTCCATG 1

RESULT 85

ABR63892 standard; DNA; 21 BP.

ABR63892;

18-JUN-2002 (first entry)

Neurokinin 1 receptor (NK-1) antisense oligonucleotide #37.

Human; neurokinin receptor-1; NK-1; dermatological disorder; immune disorder; autoimmune disorder; cardiovascular disorder; vascular disorder; airway disorder; neuropathic disorder; pain; psychiatric disorder; central nervous system disorder; inflammation; respiratory condition; ophthalmic condition; intestinal condition; demyelinating disease; small cell lung cancer; depression; hypersensitivity disorder; allergy; vasospastic disease; alcoholism; neurodegenerative disorder; acquired immune deficiency syndrome; AIDS; neuro-pathological disorder; stress; antisense; primer; ss.

Homo sapiens.

WO200213799-A2.

21-FEB-2002.

17-AUG-2001; 2001WO-1B001510.

18-AUG-2000; 2000US-0226086P.

(UYMC-) UNIV MCGILL.

Henry JL, Cahill CM, Yashpal K;

WPI; 2002-241835/29.

Treating pathological condition involving neurokinin receptor-1, e.g. pain or inflammation, by administering oligonucleotide or a non-nucleotide disruptor compound which modulate NK-1 receptor biosynthetic pathway.

Example 18; Page 65; 100pp; English.

The invention relates to a method of treating a pathological condition characterised partially by involvement of neurokinin receptor-1 (NK-1) receptor, especially treating, attenuating or preventing pain or inflammation, by administering oligonucleotide, its analogue, and a disruptor which interferes with function or production of NK-1 receptors. The method is useful for treating a pathological condition characterised by involvement of NK-1 receptor such as dermatological, immune, autoimmune, cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic, psychiatric and central nervous system disorders (e.g. anxiety, psychosis, schizophrenia), gut inflammation, arthritis, and central or peripheral aspects of chronic or acute pain, and for treating, attenuating or preventing pain or inflammation such as peripheral, chronic, acute pain or inflammation, neuropathic pain, inflammation or pain relating to psychiatric disorders and central nervous system disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia in a mammal, in particular human, NK-1 receptor related disorders, diseases, or pathological conditions treatable by this method include respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic conditions (e.g. conjunctivitis), cutaneous/dermatological conditions and (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and Crohn's disease), cardiovascular conditions (stroke), chronic gastrointestinal tract inflammation, and inflammatory diseases such as inflammatory bowel diseases. Other disorders and diseases include cardiovascular pathologies including stroke, chronic inflammatory diseases such as rheumatoid arthritis, demyelinating diseases such as multiple sclerosis, small cell lung cancer, depression, hypersensitivity disorders such as allergies and poison ivy, vasospastic diseases such as angina, addiction disorders such as alcoholism, neurodegenerative disorders such as acquired immune deficiency syndrome (AIDS) related dementia, epilepsy, Alzheimer's disease, and other neuro-pathological disorders such as peripheral neuropathy, oedema, stress related and somatic disorders, and osteoarthritis. Antisense oligonucleotides effectively treat chronic conditions and other pathological states without the co-administration of substance P, and reduce the number of activated receptors while not reducing the number of quiescent NK-1 receptors. Receptors not chronically stimulated are less affected, reducing side effects of treatment. ABR63834-ABR63906 represent NK-1 receptor coding sequences and oligonucleotides of the invention

Sequence 21 BP; 3 A; 2 C; 8 G; 8 T; 0 U; 0 Other;

Query Match Best Local Similarity 1.2%; Score 21; DB 1; Length 21;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

956 TGATGATTTGTCGTGTCGCA 976
1 TGATGATTTGTCGTGTCGCA 21

RESULT 86

ABR63900 standard; DNA; 21 BP.

ABR63900;

18-JUN-2002 (first entry)

Neurokinin 1 receptor (NK-1) antisense oligonucleotide #45.

Human; neurokinin receptor-1; NK-1; dermatological disorder; immune disorder; autoimmune disorder; cardiovascular disorder;

KM vascular disorder; airway disorder; neuropathic disorder; pain;
 KM psychiatric disorder; central nervous system disorder; inflammation;
 KM respiratory condition; ophthalmic condition; intestinal condition;
 KM demyelinating disease; small cell lung cancer; depression;
 KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
 KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
 KM neuro-pathological disorder; stress; antisense; primer; ss.

OS Homo sapiens.

XX W0200213799-A2.

XX 21-FEB-2002.

XX 17-AUG-2001; 2001WO-IB001510.

XX 18-AUG-2000; 2000US-0226086P.

XX (UYMC-) UNIV MCGILL.

XX Henry JL, Cahill CM, Yashpal K;

XX WPI; 2002-241835/29.

XX Treating pathological condition involving neurokinin receptor-1, e.g.

XX pain or inflammation, by administering oligonucleotide or a non-

XX nucleotide disruptor compound which modulate NK-1 receptor biosynthetic

XX pathway.

XX Example 18; Page 65; 100pp; English.

XX The invention relates to a method of treating a pathological condition

XX characterised partially by involvement of neurokinin receptor-1 (NK-1)

XX receptor, especially treating, attenuating or preventing pain or

XX inflammatory condition. The method comprises administering to a mammal, a

XX compound chosen from an oligonucleotide, its analogue, and a disruptor

XX which interferes with function or production of NK-1 receptors. The

XX method is useful for treating a pathological condition characterised by

XX involvement of NK-1 receptor such as dermatological, immune, autoimmune,

XX cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,

XX psychiatric and central nervous system disorders (e.g. anxiety,

XX psychoses, schizophrenia), gut inflammation, arthritis, and central or

XX peripheral aspects of chronic or acute pain, and for treating,

XX attenuating or preventing pain or inflammation such as peripheral,

XX chronic, acute pain or inflammation, neuropathic pain, inflammation or

XX pain relating to psychiatric disorders and central nervous system

XX disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia

XX in a mammal, in particular human. NK-1 receptor related disorders,

XX diseases, or pathological conditions treatable by this method include

XX respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic

XX conditions (e.g. conjunctivitis), cutaneous/dermatological conditions

XX (allergic dermatitis), intestinal conditions (stroke), chronic

XX Crohn's disease), cardiovascular conditions (stroke), chronic

XX gastrointestinal tract inflammation, and inflammatory diseases such as

Query Match 1.2%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1105 ATGTACACACCCATCATCTAC 1125
 DB 1 ATGTACACACCCATCATCTAC 21

RESULT 87

ADU26730

ID ADU26730 standard; DNA; 21 BP.

XX ADU26730;

XX 27-JAN-2005 (first entry)

XX Knock-down target sequence #128.

XX ds; RNA production; protein production; drug development;

XX knock-down target.

XX Unidentified.

XX W02004094636-A1.

XX 24-APR-2003; 2003WO-EP004362.

XX 24-APR-2003; 2003WO-EP004362.

XX 24-APR-2003; 2003WO-EP004362.

XX (GALA-) GALAPAGOS GENOMICS NV.

XX (VSC/)/ VAN DER SCHUEREN J.

XX Arts GJF, Lambrecht MJT, Djokic K, Claesen RJ, Wesic E;

XX Griffioen S, Bergs CUL;

XX WPI; 2004-775940/76.

XX New knockdown sequences, useful in lowering the amount of RNA and/or

XX protein production in cells used in drug development processes.

XX Claim 11; SEQ ID NO 131; 402pp; English.

XX The invention relates to a polynucleotide comprising an RNA sequence. The

XX amount of RNA and/or protein production in cells used in drug development

XX process. The present sequence represents a knock-down target sequence.

XX Sequence 21 BP; 7 A; 9 C; 1 G; 4 T; 0 U; 0 Other;

XX Query Match 1.2%; Score 21; DB 1; Length 21;

XX Best Local Similarity 100.0%; Pred. No. 37;

XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1025 ACATCAACCCAGATCTTACC 1045

DB 1 ACATCAACCCAGATCTTACC 21

RESULT 88

ADU26729

ID ADU26729 standard; DNA; 21 BP.

XX ADU26729;

XX 27-JAN-2005 (first entry)

XX Knock-down target sequence #127.

Query Match 1.2%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1105 ATGTACACACCCATCATCTAC 1125
 DB 1 ATGTACACACCCATCATCTAC 21

RESULT 87

ADU26730

ID ADU26730 standard; DNA; 21 BP.

XX ADU26730;

XX 27-JAN-2005 (first entry)

XX Knock-down target sequence #128.

XX ds; RNA production; protein production; drug development;

XX knock-down target.

XX Unidentified.

XX W02004094636-A1.

XX 24-APR-2003; 2003WO-EP004362.

XX 24-APR-2003; 2003WO-EP004362.

XX (GALA-) GALAPAGOS GENOMICS NV.

XX (VSC/)/ VAN DER SCHUEREN J.

XX Arts GJF, Lambrecht MJT, Djokic K, Claesen RJ, Wesic E;

XX Griffioen S, Bergs CUL;

XX WPI; 2004-775940/76.

XX New knockdown sequences, useful in lowering the amount of RNA and/or

XX protein production in cells used in drug development processes.

XX Claim 11; SEQ ID NO 131; 402pp; English.

XX The invention relates to a polynucleotide comprising an RNA sequence. The

XX amount of RNA and/or protein production in cells used in drug development

XX process. The present sequence represents a knock-down target sequence.

XX Sequence 21 BP; 7 A; 9 C; 1 G; 4 T; 0 U; 0 Other;

XX Query Match 1.2%; Score 21; DB 1; Length 21;

XX Best Local Similarity 100.0%; Pred. No. 37;

XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1025 ACATCAACCCAGATCTTACC 1045

DB 1 ACATCAACCCAGATCTTACC 21

RESULT 88

ADU26729

ID ADU26729 standard; DNA; 21 BP.

XX ADU26729;

XX 27-JAN-2005 (first entry)

XX Knock-down target sequence #127.


```
XX OS Unidentified.
XX PN WO2004094636-A1.
XX PD 04-NOV-2004.
XX PF 24-APR-2003; 2003WO-EP004362.
XX PR 24-APR-2003; 2003WO-EP004362.
XX PA (GALA-) GALAPAGOS GENOMICS NV.
XX PA (VSC/) VAN DER SCHUEREN J.
XX PI Artb GJF, Lambrecht MJT, Djokic K, Claesen RJ, Mesic E;
XX PI Griffiths S, Berge CUL;
XX DR WPI; 2004-775940/76.
XX PT New knockdown sequences, useful in lowering the amount of RNA and/or
XX PT protein production in cells used in drug development process.
XX PS Claim 11, SEQ ID NO 130; 402pp; English.
XX CC The invention relates to a polynucleotide comprising an RNA sequence. The
XX CC polynucleotide, vector, libraries, and method are useful in lowering the
XX CC amount of RNA and/or protein production in cells used in drug development
XX CC process. The present sequence represents a knock-down target sequence.
XX SQ Sequence 21 BP; 4 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 21; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 37;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 797 ACCACATCTGTGACTGTGC 817
Db 1 ACCACATCTGTGACTGTGC 21
RESULT 89
AAQ37208
ID AAQ37208 standard; DNA; 26 BP.
XX
XX AAQ37208;
XX AC
XX DT 25-MAR-2003 (revised)
XX DT 17-JUN-1993 (first entry)
XX DE PCR primer #1 to amplify substance P receptor coding region.
XX KW human substance P receptor protein; SP; neurotransmitter; neuromodulator;
XX KW central nervous system; peripheral nervous system;
XX KW gastrointestinal disorders; inflammation; immune disease.
XX OS Synthetic.
XX PN WO9303137-A1.
XX PD 18-FEB-1993.
XX PF 05-AUG-1992; 92MO-US0006532.
XX PR 07-AUG-1991; 91US-00741200.
XX PA (UNIW ) UNIV WASHINGTON.
XX PI Krause JE;
XX DR WPI; 1993-076495/09.
XX PT New human substance P receptor protein and DNA encoding it - used e.g.
XX PT for screening substance P antagonists.
```

```
XX PS Example; Page 9; 40pp; English.
XX CC This PCR primer was used with AAQ37209 to amplify the predicted human
XX CC substance P receptor coding region from 1M-9 cDNA. The amplified fragment
XX CC was blunt end ligated into SmaI-digested pBS. Transformants were further
XX CC analysed by restriction mapping and by sequence analysis. One cDNA was
XX CC isolated after restriction with HindIII and BamHI (present in the pBS
XX CC polylinker) and made blunt ended with Klenow, as was pM2 after BamHI
XX CC digestion. The cDNA was ligated to pM2 and used to transform E. coli XL-1
XX CC Blue cells by electroporation. (Updated on 25-MAR-2003 to correct PN
XX CC field.)
XX SQ Sequence 26 BP; 5 A; 10 C; 6 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 21; DB 1; Length 26;
XX Best Local Similarity 100.0%; Pred. No. 65;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 211 ATGATTAACGTCTCTCCCGTG 231
Db 6 ATGATTAACGTCTCTCCCGTG 26
RESULT 90
AAQ30778/C
ID AAQ30778 standard; DNA; 24 BP.
XX
XX AAQ30778;
XX AC
XX DT 25-MAR-2003 (revised)
XX DT 22-MAR-1993 (first entry)
XX DE PCR primer rspr7a1h to amplify human NK1R 5' core region.
XX KW Neurokinin-1 receptor short form; arthritis; Substance P;
XX KW polymerase chain reaction; rat NK1R; se.
XX OS Synthetic.
XX PN EP514207-A2.
XX PD 19-NOV-1992.
XX PF 15-MAY-1992; 92EP-00304432.
XX PR 17-MAY-1991; 91US-00701930.
XX PR 17-MAY-1991; 91US-00701935.
XX PR 17-MAY-1991; 91US-00701937.
XX PA (MERI ) MERCK & CO INC.
XX PI Strader CD, Fong TM;
XX DR WPI; 1992-384034/47.
XX PT New human neurokinin-1 receptor short form protein - useful for
XX PT identifying and determining substance P antagonists in arthritic
XX PT patients.
XX PS Example 1; Page 8; 36pp; English.
XX CC Human mRNA was prepared from 3 glioblastoma cell lines T98G, CCF-STG1
XX CC and U87MG. First strand cDNA was synthesised and used as template with
XX CC rat primers rspr2s4, rspr2s4h and rspr7a2 (AAQ30774-6) in first round PCR
XX CC amplification. Secondary PCR was performed on the amplified product using
XX CC the same 3 primers prior to a third round of amplification, this time
XX CC using the primers rspr2s4, rspr2s4h, rspr7a1 (AAQ30777) and rspr7a1h
XX CC (AAQ30778). The tertiary PCR product was sequenced and was found to have
XX CC 90% identity at the nucleotide level with the central core region of the
XX CC rat NK1R from amino acid 91 to 280. Primer rspr7a1h is an antisense
XX CC primer based on the rat NK1R sequence 864-841 (numbering as in
XX CC J Biol. Chem. 264: 17649-17652, 1989), but designed to incorporate the
```

CC human codon bias. (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 24 BP; 6 A; 6 C; 6 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 1.2%; Score 20.8; DB 1; Length 24;
 Best Local Similarity 91.7%; Pred. No. 57;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1051 AAGTTATCCAGCAGTCTACTCTG 1074
 DB 24 AAGTTATCCAGCAGCAGTCTACTCTG 1
 RESULT 91
 ABS60911/c
 ID ABS60911 standard; DNA; 21 BP.
 XX
 AC ABS60911;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Human genotyping PCR primer #64.
 XX
 XX Human; ss; aminopeptidase P; XPNP2; bradykinin receptor B1; primer;
 XX BDKRB1; tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH;
 XX Kallikrein 1; K1K1; bradykinin receptor B2; BDKRB2; gene therapy;
 XX angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;
 XX polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
 XX cardiovascular disease; angina pectoris; hypertension; heart failure;
 XX myocardial infarction; ventricular hypertrophy; vascular disease;
 XX aneurysm; embolism; thrombosis; coronary artery disease; angioedema;
 XX arteriosclerosis; atherosclerosis; hypersensitivity; sepsis; PCR;
 XX autoimmune disease; bacterial infection; arthritis; cancer; wound; genotyping;
 XX viral infection; bacterial infection; fungal infection; COPD;
 XX Chronic obstructive pulmonary disease; enterocolitis.
 OS
 XX Homo sapiens.
 XX
 PN WO200261131-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 03-DEC-2001; 2001WO-US047235.
 XX
 PR 04-DEC-2000; 2000US-0251015P.
 XX 23-JAN-2001; 2001US-0263678P.
 PR 02-MAR-2001; 2001US-0273037P.
 XX
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 PA (TSUC/) TSUCHIHASHI Z.
 PA (HUI/) HUI L.
 XX
 PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;
 PI Swanson BN, Powell JR;
 DR WPI; 2002-619265/66.
 XX
 XX New isolated nucleic acid with at least one polymorphic position, useful
 PT for detecting, diagnosing and treating disorders such as angioedema,
 PT cancer, viral, bacterial or fungal infection, cardiovascular and
 PT autoimmune diseases.
 XX
 PS Example 3; Page 899; 977pp; English.
 XX
 XX The invention relates to an isolated nucleic acid from a human gene
 CC encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDKRB1),
 CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein
 CC 1 (K1K1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme
 CC 2 (ACE2) or protease inhibitor 4 (P14), comprising at least one
 CC polymorphic position. Also included are (1) a probe that hybridises to a
 CC polymorphic position as provided in the detailed summary of single
 CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
 CC sequence; (2) analysing (MI) at least one nucleic acid sample comprising

CC obtaining the sample from one or more individuals and determining the
 CC nucleic acid sequence at one or more polymorphic positions in a gene
 CC encoding a protein selected from the group above; (3) constructing (M2)
 CC haplotypes using the genes comprising groupings at least two nucleic acids
 CC ; (4) identifying (M3) an individual at risk of developing a disorder
 CC upon administration of an ACE inhibitor and/or vasopressinase inhibitor
 CC using the polymorphic data; (5) a library of nucleic acids, each of which
 CC comprises one or more polymorphic positions within a gene encoding a
 CC human protein selected from the group above; and (6) genotyping (M4) an
 CC individual comprising obtaining a nucleic acid sample, determining the
 CC nucleotide present in at least one polymorphic position, and comparing at
 CC least one position with a known data set. The genes, (M1, M2, M3 and M4)
 CC and compositions are useful for detecting, diagnosing, treating,
 CC preventing various disorders such as angioedema and diseases which
 CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's
 CC disease, trachomas, and cardiovascular diseases like angina pectoris,
 CC hypertension, heart failure, myocardial infarction, thrombosis, coronary
 CC artery disease, arteriosclerosis and/or atherosclerosis, and
 CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory
 CC arthritis, cancer, wounds, viral, bacterial or fungal infection. Chronic
 CC obstructive pulmonary disease (COPD) and enterocolitis (many other
 CC diseases and disorders are listed in the specification). The
 CC polymucleotides are also useful for chromosome identification. Antibodies
 CC against the proteins may be utilised for immunophenotyping of cell lines
 CC and biological samples. The present sequence is a genotyping PCR primer
 CC for the gene encoding one of the proteins listed above
 XX
 SQ Sequence 21 BP; 6 A; 3 C; 6 G; 5 T; 0 U; 1 Other;
 Query Match 1.2%; Score 20.6; DB 1; Length 21;
 Best Local Similarity 95.2%; Pred. No. 43;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1624 CCTCATCTCTGTGACTCTCAA 1644
 DB 21 CCTCATCTCTGTGACTCTCAA 1
 RESULT 92
 AAT18361/c
 ID AAT18361 standard; DNA; 24 BP.
 XX
 AC AAT18361;
 XX
 DT 26-AUG-1996 (first entry)
 XX
 DE G-protein coupled receptor protein DNA primer TM6-E2.
 XX
 XX G-protein coupled receptor protein; G-PCR; agonist; antagonist;
 KW cystic fibrosis; incontinence; diabetes; diagnosis; gene therapy;
 KW transgenic animal; polymerase chain reaction; PCR; primer; ss.
 KW
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH modified_base 18
 FT /*tag= a
 FT /*mod_base= i
 XX
 PN WO9605302-A1.
 XX
 PD 22-FEB-1996.
 XX
 PF 10-AUG-1995; 95WO-JP001599.
 XX
 PR 11-AUG-1994; 94JP-00189272.
 XX 11-AUG-1994; 94JP-00189273.
 PR 11-AUG-1994; 94JP-00189274.
 XX 30-SEP-1994; 94JP-00236356.
 PR 30-SEP-1994; 94JP-00236357.
 XX 02-NOV-1994; 94JP-00270017.
 PR 28-DEC-1994; 94JP-00326611.
 XX

PR 20-JAN-1995; 95JP-00007177.
PR 16-MAR-1995; 95JP-00057186.
PR 19-APR-1995; 95JP-00093989.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
PI Hinuma S, Hosoya M, Fujii R, Ohtaki T, Fukusumi S, Ohgi K;
XX WPI; 1996-139698/14.
XX
XX G-protein coupled receptor protein DNA and protein - also methods for
PT isolating (ant)agonists for treatment of cystic fibrosis, incontinence
PT and diabetes.
XX
PS Claim 1; Page 242; 360pp; English.
XX
CC PCR primer TM6-E2 (AAT18361) is complementary to DNA coding for a region
CC corresponding to, or near, the sixth transmembrane domain of known G-
CC protein coupled receptor proteins (G-PCRs). TM6-E2 and other primers
CC (see also AAT18347-60 and AAT18362-65) based on G-PCR transmembrane
CC domains are used for the PCR amplification of mammalian DNAs to obtain G-
CC PCR-encoding sequences (see also AAT18366-73 and AAT13901-09)
CC
XX
SQ Sequence 24 BP; 6 A; 4 C; 7 G; 0 T; 0 U; 7 Other;

Query Match 1.2%; Score 20.6; DB 1; Length 24;
Best Local Similarity 70.8%; Pred. No. 61;
Matches 17; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 979 TTGCGCATCTGTCGTGCGTCCCTTC 1002
Db |||||:|||||:|||||:|||||:
24 TTGCGCNTSTGCTGAGTSCCWC 1

RESULT 93
ID AAQ30792 standard; DNA; 20 BP.
XX
AC AAQ30792;
XX
DT 25-MAR-2003 (revised)
DT 22-MAR-1993 (first entry)
XX
DE PCR primer hsp664 to amplify human NK1R sf C-terminal region.
XX
XX Neurokinin-1 receptor short form; arthritis; Substance P;
KM anchored polymerase chain reaction; rat NK1R; ss.
XX
OS Synthetic.
XX
PN EP514207-A2.
XX
PD 19-NOV-1992.
XX
PE 15-MAY-1992; 92EP-00304432.
XX
PR 17-MAY-1991; 91US-00701930.
PR 17-MAY-1991; 91US-00701935.
PR 17-MAY-1991; 91US-00701937.
XX
PA (MERI) MERCK & CO INC.
XX
XX Strader CD, Fong TM;
PI WPI; 1992-384034/47.
DR
XX
XX New human neurokinin-1 receptor short form protein - useful for
PT identifying and determining substance P antagonists in arthritic
PT patients.
XX
PS Example 1; Page 8; 36pp; English.
XX
CC Double-stranded cDNA was prepared from human glioblastoma mRNA and large-

CC size cDNA was ligated to EcoRI linkers. linker-ligated cDNA was then
CC ligated to the calf intestinal phosphatase-treated EcoRI site of the
CC vector Bluescript SK+. The ligated plasmid DNA was used as template in a
CC primary PCR amplification with human primers hsp661 and hsp662
CC (AAQ30789 and AAQ30790) and the vector-specific primer t3 (from
CC "Stratagene"). The primary PCR product was used as template for secondary
CC PCR with the human primer hsp663 (AAQ30791) and t3. The product of this
CC reaction was amplified in a tertiary PCR amplification with hsp664
CC (AAQ30792) and vector-specific primer SK (also from "Stratagene"). A
CC 400bp DNA fragment was detected which hybridized to human oligoprobe
CC hsp665 (AAQ30793). This fragment was subcloned and sequenced. It was
CC found to encode the C-terminal region of human NK1R sf and also contains
CC 3'UTR. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 20 BP; 6 A; 8 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1023 CTACATCAACCCAGATCTCT 1042
Db |||||:|||||:|||||:|||||:
1 CTACATCAACCCAGATCTCT 20

RESULT 94
ID AAQ30788/c
ID AAQ30788 standard; DNA; 20 BP.
XX
AC AAQ30788;
XX
DT 25-MAR-2003 (revised)
DT 22-MAR-1993 (first entry)
XX
XX
DE PCR primer hsp662 to amplify human NK1R sf N-terminal region.
XX
XX Neurokinin-1 receptor short form; arthritis; Substance P;
KM polymerase chain reaction; rat NK1R; ss.
XX
OS Synthetic.
XX
PN EP514207-A2.
XX
PD 19-NOV-1992.
XX
PE 15-MAY-1992; 92EP-00304432.
XX
PR 17-MAY-1991; 91US-00701930.
PR 17-MAY-1991; 91US-00701935.
PR 17-MAY-1991; 91US-00701937.
XX
PA (MERI) MERCK & CO INC.
XX
XX Strader CD, Fong TM;
PI WPI; 1992-384034/47.
DR
XX
XX New human neurokinin-1 receptor short form protein - useful for
PT identifying and determining substance P antagonists in arthritic
PT patients.
XX
PS Example 1; Page 8; 36pp; English.
XX
XX The core region of human NK1R sf was isolated by PCR and sequenced (see
CC AAQ30774-Q30778). The antisense primers hsp345, hsp541, hsp542,
CC hsp661 and hsp662 (AAQ30784-Q30788) were synthesised based on the human
CC core sequence. Human glioblastoma mRNA and each of these primers were
CC used in first strand cDNA synthesis to produce the template for a primary
CC PCR amplification. Primer hsp345 was used with 2 rat sense primers rsnrn
CC and rsnrth (AAQ30779 and AAQ30780) for the primary PCR with the same rat
CC product was then used as template for secondary PCR with the same rat
CC primers and the human antisense primer hsp344 (AAQ30783). The secondary
CC PCR product was the template for tertiary PCR amplification, again using

CC the same rat sense primers but with human antisense primer hsp3a1
CC (AAQ30782). The amplified DNA fragment hybridised to hsp3a2 (AAQ30781),
CC indicating it is not a non-specific by-product. The DNA was sequenced and
CC found to encode the human NK1R sf N-terminal region and also contains a
CC 5' UTR. (Updated on 25-MAR-2003 to correct PN field.)
CC
XX

SQ Sequence 20 BP; 6 A; 1 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1012 TTCCCTGCGCCCTACATCAA 1031
20 TTCTCTGCGCCCTACATCAA 1

RESULT 95
AAQ30791
ID AAQ30791 standard; DNA; 20 BP.

AC AAQ30791;
DT 25-MAR-2003 (revised)
DT 22-MAR-1993 (first entry)

DE PCR primer hsp663 to amplify human NK1R sf C-terminal region.

KW Neurokinin-1 receptor short form; arthritis; Substance P;
KW anchored polymerase chain reaction; rat NK1R; ss.

OS Synthetic.

PN EP514207-A2.

PD 19-NOV-1992.

PF 15-MAY-1992; 92BP-00304432.

PR 17-MAY-1991; 91US-00701930.

PR 17-MAY-1991; 91US-00701935.

PR 17-MAY-1991; 91US-00701937.

PA (MERI) MERCK & CO INC.

PI Strader CD, Fong TM;

DR WPI; 1992-384034/47.

XX New human neurokinin-1 receptor short form protein - useful for
PT identifying and determining substance P antagonists in arthritic
PT patients.

PS Example 1; Page 8; 36pp; English.

XX Double-stranded cDNA was prepared from human glioblastoma mRNA and large-
CC size cDNA was ligated to EcoRI linkers. Linker-ligated cDNA was then
CC ligated to the calf intestinal phosphatase-treated EcoRI site of the
CC vector Bluescript SK+. The ligated plasmid DNA was used as template in a
CC primary PCR amplification with human primers hsp661 and hsp662
CC (AAQ30789 and AAQ30790) and the vector-specific primer t3 (from
CC "Stratagene"). The primary PCR product was used as template for secondary
CC PCR with the human primer hsp663 (AAQ30791) and t3. The product of this
CC reaction was amplified in a tertiary PCR amplification with hsp664
CC (AAQ30792) and vector-specific primer SK (also from "Stratagene"). A
CC 400bp DNA fragment was detected which hybridised to human oligoprobe
CC hsp665 (AAQ30793). This fragment was subcloned and sequenced. It was
CC found to encode the C-terminal region of human NK1R sf and also contains
CC 3' UTR. (Updated on 25-MAR-2003 to correct PN field.)
CC
XX
SQ

Query Match 1.1%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1000 TTCCACATCTTCTCTCTCT 1019
1 TTCCACATCTTCTCTCTCT 20

RESULT 96
AAQ30786/c
ID AAQ30786 standard; DNA; 20 BP.

AC AAQ30786;

DT 25-MAR-2003 (revised)

DT 22-MAR-1993 (first entry)

DE PCR primer hsp5a2 to amplify human NK1R sf N-terminal region.

KW Neurokinin-1 receptor short form; arthritis; Substance P;
KW polymerase chain reaction; rat NK1R; ss.

OS Synthetic.

PN EP514207-A2.

PD 19-NOV-1992.

PF 15-MAY-1992; 92BP-00304432.

PR 17-MAY-1991; 91US-00701930.

PR 17-MAY-1991; 91US-00701935.

PR 17-MAY-1991; 91US-00701937.

PA (MERI) MERCK & CO INC.

PI Strader CD, Fong TM;

DR WPI; 1992-384034/47.

XX New human neurokinin-1 receptor short form protein - useful for
PT identifying and determining substance P antagonists in arthritic
PT patients.

PS Example 1; Page 8; 36pp; English.

XX The core region of human NK1R sf was isolated by PCR and sequenced (see
CC AAQ30774-Q30778). The antisense primers hsp3a5, hsp5a1, hsp5a2,
CC hsp6a1 and hsp6a2 (AAQ30784-Q30788) were synthesised based on the human
CC core sequence. Human glioblastoma mRNA and each of these primers were
CC used in first strand cDNA synthesis to produce the template for a primary
CC PCR amplification. Primer hsp3a5 was used with 2 rat sense primers rsn1
CC and rsnph (AAQ30779 and AAQ30780) for the primary amplification. The PCR
CC product was then used as template for secondary PCR with the same rat
CC primers and the human antisense primer hsp3a4 (AAQ30783). The secondary
CC PCR product was the template for tertiary PCR amplification, again using
CC the same rat sense primers but with human antisense primer hsp3a1
CC (AAQ30782). The amplified DNA fragment hybridised to hsp3a2 (AAQ30781),
CC indicating it is not a non-specific by-product. The DNA was sequenced and
CC found to encode the human NK1R sf N-terminal region and also contains a
CC 5' UTR. (Updated on 25-MAR-2003 to correct PN field.)
CC
XX
SQ

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

862 GTAGTGGGATCACTATG 861
20 GTAGTGGGATCACTATG 1

RESULT 97
AAQ30783/c
ID AAQ30783 standard; DNA; 20 BP.
XX
XX AAQ30783;
AC
XX
XX 25-MAR-2003 (revised)
DT 22-MAR-1993 (first entry)
XX
XX PCR primer hsp34 to amplify human NK1R 5' N-terminal region.
DE
XX Neurokinin-1 receptor short form; arthritis; Substance P;
KW polymerase chain reaction; rat NK1R; ss.
XX
XX Synthetic.
OS
XX EP514207-A2.
PN
XX 19-NOV-1992.
PD
XX 15-MAY-1992; 92EP-00304432.
PF
XX 17-MAY-1991; 91US-00701930.
PR 17-MAY-1991; 91US-00701935.
PR 17-MAY-1991; 91US-00701937.
XX
XX (MERI) MERCK & CO INC.
XX
XX Strader CD, Fong TW;
PI
XX WPI; 1992-384034/47.
DR
XX New human neurokinin-1 receptor short form protein - useful for
PT identifying and determining substance P antagonists in arthritic
PT patients.
XX
XX Example 1; Page 8; 36pp; English.
PS
XX The core region of human NK1R 5' was isolated by PCR and sequenced (see
XX AAQ30774-Q30778). The antisense primers hsp3a5, hsp5a1, hsp5a2,
XX hsp6a1 and hsp6a2 (AAQ30784-Q30788) were synthesised based on the human
XX core sequence. Human glioblastoma mRNA and each of these primers were
XX used in first strand cDNA synthesis to produce the template for a primary
XX PCR amplification. Primer hsp3a5 was used with 2 rat sense primers repm
XX and repm (AAQ30779 and AAQ30780) for the primary amplification. The PCR
XX product was then used as template for secondary PCR with the same rat
XX primers and the human antisense primer hsp3a4 (AAQ30783). The secondary
XX PCR product was the template for tertiary PCR amplification, again using
XX the same rat sense primers but with human antisense primer hsp3a1
XX (AAQ30782). The amplified DNA fragment hybridised to hsp3a2 (AAQ30781),
XX indicating it is not a non-specific by-product. The DNA was sequenced and
XX found to encode the human NK1R 5' N-terminal region and also contains a
XX 5' UTR. (Updated on 25-MAR-2003 to correct PN field.)
SQ
XX Sequence 20 BP; 5 A; 2 C; 7 G; 6 T; 0 U; 0 Other;
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 601 TCATGGCCATCATCATCC 620
DB 20 TCATGGCCATCATCATCC 1

XX
XX PCR primer hsp3a5 to amplify human NK1R 5' N-terminal region.
DE
XX Neurokinin-1 receptor short form; arthritis; Substance P;
KW polymerase chain reaction; rat NK1R; ss.
XX
XX Synthetic.
OS
XX EP514207-A2.
PN
XX 19-NOV-1992.
PD
XX 15-MAY-1992; 92EP-00304432.
PF
XX 17-MAY-1991; 91US-00701930.
PR 17-MAY-1991; 91US-00701935.
PR 17-MAY-1991; 91US-00701937.
XX
XX (MERI) MERCK & CO INC.
XX
XX Strader CD, Fong TW;
PI
XX WPI; 1992-384034/47.
DR
XX New human neurokinin-1 receptor short form protein - useful for
PT identifying and determining substance P antagonists in arthritic
PT patients.
XX
XX Example 1; Page 8; 36pp; English.
PS
XX The core region of human NK1R 5' was isolated by PCR and sequenced (see
XX AAQ30774-Q30778). The antisense primers hsp3a5, hsp5a1, hsp5a2,
XX hsp6a1 and hsp6a2 (AAQ30784-Q30788) were synthesised based on the human
XX core sequence. Human glioblastoma mRNA and each of these primers were
XX used in first strand cDNA synthesis to produce the template for a primary
XX PCR amplification. Primer hsp3a5 was used with 2 rat sense primers repm
XX and repm (AAQ30779 and AAQ30780) for the primary amplification. The PCR
XX product was then used as template for secondary PCR with the same rat
XX primers and the human antisense primer hsp3a4 (AAQ30783). The secondary
XX PCR product was the template for tertiary PCR amplification, again using
XX the same rat sense primers but with human antisense primer hsp3a1
XX (AAQ30782). The amplified DNA fragment hybridised to hsp3a2 (AAQ30781),
XX indicating it is not a non-specific by-product. The DNA was sequenced and
XX found to encode the human NK1R 5' N-terminal region and also contains a
XX 5' UTR. (Updated on 25-MAR-2003 to correct PN field.)
SQ
XX Sequence 20 BP; 2 A; 3 C; 8 G; 7 T; 0 U; 0 Other;
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 637 TCAGCCACAGCCACCAAGT 656
DB 20 TCAGCCACAGCCACCAAGT 1

RESULT 99
AAQ29672/c
ID AAQ29672 standard; DNA; 20 BP.
XX
XX AAQ29672;
AC
XX
XX 25-MAR-2003 (revised)
DT 15-MAR-1993 (first entry)
XX
XX hsp3a4 primer 532-513.
DE
XX Human; neurokinin-1 receptor; NK1R; membrane receptor; substance P;
KW neurotransmitter; polymerase chain reaction; PCR; rat NK1R; primer;
KW amplify; probe; ss.
XX
XX Homo sapiens.

XX EP510878-A1.
 XX 28-OCT-1992.
 XX 16-APR-1992; 92EP-00303457.
 XX 25-APR-1991; 91US-00691197.
 XX 25-APR-1991; 91US-00691198.
 XX 25-APR-1991; 91US-00691200.
 XX (MERI) MERCK & CO INC.
 XX Fong TM, Strader CD;
 XX WPI; 1992-359073/44.
 XX New recombinant human neurokinin-1 receptor - used to detect and evaluate
 PT substances that bind to substance P receptor, and to determine substance
 PT P in body fluid of arthritis patients.
 XX Disclosure; Page 8; 35pp; English.
 XX The sequences given in AAQ29670-82, AAQ29783 and AAQ29746-48 are primers
 CC which were used in the isolation of fragments of the human neurokinin-1
 CC receptor (NK1R) cDNA. Human NK1R is a membrane receptor for the
 CC neurotransmitter substance P. The primers were designed using regions of
 CC the human NK1R cDNA and also regions of the rat NK1R which were thought
 CC to be similar to human regions. Part of the human cDNA sequence was
 CC derived by amplification using these primers. The remaining part of human
 CC NK1R cDNA was obtained from a human cDNA library utilising portions of
 CC PCR generated fragments as probes. See also AAQ29749. (Updated on 25-MAR-
 CC 2003 to correct PN field.)
 XX Sequence 20 BP; 5 A; 2 C; 7 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 601 TACATGGCCATCATCATCC 620
 DB 20 TACATGGCCATCATCATCC 1
 RESULT 100
 AAQ29675/C
 ID AAQ29675 standard; DNA; 20 BP.
 XX AAQ29675;
 AC
 XX 25-MAR-2003 (revised)
 DT 15-MAR-1993 (first entry)
 XX
 DE hsp5a2 primer 793-774.
 XX
 XX Human; neurokinin-1 receptor; NK1R, membrane receptor; substance P;
 KW neurotransmitter; polymerase chain reaction; PCR; rat NK1R; primer;
 KW amplify; probe; ss.
 XX
 XX Homo sapiens.
 XX
 XX EP510878-A1.
 XX 28-OCT-1992.
 XX 16-APR-1992; 92EP-00303457.
 XX 25-APR-1991; 91US-00691197.
 XX 25-APR-1991; 91US-00691198.
 XX 25-APR-1991; 91US-00691200.
 XX (MERI) MERCK & CO INC.

XX Fong TM, Strader CD;
 XX WPI; 1992-359073/44.
 XX New recombinant human neurokinin-1 receptor - used to detect and evaluate
 PT substances that bind to substance P receptor, and to determine substance
 PT P in body fluid of arthritis patients.
 XX Disclosure; Page 8; 35pp; English.
 XX The sequences given in AAQ29670-82, AAQ29783 and AAQ29746-48 are primers
 CC which were used in the isolation of fragments of the human neurokinin-1
 CC receptor (NK1R) cDNA. Human NK1R is a membrane receptor for the
 CC neurotransmitter substance P. The primers were designed using regions of
 CC the human NK1R cDNA and also regions of the rat NK1R which were thought
 CC to be similar to human regions. Part of the human cDNA sequence was
 CC derived by amplification using these primers. The remaining part of human
 CC NK1R cDNA was obtained from a human cDNA library utilising portions of
 CC PCR generated fragments as probes. See also AAQ29749. (Updated on 25-MAR-
 CC 2003 to correct PN field.)
 XX Sequence 20 BP; 5 A; 6 C; 3 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 862 GTAGTGGGAATCAGCTATG 881
 DB 20 GTAGTGGGAATCAGCTATG 1
 RESULT 101
 AAQ29680
 ID AAQ29680 standard; DNA; 20 BP.
 XX AAQ29680;
 AC
 XX 25-MAR-2003 (revised)
 DT 15-MAR-1993 (first entry)
 XX
 DE hsp683 primer 912-931.
 XX
 XX Human; neurokinin-1 receptor; NK1R, membrane receptor; substance P;
 KW neurotransmitter; polymerase chain reaction; PCR; rat NK1R; primer;
 KW amplify; probe; ss.
 XX
 XX Homo sapiens.
 XX
 XX EP510878-A1.
 XX 28-OCT-1992.
 XX 16-APR-1992; 92EP-00303457.
 XX 25-APR-1991; 91US-00691197.
 XX 25-APR-1991; 91US-00691198.
 XX 25-APR-1991; 91US-00691200.
 XX (MERI) MERCK & CO INC.
 XX Fong TM, Strader CD;
 XX WPI; 1992-359073/44.
 XX New recombinant human neurokinin-1 receptor - used to detect and evaluate
 PT substances that bind to substance P receptor, and to determine substance
 PT P in body fluid of arthritis patients.
 XX Disclosure; Page 8; 35pp; English.
 XX The sequences given in AAQ29670-82, AAQ29783 and AAQ29746-48 are primers

CC which were used in the isolation of fragments of the human neurokinin-1
CC receptor (NK1R) cDNA. Human NK1R is a membrane receptor for the
CC neurotansmitter substance P. The primers were designed using regions of
CC the human NK1R cDNA and also regions of the rat NK1R which were thought
CC to be similar to human regions. Part of the human cDNA sequence was
CC derived by amplification using these primers. The remaining part of human
CC NK1R cDNA was obtained from a human cDNA library utilising portions of
CC PCR generated fragments as probes. See also AAQ29749. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 20 BP; 2 A; 9 C; 0 G; 9 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1000 TTCCACATCTTCTCTCTCT 1019
Db 1 TTCCACATCTTCTCTCTCT 20
XX
RESULT 102
AAQ29677/c
ID AAQ29677 standard; DNA; 20 BP.
XX
AC AAQ29677;
XX
DT 25-MAR-2003 (revised)
DT 15-MAR-1993 (first entry)
XX
DE hsp662 primer 943-924.
XX
KW Human; neurokinin-1 receptor; NK1R; membrane receptor; substance P;
KW neurotansmitter; polymerase chain reaction; PCR; rat NK1R; primer;
KW amplify; probe; ss.
OS Homo sapiens.
XX
PN EP510878-A1.
XX
PD 28-OCT-1992.
XX
PF 16-APR-1992; 92EP-00303457.
XX
PR 25-APR-1991; 91US-00691197.
PR 25-APR-1991; 91US-00691198.
PR 25-APR-1991; 91US-00691200.
XX
PA (MERI) MERCK & CO INC.
XX
PI Fong TM, Strader CD;
XX
DR WPI; 1992-359073/44.
XX
PT New recombinant human neurokinin-1 receptor - used to detect and evaluate
PT substances that bind to substance P receptor, and to determine substance
PT P in body fluid of arthritis patients.
XX
PS Disclosure; Page 8; 35pp; English.
XX
CC The sequences given in AAQ29670-82, AAQ29783 and AAQ29746-48 are primers
CC which were used in the isolation of fragments of the human neurokinin-1
CC receptor (NK1R) cDNA. Human NK1R is a membrane receptor for the
CC neurotansmitter substance P. The primers were designed using regions of
CC the human NK1R cDNA and also regions of the rat NK1R which were thought
CC to be similar to human regions. Part of the human cDNA sequence was
CC derived by amplification using these primers. The remaining part of human
CC NK1R cDNA was obtained from a human cDNA library utilising portions of
CC PCR generated fragments as probes. See also AAQ29749. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 20 BP; 6 A; 1 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1012 TTCTCTGCGCCATCATCAA 1031
Db 20 TTCTCTGCGCCATCATCAA 1
XX
RESULT 103
AAQ29681
ID AAQ29681 standard; DNA; 20 BP.
XX
AC AAQ29681;
XX
DT 25-MAR-2003 (revised)
DT 15-MAR-1993 (first entry)
XX
DE hsp664 primer 935-954.
XX
KW Human; neurokinin-1 receptor; NK1R; membrane receptor; substance P;
KW neurotansmitter; polymerase chain reaction; PCR; rat NK1R; primer;
KW amplify; probe; ss.
OS Homo sapiens.
XX
PN EP510878-A1.
XX
PD 28-OCT-1992.
XX
PF 16-APR-1992; 92EP-00303457.
XX
PR 25-APR-1991; 91US-00691197.
PR 25-APR-1991; 91US-00691198.
PR 25-APR-1991; 91US-00691200.
XX
PA (MERI) MERCK & CO INC.
XX
PI Fong TM, Strader CD;
XX
DR WPI; 1992-359073/44.
XX
PT New recombinant human neurokinin-1 receptor - used to detect and evaluate
PT substances that bind to substance P receptor, and to determine substance
PT P in body fluid of arthritis patients.
XX
PS Disclosure; Page 8; 35pp; English.
XX
CC The sequences given in AAQ29670-82, AAQ29783 and AAQ29746-48 are primers
CC which were used in the isolation of fragments of the human neurokinin-1
CC receptor (NK1R) cDNA. Human NK1R is a membrane receptor for the
CC neurotansmitter substance P. The primers were designed using regions of
CC the human NK1R cDNA and also regions of the rat NK1R which were thought
CC to be similar to human regions. Part of the human cDNA sequence was
CC derived by amplification using these primers. The remaining part of human
CC NK1R cDNA was obtained from a human cDNA library utilising portions of
CC PCR generated fragments as probes. See also AAQ29749. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 20 BP; 6 A; 8 C; 1 G; 5 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1023 CTACATCAACCCAGATCTCT 1042
Db 1 CTACATCAACCCAGATCTCT 20
XX
RESULT 104
AAQ29673/c
ID AAQ29673 standard; DNA; 20 BP.

```
XX AC AAQ29673;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 15-MAR-1993 (first entry)
XX DE hepr3a5 primer 568-549.
XX XX
XX XX Human; neurokinin-1 receptor; NK1R; membrane receptor; substance P;
XX KM neurotransmitter; polymerase chain reaction; PCR; rat NK1R; primer;
XX KM amplify; probe; ss.
XX OS
XX XX Homo sapiens.
XX PN EP510878-A1.
XX PD 28-OCT-1992.
XX PF 16-APR-1992; 92EP-00303457.
XX PR 25-APR-1991; 91US-00691197.
XX PR 25-APR-1991; 91US-00691198.
XX PR 25-APR-1991; 91US-00691200.
XX PA (MERI ) MERCK & CO INC.
XX PI Fong TM, Strader CD;
XX DR WPI, 1992-359073/44.
XX PT New recombinant human neurokinin-1 receptor - used to detect and evaluate
XX PT substances that bind to substance P receptor, and to determine substance
XX PT P in body fluid of arthritis patients.
XX PS Disclosure; Page 8; 35pp; English.
XX XX
XX CC The sequences given in AAQ29670-82, AAQ29783 and AAQ29746-48 are primers
XX CC which were used in the isolation of fragments of the human neurokinin-1
XX CC receptor (NK1R) cDNA. Human NK1R is a membrane receptor for the
XX CC neurotransmitter substance P. The primers were designed using regions of
XX CC the human NK1R cDNA and also regions of the rat NK1R which were thought
XX CC to be similar to human regions. Part of the human cDNA sequence was
XX CC derived by amplification using these primers. The remaining part of human
XX CC NK1R cDNA was obtained from a human cDNA library utilising portions of
XX CC PCR generated fragments as probes. See also AAQ29749. (Updated on 25-MAR-
XX CC 2003 to correct PN field.)
XX SQ Sequence 20 BP; 2 A; 3 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 637 TCAGCCACAGCCACCAAGT 656
DB 20 TCAGCCACAGCCACCAAGT 1

RESULT 105
AAZ92287
ID AAZ92287 standard; DNA; 20 BP.
XX
XX AC AAZ92287;
XX DT 05-JUN-2000 (first entry)
XX DE Allele specific primer for NK1R exon 1 polymorphism detection.
XX KM Neurokinin 1 receptor; NK1R; human; single nucleotide polymorphism; SNP;
XX KM diagnosis; treatment; asthma; depression; urinary incontinence;
XX KM inflammatory bowel disease; primer; ss.
XX OS Homo sapiens.
```

```
XX XX WO200006768-A1.
XX XX
XX PD 10-FEB-2000.
XX PF 20-JUL-1999; 99WO-GB002340.
XX PR 25-JUL-1998; 98GB-00016192.
XX PR 22-AUG-1998; 98GB-00018280.
XX PA (ZENEC ) ZENECA LTD.
XX PI Smith JC, Anand R, Morten JEN;
XX DR WPI, 2000-183135/16.
XX PT Novel polymorphisms in the human neurokinin 1 receptor gene used for
XX PT diagnosis and treatment of NK1R ligand mediated diseases such as asthma.
XX PS Disclosure; Page 10; 43pp; English.
XX XX
XX CC This sequence represents an allele specific primer used to detect the
XX CC 2361 'T' polymorphism in exon 1 of the human neurokinin 1 receptor gene
XX CC (see AAZ92286). The invention relates to single nucleotide polymorphisms
XX CC (SNPs) in human neurokinin 1 receptor (NK1R). Detection of these
XX CC polymorphisms is useful for the diagnosis and treatment of NK1R ligand
XX CC mediated diseases. A method for the diagnosis of one or more SNPs in the
XX CC NK1R gene in a human, comprises determining the sequence of the nucleic
XX CC acid at one or more of the polymorphic positions. Diagnostic primers can
XX CC be used to detect the presence of the polymorphisms. The methods of the
XX CC invention are used to identify SNPs in the human neurokinin 1 receptor
XX CC (NK1R) gene. The presence or absence of these polymorphisms can be used
XX CC in the diagnosis and treatment of NK1R-ligand mediated diseases, such as
XX CC asthma and depression. A NK1R ligand antagonist drug can also be used to
XX CC treat pain, migraine, anxiety, depression, urinary incontinence, and
XX CC inflammatory bowel disease. The methods may also be used for the
XX CC development of new drug therapies which selectively target one or more
XX CC allelic variants of the NK1R gene
XX SQ Sequence 20 BP; 5 A; 6 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 524 GCAAGTTCACACACTCTTT 543
DB 1 GCAAGTTCACACACTCTTT 20

RESULT 106
ABS60995
ID ABS60995 standard; DNA; 20 BP.
XX
XX AC ABS60995;
XX DT 05-NOV-2002 (first entry)
XX DE Human genotyping PCR primer #148.
XX KM Human; ss; aminopeptidase P; XPNP2; bradykinin receptor B1; primer;
XX KM BDKRB1; tachykinin receptor B1; TACR1; cI esterase inhibitor; CINH;
XX KM kallikrein 1; KLK1; bradykinin receptor B2; BDKRB2; gene therapy;
XX KM angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;
XX KM polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
XX KM cardiovascular disease; angina pectoris; hypertension; heart failure;
XX KM myocardial infarction; ventricular hypertrophy; vascular disease; angioedema;
XX KM aneurysm; embolism; thrombosis; coronary artery disease; sepsis; PCR;
XX KM atherosclerosis; hypercholesterols; hyperreactivity; sepsis; PCR;
XX KM autoimmune disease; inflammatory arthritis; cancer; wound; genotyping;
XX KM viral infection; bacterial infection; fungal infection; COPD;
XX KM Chronic obstructive pulmonary disease; enterocolitis.
```


OS Homo sapiens.
XX
XX MO200261131-A2.
XX
XX 08-AUG-2002.
XX
XX 03-DEC-2001; 2001WO-US047235.
XX
XX 04-DEC-2000; 2000US-0251015P.
XX 23-JAN-2001; 2001US-0263678P.
XX 02-MAR-2001; 2001US-0273037P.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX (TSUC/) TSUCHIHASHI Z.
XX (HUI/L/) HUI L.
XX Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH,
XX Swanson BN, Powell JR;
XX WPI; 2002-619265/66.
XX
XX New isolated nucleic acid with at least one polymorphic position, useful
XX for detecting, diagnosing and treating disorders such as angioedema,
XX cancer, viral, bacterial or fungal infection, cardiovascular and
XX autoimmune diseases.
XX
XX Example 3; Page 912; 977pp; English.
XX
XX The invention relates to an isolated nucleic acid from a human gene
XX encoding aminopeptidase P (XPNEP2), bradykinin receptor B1 (BDKRB1),
XX tachykinin receptor B1 (TACR1), Cl esterase inhibitor (C1NH), kallikrein
XX 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme
XX 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one
XX polymorphic position. Also included are (1) a probe that hybridises to a
XX nucleotide polymorphism comprising additional 5' and 3' flanking genomic
XX sequence; (2) analysing (M1) at least one nucleic acid sample comprising
XX obtaining the sample from one or more individuals and determining the
XX nucleic acid sequence at one or more polymorphic positions in a gene
XX encoding a protein selected from the group above; (3) constructing (M2)
XX haplotypes using the genes comprising grouping at least two nucleic acids
XX (4) identifying (M3) an individual at risk of developing a disorder
XX upon administration of an ACE inhibitor and/or vasopressinase inhibitor
XX using the polymorphic data; (5) a library of nucleic acids, each of which
XX comprises one or more polymorphic positions within a gene encoding a
XX human protein selected from the group above; and (6) genotyping (M4) an
XX individual comprising obtaining a nucleic acid sample, determining the
XX nucleotide present in at least one polymorphic position, and comparing at
XX least one position with a known data set. The genes, (M1, M2, M3 and M4)
XX and compositions are useful for detecting, diagnosing, treating,
XX preventing various disorders such as angioedema and diseases which
XX involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's
XX disease, trachomas, and cardiovascular diseases like angina pectoris,
XX hypertension, heart failure, myocardial infarction, ventricular
XX hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
XX artery disease, arteriosclerosis and/or atherosclerosis, and
XX hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory
XX arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic
XX obstructive pulmonary disease (COPD) and enterocolitis (many other
XX diseases and disorders are listed in the specification). The
XX polynucleotides are also useful for chromosome identification. Antibodies
XX against the proteins may be utilised for immunophenotyping of cell lines
XX and biological samples. The present sequence is a genotyping PCR primer
XX for the gene encoding one of the proteins listed above
XX
XX Sequence 20 BP; 5 A; 10 C; 1 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 47;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

609 CATCATATCCCTCCAGC 628
|||||

Db 1 CATCATATCCCTCCAGC 20
RESULT 107
ABS60996
ID ABS60996 standard; DNA; 20 BP.
XX
XX AC ABS60996;
XX
XX 05-NOV-2002 (first entry)
XX
XX Human genotyping PCR primer #149.
XX
XX Human; ser; aminopeptidase P; XPNEP2, bradykinin receptor B1; primer;
XX BDKRB1, tachykinin receptor B1; TACR1; Cl esterase inhibitor; C1NH;
XX kallikrein 1; KLK1; bradykinin receptor B2; BDKRB2; gene therapy;
XX angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;
XX polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
XX cardiovascular disease; angina pectoris; hypertension; heart failure;
XX myocardial infarction; ventricular hypertrophy; vascular disease;
XX aneurysm; embolism; thrombosis; coronary artery disease; angioedema;
XX arteriosclerosis; atherosclerosis; hypersensitivity; sepsis; PCR;
XX autoimmune disease; inflammatory arthritis; cancer; wound; genotyping;
XX viral infection; bacterial infection; fungal infection; COPD;
XX Chronic obstructive pulmonary disease; enterocolitis.
XX
XX OS Homo sapiens.
XX
XX MO200261131-A2.
XX
XX 08-AUG-2002.
XX
XX 03-DEC-2001; 2001WO-US047235.
XX
XX 04-DEC-2000; 2000US-0251015P.
XX 23-JAN-2001; 2001US-0263678P.
XX 02-MAR-2001; 2001US-0273037P.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX (TSUC/) TSUCHIHASHI Z.
XX (HUI/L/) HUI L.
XX Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH,
XX Swanson BN, Powell JR;
XX WPI; 2002-619265/66.
XX
XX New isolated nucleic acid with at least one polymorphic position, useful
XX for detecting, diagnosing and treating disorders such as angioedema,
XX cancer, viral, bacterial or fungal infection, cardiovascular and
XX autoimmune diseases.
XX
XX Example 3; Page 912; 977pp; English.
XX
XX The invention relates to an isolated nucleic acid from a human gene
XX encoding aminopeptidase P (XPNEP2), bradykinin receptor B1 (BDKRB1),
XX tachykinin receptor B1 (TACR1), Cl esterase inhibitor (C1NH), kallikrein
XX 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme
XX 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one
XX polymorphic position. Also included are (1) a probe that hybridises to a
XX nucleotide polymorphism comprising additional 5' and 3' flanking genomic
XX sequence; (2) analysing (M1) at least one nucleic acid sample comprising
XX obtaining the sample from one or more individuals and determining the
XX nucleic acid sequence at one or more polymorphic positions in a gene
XX encoding a protein selected from the group above; (3) constructing (M2)
XX haplotypes using the genes comprising grouping at least two nucleic acids
XX (4) identifying (M3) an individual at risk of developing a disorder
XX upon administration of an ACE inhibitor and/or vasopressinase inhibitor
XX using the polymorphic data; (5) a library of nucleic acids, each of which
XX comprises one or more polymorphic positions within a gene encoding a
XX human protein selected from the group above; and (6) genotyping (M4) an
XX individual comprising obtaining a nucleic acid sample, determining the

CC nucleotide present in at least one polymorphic position, and comparing at
CC last one position with a known data set. The genes, (M1, M2, M3 and M4)
CC and compositions are useful for detecting, diagnosing, treating,
CC preventing various disorders such as angioedema and diseases which
CC involve angioedema like haemangiomas, tumours, sarcomas, Cronin's
CC disease, trichomas, and cardiovascular diseases like angina pectoris,
CC hypertension, heart failure, myocardial infarction, ventricular
CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
CC artery disease, arteriosclerosis and/or atherosclerosis, and
CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory
CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic
CC obstructive pulmonary disease (COPD) and enterocolitis (many other
CC diseases and disorders are listed in the specification). The
CC polynucleotides are also useful for chromosome identification. Antibodies
CC against the proteins may be utilised for immunophotyping of cell lines
CC and biological samples. The present sequence is a genotyping PCR primer
CC for the gene encoding one of the proteins listed above
XX
XX Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

Query Match	1.1%;	Score 20;	DB 1;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 47;		
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

```
OY      915 CTACCACGAGCAAGTCTCTG 934  
         |||||  
Db       1 CTACCACGAGCAAGTCTCTG 20
```

RESULT 108
ABK63858/c
ID ABK63858 standard; DNA; 20 BP.

AC ABK63858;

DT 18-JUN-2002 (first entry)

Neurokinin 1 receptor (NK-1) sense oligonucleotide #9.

KM Human, neurokinin receptor-1; NK-1; dermatological disorder;
KM immune disorder; autoimmune disorder; cardiovascular disorder;
KM vaccine disorder; airway disorder; neuropathic disorder; pain;
KM psychiatric disorder; central nervous system disorder; inflammation;
KM respiratory condition; ophthalmic condition; intestinal condition;
KM deforming disease; small cell lung cancer; depression;
KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
KM hypergenerative disorder; acquired immune deficiency syndrome; AIDS;
KM neuro-pathological disorder; stress; antinease; pimezi ss.

OS Homo sapiens.

PN WO200213799-A2.

PD 21-FEB-2002.

PF 17-AUG-2001; 2001WO-IB001510.

PR 18-AUG-2000; 2000US-0226086P.

PA (UYMC-) UNIV MCGILL.

PI Henry JL, Cahill CM, Yashpal K;

DR WPI: 2002-241835/29.

PT Treating pathological condition involving neurokinin receptor-1, e.g.

PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic

PT pathway.

PS Claim 24; Page 20; 100pp; English

The invention relates to a method of treating a pathological condition

characterised partially by involvement of neurokinin receptor-1 (NK-1) receptor, especially treating, attenuating or preventing pain or inflammatory condition. The method comprises administering to a mammal, a compound chosen from an oligonucleotide, its analogue, and a disruptor which interferes with function or production of NK-1 receptors. The method is useful for treating a pathological condition characterised by involvement of NK-1 receptor such as dermatological, immune, autoimmune, cardiovascular, vascular disorders (e.g. migraines), allergy, neuropathic, psychiatric and central nervous system disorders (e.g. anxiety, psychosis, schizophrenia), gut inflammation, arthritis, and for treating, attenuating or preventing pain or inflammation such as peripheral, peripheral aspects of chronic or acute pain, and for treating, attenuating or preventing pain or inflammation such as peripheral, chronic, acute pain or inflammation, neuropathic pain, inflammation or pain relating to psychiatric disorders and central nervous system disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia in a mammal, in particular human, NK-1 receptor related disorders, diseases, or pathological conditions treatable by this method include respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic conditions (e.g. conjunctivitis), cutaneous/dermatological conditions (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and Crohn's disease), cardiovascular conditions (stroke), chronic gastrointestinal tract inflammation, and inflammatory diseases such as inflammatory bowel diseases. Other disorders and diseases include cardiovascular pathologies including stroke, chronic inflammatory diseases such as rheumatoid arthritis, demyelinating diseases such as multiple sclerosis, small cell lung cancer, depression, hypersensitivity disorders such as allergies and poison ivy, vasospastic diseases such as angina, addiction disorders such as alcoholism, neurodegenerative disorders such as acquired immune deficiency syndrome (AIDS) related dementia, epilepsy, Alzheimer's disease, and other neuro-pathological disorders, such as peripheral neuropathy, oedema, stress related and somatic disorders, and osteoarthritis. Antisense oligonucleotides effectively treat chronic conditions and other pathological states without the co-administration of substance P, and reduce the number of activated receptors while not reducing the number of quiescent NK-1 receptors. Receptors not chronically stimulated are less affected, reducing side effects of treatment. ABK6384-ABK63906 represent NK-1 receptor coding sequences and oligonucleotides of the invention

Sequence 20 BP; 5 A; 2 C; 7 G; 6 T; 0 U; 0 Other;

Query Match	1.1%;	Score 20;	DB 1;	Length 20;
Best Local Similarity	100.0%;	Pred. Nc.	47	
Matches 20; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

	601	TACATGGCCATCATCATCC	620
QY			
Dd	20	TACATGGCCATCATCATCC	1

RESULT

ABK63876 standard; DNA; 20 BP.

AC ABK63876

18-JUN-2002 (first entry)

Neurokinin 1 receptor (NK-1) antisense oligonucleotide #21.

XX Human; neurokinin receptor-1, NK-1, dermatological disorder;
XX immune disorder; autoimmune disorder; cardiovascular disorder;
KW vascular disorder; airway disorder; neuropathic disorder; pain;
KW psychiatric disorder; central nervous system disorder; inflammation;
KW respiratory condition; ophthalmic condition; intestinal condition;
KW demyelinating disease; small cell lung cancer; depression;
KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
KW neuro-rheological disorder; stress; antisense; primer; ss.

OS Homo sapiens.

PN WO200213799-A2

XX 21-FEB-2002.
PD
XX 17-AUG-2001; 2001WO-IB001510.
PF
XX 18-AUG-2000; 2000US-0226086P.
PR
XX (UYMC-) UNIV MCGILL.
PA
XX Henry JL, Cahill CM, Yashpal K;
PI
XX WPI; 2002-241835/29.
DR
XX
PT Treating pathological condition involving neurokinin receptor-1, e.g.
PT pain or inflammation, by administering oligonucleotide or a non-
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
PT pathway.
XX
XX
PS Claim 24; Page 65; 100pp; English.
XX
XX The invention relates to a method of treating a pathological condition
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)
CC receptor, especially treating, attenuating or preventing pain or
CC inflammatory condition. The method comprises administering to a mammal, a
CC compound chosen from an oligonucleotide, its analogue, and a disruptor
CC which interferes with function or production of NK-1 receptors. The
CC method is useful for treating a pathological condition characterised by
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,
CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,
CC psychiatric and central nervous system disorders (e.g. anxiety,
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or
CC peripheral aspects of chronic or acute pain, and for treating,
CC attenuating or preventing pain or inflammation such as peripheral,
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or
CC pain relating to psychiatric disorders and central nervous system
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
CC in a mammal, in particular human. NK-1 receptor related disorders,
CC diseases, or pathological conditions treatable by this method include
CC respiratory conditions (e.g. asthma, allergic rhinitis), opthalmic
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and
CC gastrointestinal tract inflammation, and inflammatory diseases such as
CC inflammatory bowel diseases. Other disorders and diseases include
CC cardiovascular pathologies including stroke, chronic inflammatory
CC diseases such as rheumatoid arthritis, demyelinating diseases such as
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
CC disorders such as allergies and poison ivy, vasospastic diseases such as
CC angina, addiction disorders such as alcoholism, neurodegenerative
CC disorders such as acquired immune deficiency syndrome (AIDS) related
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
CC disorders such as peripheral neuropathy, oedema, stress related and
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
CC effectively treat chronic conditions and other pathological states
CC without the co-administration of substance P, and reduce the number of
CC activated receptors while not reducing the number of quiescent NK-1
CC receptors. Receptors not chronically stimulated are less affected,
CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1
CC receptor coding sequences and oligonucleotides of the invention
XX
SQ Sequence 20 BP; 7 A; 8 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ID ABK63857 standard; DNA; 20 BP.
XX
XX AC ABK63857;
XX
XX 18-JUN-2002 (first entry)
DT
XX
XX
DE Neurokinin 1 receptor (NK-1) sense oligonucleotide #8.
XX
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;
XX immune disorder; autoimmune disorder; cardiovascular disorder;
XX vascular disorder; airway disorder; neuropathic disorder; pain;
XX psychiatric disorder; central nervous system disorder; inflammation;
XX respiratory condition; opthalmic condition; intestinal condition;
XX demyelinating disease; small cell lung cancer; depression;
XX hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
XX neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
XX neuro-pathological disorder; stress; antisense; primer; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200213799-A2.
PN
XX
XX 21-FEB-2002.
PD
XX
XX 17-AUG-2001; 2001WO-IB001510.
PF
XX
XX 18-AUG-2000; 2000US-0226086P.
PR
XX
XX (UYMC-) UNIV MCGILL.
PA
XX
PI Henry JL, Cahill CM, Yashpal K;
XX
XX WPI; 2002-241835/29.
DR
XX
XX Treating pathological condition involving neurokinin receptor-1, e.g.
PT pain or inflammation, by administering oligonucleotide or a non-
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
PT pathway.
XX
XX
PS Claim 24; Page 20; 100pp; English.
XX
XX The invention relates to a method of treating a pathological condition
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)
CC receptor, especially treating, attenuating or preventing pain or
CC inflammatory condition. The method comprises administering to a mammal, a
CC compound chosen from an oligonucleotide, its analogue, and a disruptor
CC which interferes with function or production of NK-1 receptors. The
CC method is useful for treating a pathological condition characterised by
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,
CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,
CC psychiatric and central nervous system disorders (e.g. anxiety,
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or
CC peripheral aspects of chronic or acute pain, and for treating,
CC attenuating or preventing pain or inflammation such as peripheral,
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or
CC pain relating to psychiatric disorders and central nervous system
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
CC in a mammal, in particular human. NK-1 receptor related disorders,
CC diseases, or pathological conditions treatable by this method include
CC respiratory conditions (e.g. asthma, allergic rhinitis), opthalmic
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and
CC gastrointestinal tract inflammation, and inflammatory diseases such as
CC inflammatory bowel diseases. Other disorders and diseases include
CC cardiovascular pathologies including stroke, chronic inflammatory
CC diseases such as rheumatoid arthritis, demyelinating diseases such as
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
CC disorders such as allergies and poison ivy, vasospastic diseases such as
CC angina, addiction disorders such as alcoholism, neurodegenerative
CC disorders such as acquired immune deficiency syndrome (AIDS) related
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
CC disorders such as peripheral neuropathy, oedema, stress related and

CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
 CC effectively treat chronic conditions and other pathological states
 CC without the co-administration of substance P, and reduce the number of
 CC activated receptors while not reducing the number of quiescent NK-1
 CC receptors. Receptors not chronically stimulated are less affected.
 CC reducing side effects of treatment. ABRK3834-ABK63906 represent NK-1
 CC receptor coding sequences and oligonucleotides of the invention
 CC
 XX Sequence 20 BP; 2 A; 3 C; 8 G; 7 T; 0 U; 0 Other;
 QQ
 Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 637 TCAGCCACAGCCACCAAGT 656
 Db 20 TCAGCCACAGCCACCAAGT 1
 RESULT 111
 ABRK63893
 ID ABRK63893 standard; DNA; 20 BP.
 XX
 AC ABRK63893;
 XX
 DT 18-JUN-2002 (first entry)
 DE
 XX Neurokinin 1 receptor (NK-1) antisense oligonucleotide #38.
 XX
 KW Human; neurokinin receptor-1; NK-1; dermatological disorder;
 KW immune disorder; autoimmune disorder; cardiovascular disorder;
 KW vascular disorder; airway disorder; neuropathic disorder; pain;
 KW psychiatric disorder; central nervous system disorder; inflammation;
 KW respiratory condition; ophthalmic condition; intestinal condition;
 KW demyelinating disease; small cell lung cancer; depression;
 KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
 KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
 KW neuro-pathological disorder; stress; antisense; primer; ss.
 KM
 OS Homo sapiens.
 XX
 PN WO200213799-A2.
 XX
 PD 21-FEB-2002.
 XX
 PF 17-AUG-2001; 2001WO-IB001510.
 XX
 PR 18-AUG-2000; 2000US-0226086P.
 XX
 PA (UNWC-) UNIV MCGILL.
 XX
 PI Henry JL, Cahill CM, Yashpal K;
 XX
 DR WPI; 2002-241835/29.
 XX
 PT Treating pathological condition involving neurokinin receptor-1, e.g.
 PT pain or inflammation, by administering oligonucleotide or a non-
 PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
 PT pathway.
 XX
 PS Example 18; Page 65; 100pp; English.
 XX
 CC The invention relates to a method of treating a pathological condition
 CC characterised partially by involvement of neurokinin receptor-1 (NK-1)
 CC receptor, especially treating, attenuating or preventing pain or
 CC inflammatory condition. The method comprises administering to a mammal, a
 CC compound chosen from an oligonucleotide, its analogue, and a disruptor
 CC which interferes with function or production of NK-1 receptors. The
 CC method is useful for treating a pathological condition characterised by
 CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,
 CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,
 CC psychiatric and central nervous system disorders (e.g. anxiety,
 CC psychosis, schizophrenia), gut inflammation, arthritis, and central or

CC peripheral aspects of chronic or acute pain, and for treating,
 CC attenuating or preventing pain or inflammation such as peripheral,
 CC chronic, acute pain or inflammation, neuropathic pain, inflammation or
 CC pain relating to psychiatric disorders and central nervous system
 CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
 CC in a mammal, in particular human. NK-1 receptor related disorders,
 CC diseases, or pathological conditions treatable by this method include
 CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
 CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
 CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and
 CC Crohn's disease), cardiovascular conditions (stroke), chronic
 CC gastrointestinal tract inflammation, and inflammatory diseases such as
 CC inflammatory bowel diseases. Other disorders and diseases include
 CC cardiovascular pathologies including stroke, chronic inflammatory
 CC diseases such as rheumatoid arthritis, demyelinating diseases such as
 CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
 CC disorders such as allergies and poison ivy, vasospastic diseases such as
 CC angina, addiction disorders such as alcoholism, neurodegenerative
 CC disorders such as acquired immune deficiency syndrome (AIDS) related
 CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
 CC disorders, such as peripheral neuropathy, edema, stress related and
 CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
 CC effectively treat chronic conditions and other pathological states
 CC without the co-administration of substance P, and reduce the number of
 CC activated receptors while not reducing the number of quiescent NK-1
 CC receptors. Receptors not chronically stimulated are less affected,
 CC reducing side effects of treatment. ABRK3834-ABK63906 represent NK-1
 CC receptor coding sequences and oligonucleotides of the invention
 CC
 XX Sequence 20 BP; 6 A; 3 C; 6 G; 5 T; 0 U; 0 Other;
 QQ
 Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 862 GTAGTGGGAATTCACACTATG 881
 Db 1 GTAGTGGGAATTCACACTATG 20
 RESULT 112
 ABRK63895
 ID ABRK63895 standard; DNA; 20 BP.
 XX
 AC ABRK63895;
 XX
 DT 18-JUN-2002 (first entry)
 DE
 XX Neurokinin 1 receptor (NK-1) antisense oligonucleotide #40.
 XX
 KW Human; neurokinin receptor-1; NK-1; dermatological disorder;
 KW immune disorder; autoimmune disorder; cardiovascular disorder;
 KW vascular disorder; airway disorder; neuropathic disorder; pain;
 KW psychiatric disorder; central nervous system disorder; inflammation;
 KW respiratory condition; ophthalmic condition; intestinal condition;
 KW demyelinating disease; small cell lung cancer; depression;
 KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
 KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
 KW neuro-pathological disorder; stress; antisense; primer; ss.
 KM
 OS Homo sapiens.
 XX
 PN WO200213799-A2.
 XX
 PD 21-FEB-2002.
 XX
 PF 17-AUG-2001; 2001WO-IB001510.
 XX
 PR 18-AUG-2000; 2000US-0226086P.
 XX
 PA (UNWC-) UNIV MCGILL.
 XX
 PI Henry JL, Cahill CM, Yashpal K;

XX WPI; 2002-241835/29.
DR
XX
XX Treating pathological condition involving neurokinin receptor-1, e.g.
PT pain or inflammation, by administering oligonucleotide or a non-
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
PT pathway.
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XX Example 18; Page 65; 100pp; English.
XX
XX The invention relates to a method of treating a pathological condition
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)
CC receptor, especially treating, attenuating or preventing pain or
CC inflammatory condition. The method comprises administering to a mammal, a
CC compound chosen from an oligonucleotide, its analogue, and a disruptor
CC which interferes with function or production of NK-1 receptors. The
CC method is useful for treating a pathological condition characterised by
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,
CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,
CC psychiatric and central nervous system disorders (e.g. anxiety,
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or
CC peripheral aspects of chronic or acute pain, and for treating,
CC attenuating or preventing pain or inflammation such as peripheral,
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or
CC pain relating to psychiatric disorders and central nervous system
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
CC in a mammal, in particular human. NK-1 receptor related disorders,
CC diseases, or pathological conditions treatable by this method include
CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and
CC Crohn's disease), cardiovascular conditions (stroke), chronic
CC gastrointestinal tract inflammation, and inflammatory diseases such as
CC cardiovascular pathologies including stroke, chronic inflammatory
CC diseases such as rheumatoid arthritis, demyelinating diseases such as
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
CC disorders such as allergies and poison ivy, vasospastic diseases such as
CC angina, addiction disorders such as alcoholism, neurodegenerative
CC disorders such as acquired immune deficiency syndrome (AIDS) related
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
CC disorders such as peripheral neuropathy, oedema, stress related and
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
CC effectively treat chronic conditions and other pathological states
CC without the co-administration of substance P, and reduce the number of
CC activated receptors while not reducing the number of quiescent NK-1
CC receptors. Receptors not chronically stimulated are less affected,
CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1
CC receptor coding sequences and oligonucleotides of the invention
XX
XX Sequence 20 BP; 7 A; 8 C; 3 G; 2 T; 0 U; 0 Other;
SQ
Query March 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 637 TCAGCCACAGCCACCAAGT 656
Db 1 TCAGCCACAGCCACCAAGT 20
RESULT 113
ABK63869/c
ID ABK63869 standard; DNA; 20 BP.
XX
XX ABK63869;
AC
XX 18-JUN-2002 (first entry)
DT
XX Neurokinin 1 receptor (NK-1) antisense oligonucleotide #14.
DE
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;
XX immune disorder; autoimmune disorder; cardiovascular disorder;
KM

KM vascular disorder; airway disorder; neuropathic disorder; pain;
KM psychiatric disorder; central nervous system disorder; inflammation;
KM respiratory condition; ophthalmic condition; intestinal condition;
KM demyelinating disease; small cell lung cancer; depression;
KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
KM neuro-pathological disorder; stress; antisense; primer; ss.
XX
XX Homo sapiens.
OS
XX
XX MO200213799-A2.
PN
XX 21-FEB-2002.
PD
XX 17-AUG-2001; 2001WO-IB001510.
PF
XX 18-AUG-2000; 2000US-0226086P.
PR
XX (UVMC-) UNIV MCGILL.
PA
XX Henry JL, Cahill CM, Yashpal K;
PI WPI; 2002-241835/29.
XX
XX
XX Treating pathological condition involving neurokinin receptor-1, e.g.
PT pain or inflammation, by administering oligonucleotide or a non-
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
PT pathway.
XX
XX Claim 24; Page 65; 100pp; English.
PS
XX The invention relates to a method of treating a pathological condition
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)
CC receptor, especially treating, attenuating or preventing pain or
CC inflammatory condition. The method comprises administering to a mammal, a
CC compound chosen from an oligonucleotide, its analogue, and a disruptor
CC which interferes with function or production of NK-1 receptors. The
CC method is useful for treating a pathological condition characterised by
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,
CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,
CC psychiatric and central nervous system disorders (e.g. anxiety,
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or
CC peripheral aspects of chronic or acute pain, and for treating,
CC attenuating or preventing pain or inflammation such as peripheral,
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or
CC pain relating to psychiatric disorders and central nervous system
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CC in a mammal, in particular human. NK-1 receptor related disorders,
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CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and
CC Crohn's disease), cardiovascular conditions (stroke), chronic
CC gastrointestinal tract inflammation, and inflammatory diseases such as
CC inflammatory bowel diseases. Other disorders and diseases include
CC cardiovascular pathologies including stroke, chronic inflammatory
CC diseases such as rheumatoid arthritis, demyelinating diseases such as
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
CC disorders such as allergies and poison ivy, vasospastic diseases such as
CC angina, addiction disorders such as alcoholism, neurodegenerative
CC disorders such as acquired immune deficiency syndrome (AIDS) related
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
CC disorders such as peripheral neuropathy, oedema, stress related and
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
CC effectively treat chronic conditions and other pathological states
CC without the co-administration of substance P, and reduce the number of
CC activated receptors while not reducing the number of quiescent NK-1
CC receptors. Receptors not chronically stimulated are less affected,
CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1
CC receptor coding sequences and oligonucleotides of the invention
XX
XX Sequence 20 BP; 9 A; 0 C; 9 G; 2 T; 0 U; 0 Other;
SQ

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1000 TTCACATCTTCTCTCCT 1019
Db 20 TTCACATCTTCTCTCCT 1
RESULT 114
ID ABR63877
XX ABR63877 standard; DNA; 20 BP.
AC ABR63877;
XX
DT 18-JUN-2002 (first entry)
XX
DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #22.
XX
KW Human; neurokinin receptor-1; NK-1; dermatological disorder;
KW immune disorder; autoimmune disorder; cardiovascular disorder;
KW vascular disorder; airway disorder; neuropathic disorder; pain;
KW psychiatric disorder; central nervous system disorder; inflammation;
KW respiratory condition; ophthalmic condition; intestinal condition;
KW demyelinating disease; small cell lung cancer; depression;
KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
KW neuro-pathological disorder; stress; antisense; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200213799-A2.
XX
PD 21-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-IB001510.
XX
PR 18-AUG-2000; 2000US-0226086P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Henry JL, Cahill CM, Yashpal K;
XX
DR WPI; 2002-241835/29.
XX
PT Treating pathological condition involving neurokinin receptor-1, e.g.
PT pain or inflammation, by administering oligonucleotide or a non-
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
PT pathway.
XX
PS Claim 24; Page 65; 100pp; English.
XX
XX The invention relates to a method of treating a pathological condition
XX characterised partially by involvement of neurokinin receptor-1 (NK-1)
XX receptor, especially treating, attenuating or preventing pain or
XX inflammatory condition. The method comprises administering to a mammal, a
XX compound chosen from an oligonucleotide, its analogue, and a disruptor
XX which interferes with function or production of NK-1 receptors. The
XX method is useful for treating a pathological condition characterised by
XX involvement of NK-1 receptor such as dermatological, immune, autoimmune,
XX cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,
XX psychiatric and central nervous system disorders (e.g. anxiety,
XX psychosis, schizophrenia), gut inflammation, arthritis and central or
XX peripheral aspects of chronic or acute pain, and for treating,
XX attenuating or preventing pain or inflammation such as peripheral,
XX chronic, acute pain or inflammation, neuropathic pain, inflammation or
XX pain relating to psychiatric disorders and central nervous system
XX disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
XX in a mammal, in particular human. NK-1 receptor related disorders,
XX diseases, or pathological conditions treatable by this method include
XX respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
XX conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
XX (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and

CC Crohn's disease), cardiovascular conditions (stroke), chronic
CC gastrointestinal tract inflammation, and inflammatory diseases such as
CC inflammatory bowel diseases. Other disorders and diseases include
CC cardiovascular pathologies including stroke, chronic inflammatory
CC diseases such as rheumatoid arthritis, demyelinating diseases such as
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
CC disorders such as allergies and poison ivy, vasospastic diseases such as
CC angina, addiction disorders such as alcoholism, neurodegenerative
CC disorders such as acquired immune deficiency syndrome (AIDS) related
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
CC disorders such as peripheral neuropathy, oedema, stress related and
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
CC effectively treat chronic conditions and other pathological states
CC without the co-administration of substance P, and reduce the number of
CC activated receptors while not chronically stimulating are less affected,
CC reducing side effects of treatment. ABR63834-ABR63906 represent NK-1
CC receptor coding sequences and oligonucleotides of the invention
XX
SQ Sequence 20 BP; 6 A; 7 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 601 TACATGGCCATCATCATCC 620
Db 1 TACATGGCCATCATCATCC 20

RESULT 115
ID ABR63891
XX ABR63891 standard; DNA; 20 BP.
AC ABR63891;
XX
DT 18-JUN-2002 (first entry)
XX
DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #36.
XX
KW Human; neurokinin receptor-1; NK-1; dermatological disorder;
KW immune disorder; autoimmune disorder; cardiovascular disorder;
KW vascular disorder; airway disorder; neuropathic disorder; pain;
KW psychiatric disorder; central nervous system disorder; inflammation;
KW respiratory condition; ophthalmic condition; intestinal condition;
KW demyelinating disease; small cell lung cancer; depression;
KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
KW neuro-pathological disorder; stress; antisense; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200213799-A2.
XX
PD 21-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-IB001510.
XX
PR 18-AUG-2000; 2000US-0226086P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Henry JL, Cahill CM, Yashpal K;
XX
DR WPI; 2002-241835/29.
XX
PT Treating pathological condition involving neurokinin receptor-1, e.g.
PT pain or inflammation, by administering oligonucleotide or a non-
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
PT pathway.
XX
PS Example 18; Page 65; 100pp; English.
XX

CC The invention relates to a method of treating a pathological condition
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)
CC receptor, especially treating, attenuating or preventing pain or
CC inflammatory condition. The method comprises administering to a mammal, a
CC compound chosen from an oligonucleotide, its analogue, and a disruptor
CC which interferes with function or production of NK-1 receptors. The
CC method is useful for treating a pathological condition characterised by
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,
CC cardiovascular, vascular disorders (e.g. migraine), allergy, neuropathic,
CC psychiatric and central nervous system disorders (e.g. anxiety,
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or
CC peripheral aspects of chronic or acute pain, and for treating,
CC attenuating or preventing pain or inflammation such as peripheral,
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or
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CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and
CC Crohn's disease), cardiovascular conditions (stroke), chronic
CC gastrointestinal tract inflammation, and inflammatory diseases such as
CC inflammatory bowel diseases. Other disorders and diseases include
CC cardiovascular pathologies including stroke, chronic inflammatory
CC diseases such as rheumatoid arthritis, demyelinating diseases such as
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
CC disorders such as allergies and poison ivy, vasospastic diseases such as
CC angina, addiction disorders such as alcoholism, neurodegenerative
CC disorders such as acquired immune deficiency syndrome (AIDS) related
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
CC disorders such as peripheral neuropathy, oedema, stress related and
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
CC effectively treat chronic conditions and other pathological states
CC without the co-administration of substance P, and reduce the number of
CC activated receptors while not reducing the number of quiescent NK-1
CC receptors. Receptors not chronically stimulated are less affected,
CC reducing side effects of treatment. ABR63834-ABR63906 represent NK-1
CC receptor coding sequences and oligonucleotides of the invention
CC
XX
SQ Sequence 20 BP; 4 A; 9 C; 1 G; 6 T; 0 U; 0 Other;
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1012 TTCTCTGCTGCTCATCA 1031
Db 1 TTCTCTGCTGCTCATCA 20
RESULT 116
ABR63850
ID ABR63850 standard; DNA; 20 BP.
XX
XX ABR63850;
XX
XX 18-JUN-2002 (first entry)
XX
XX Neurokinin 1 receptor (NK-1) sense oligonucleotide #1.
XX
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;
XX immune disorder; autoimmune disorder; cardiovascular disorder;
XX vascular disorder; allergy disorder; neuropathic disorder; pain;
XX psychiatric disorder; central nervous system disorder; inflammation;
XX respiratory condition; ophthalmic condition; intestinal condition;
XX demyelinating disease; small cell lung cancer; depression;
XX hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
XX neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
XX neuro-pathological disorder; stress; antisense; primer; ss.
XX
XX Homo sapiens.

PN WO200213799-A2.
XX
XX 21-FEB-2002.
PD
XX 17-AUG-2001; 2001WO-IB001510.
PF
XX 18-AUG-2000; 2000US-0226086P.
PR
XX (UTMC-) UNIV MCGILL.
PA
XX Henry JL, Cahill CM, Yaehpal K;
PI WPI; 2002-241835/29.
XX
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XX Treating pathological condition involving neurokinin receptor-1, e.g.
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XX nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
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XX receptor, especially treating, attenuating or preventing pain or
XX inflammatory condition. The method comprises administering to a mammal, a
XX compound chosen from an oligonucleotide, its analogue, and a disruptor
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XX involvement of NK-1 receptor such as dermatological, immune, autoimmune,
XX cardiovascular, vascular disorders (e.g. migraine), allergy, neuropathic,
XX psychiatric and central nervous system disorders (e.g. anxiety,
XX psychosis, schizophrenia), gut inflammation, arthritis, and central or
XX peripheral aspects of chronic or acute pain, and for treating,
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XX conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
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XX Crohn's disease), cardiovascular conditions (stroke), chronic
XX gastrointestinal tract inflammation, and inflammatory diseases such as
XX inflammatory bowel diseases. Other disorders and diseases include
XX cardiovascular pathologies including stroke, chronic inflammatory
XX diseases such as rheumatoid arthritis, demyelinating diseases such as
XX multiple sclerosis, small cell lung cancer, depression, hypersensitivity
XX disorders such as allergies and poison ivy, vasospastic diseases such as
XX angina, addiction disorders such as alcoholism, neurodegenerative
XX disorders such as acquired immune deficiency syndrome (AIDS) related
XX dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
XX disorders such as peripheral neuropathy, oedema, stress related and
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XX receptor coding sequences and oligonucleotides of the invention
XX
XX
SQ Sequence 20 BP; 2 A; 9 C; 0 G; 9 T; 0 U; 0 Other;
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1000 TTCCACATCTTCTCTCTCT 1019
Db 1 TTCCACATCTTCTCTCTCT 20
RESULT 117

ABK63888/c
ID ABK63888 standard; DNA; 20 BP.
XX
AC ABK63888;
XX
DT 18-JUN-2002 (first entry)
XX
DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #33.
XX
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;
KM immune disorder; autoimmune disorder; cardiovascular disorder;
KM vascular disorder; airway disorder; neuropathic disorder; pain;
KM psychiatric disorder; central nervous system disorder; inflammation;
KM respiratory condition; ophthalmic condition; intestinal condition;
KM demyelinating disease; small cell lung cancer; depression;
KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
KM neuro-pathological disorder; stress; antisense; primer; ss.
XX
OS Homo sapiens.
XX
XX WO200213799-A2.
XX
PD 21-FEB-2002.
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PF 17-AUG-2001; 2001WO-IB001510.
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PA (UWMC-) UNIV MCGILL.
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PI Henry JL, Cahill CM, Yashpal K;
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DR WPI; 2002-241835/29.
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XX receptor, especially treating, attenuating or preventing pain or
XX inflammatory condition. The method comprises administering to a mammal, a
XX compound chosen from an oligonucleotide, its analogue, and a disruptor
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XX involvement of NK-1 receptor such as dermatological, immune, autoimmune,
XX cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,
XX psychiatric and central nervous system disorders (e.g. anxiety,
XX psychosis, schizophrenia), gut inflammation, arthritis, and central or
XX peripheral aspects of chronic or acute pain, and for treating,
XX attenuating or preventing pain or inflammation such as peripheral,
XX chronic, acute pain or inflammation, neuropathic pain, inflammation or
XX pain relating to psychiatric disorders and central nervous system
XX disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
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XX diseases, or pathological conditions treatable by this method include
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XX conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
XX (allergic dermatitis), intestinal conditions (stroke), chronic
XX Crohn's disease), cardiovascular conditions (stroke), chronic
XX gastrointestinal tract inflammation, and inflammatory diseases such as
XX inflammatory bowel diseases. Other disorders and diseases include
XX cardiovascular pathologies including stroke, chronic inflammatory
XX diseases such as rheumatoid arthritis, demyelinating diseases such as
XX multiple sclerosis, small cell lung cancer, depression, hypersensitivity
XX disorders such as allergies and poison ivy, vasospastic diseases such as
XX angina, addiction disorders such as alcoholism, neurodegenerative
XX disorders such as acquired immune deficiency syndrome (AIDS) related
XX dementia, epilepsy, Alzheimer's disease, and other neuro-pathological

disorders such as peripheral neuropathy, oedema, stress related and
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
CC effectively treat chronic conditions and other pathological states
CC without the co-administration of substance P, and reduce the number of
CC activated receptors while not reducing the number of quiescent NK-1
CC receptors. Receptors not chronically stimulated are less affected,
CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1
CC receptor coding sequences and oligonucleotides of the invention
XX
SQ Sequence 20 BP; 9 A; 0 C; 9 G; 2 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DY 1000 TTCCACATCTTCTTCTCTCT 1019
DB 20 TTCCACATCTTCTTCTCTCT 1
XX
RESULT 118
ABK63853/c
ID ABK63853 standard; DNA; 20 BP.
XX
AC ABK63853;
XX
DT 18-JUN-2002 (first entry)
XX
DE Neurokinin 1 receptor (NK-1) sense oligonucleotide #4.
XX
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;
KM immune disorder; autoimmune disorder; cardiovascular disorder;
KM vascular disorder; airway disorder; neuropathic disorder; pain;
KM psychiatric disorder; central nervous system disorder; inflammation;
KM respiratory condition; ophthalmic condition; intestinal condition;
KM demyelinating disease; small cell lung cancer; depression;
KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
KM neuro-pathological disorder; stress; antisense; primer; ss.
XX
OS Homo sapiens.
XX
XX WO200213799-A2.
XX
PD 21-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-IB001510.
XX
PR 18-AUG-2000; 2000US-0226086P.
XX
PA (UWMC-) UNIV MCGILL.
XX
PI Henry JL, Cahill CM, Yashpal K;
XX
DR WPI; 2002-241835/29.
XX
PT Treating pathological condition involving neurokinin receptor-1, e.g.
PT pain or inflammation, by administering oligonucleotide or a non-
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
PT pathway.
XX
PS Claim 24; Page 20; 100pp; English.
XX
XX The invention relates to a method of treating a pathological condition
XX characterised partially by involvement of neurokinin receptor-1 (NK-1)
XX receptor, especially treating, attenuating or preventing pain or
XX inflammatory condition. The method comprises administering to a mammal, a
XX compound chosen from an oligonucleotide, its analogue, and a disruptor
XX which interferes with function or production of NK-1 receptors. The
XX method is useful for treating a pathological condition characterised by
XX involvement of NK-1 receptor such as dermatological, immune, autoimmune,
XX cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,
XX psychiatric and central nervous system disorders (e.g. anxiety,

CC psychosis, schizophrenia), gut inflammation, arthritis, and central or
 CC peripheral aspects of chronic or acute pain, and for treating,
 CC attenuating or preventing pain or inflammation such as peripheral,
 CC chronic, acute pain or inflammation, neuropathic pain, inflammation or
 CC pain relating to psychiatric disorders and central nervous system
 CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
 CC in a mammal, in particular human, NK-1 receptor related disorders
 CC diseases, or pathological conditions treatable by this method include
 CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
 CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
 CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and
 CC Crohn's disease), cardiovascular conditions (stroke), chronic
 CC gastrointestinal tract inflammation, and inflammatory diseases such as
 CC inflammatory bowel diseases. Other disorders and diseases include
 CC cardiovascular pathologies including stroke, chronic inflammatory
 CC diseases such as rheumatoid arthritis, demyelinating diseases such as
 CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
 CC disorders such as allergies and poison ivy, vasospastic diseases such as
 CC angina, addiction disorders such as alcoholism, neurodegenerative
 CC disorders such as acquired immune deficiency syndrome (AIDS) related
 CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
 CC disorders such as peripheral neuropathy, oedema, stress related and
 CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
 CC effectively treat chronic conditions and other pathological states
 CC without the co-administration of substance P, and reduce the number of
 CC activated receptors while not reducing the number of quiescent NK-1
 CC receptors. Receptors not chronically stimulated are less affected,
 CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1
 CC receptor coding sequences and oligonucleotides of the invention
 XX

SO Sequence 20 BP; 6 A; 1 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1012 TTCTCTCGCCCTACATCAA 1031
 Db 20 TTCTCTCGCCCTACATCAA 1

RESULT 119
 ABK63874
 ID ABK63874 standard; DNA; 20 BP.
 XX
 AC ABK63874;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #19.
 XX

KM Human; neurokinin receptor-1; NK-1; dermatological disorder;
 KM immune disorder; autoimmune disorder; cardiovascular disorder;
 KM vascular disorder; airway disorder; neuropathic disorder; pain;
 KM psychiatric disorder; central nervous system disorder; inflammation;
 KM respiratory condition; ophthalmic condition; intestinal condition;
 KM demyelinating disease; small cell lung cancer; depression;
 KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
 KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
 KM neuro-pathological disorder; stress; antisense; primer; ss.
 XX

OS Homo sapiens.
 XX
 PN M0200213799-A2.
 XX
 PD 21-FEB-2002.
 XX
 PF 17-AUG-2001; 2001MO-IB001510.
 XX
 PR 18-AUG-2000; 2000US-0226086P.
 XX
 PA (UYMC-) UNIV MCGILL.
 XX

PT Henry JL, Cahill CM, Yashpal K;
 XX
 XX WPI; 2002-241835/29.
 XX
 PT Treating pathological condition involving neurokinin receptor-1, e.g.
 PT pain or inflammation, by administering oligonucleotide or a non-
 PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
 PT pathway.
 XX
 XX
 PS Claim 24; Page 65; 100pp; English.
 XX

CC The invention relates to a method of treating a pathological condition
 CC characterised partially by involvement of neurokinin receptor-1 (NK-1)
 CC receptor, especially treating, attenuating or preventing pain or
 CC inflammatory condition. The method comprises administering to a mammal, a
 CC compound chosen from an oligonucleotide, its analogue, and a disruptor
 CC which interferes with function or production of NK-1 receptors. The
 CC method is useful for treating a pathological condition characterised by
 CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,
 CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,
 CC psychiatric and central nervous system disorders (e.g. anxiety,
 CC psychosis, schizophrenia), gut inflammation, arthritis, and central or
 CC peripheral aspects of chronic or acute pain, and for treating,
 CC attenuating or preventing pain or inflammation such as peripheral,
 CC chronic, acute pain or inflammation, neuropathic pain, inflammation or
 CC pain relating to psychiatric disorders and central nervous system
 CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
 CC in a mammal, in particular human, NK-1 receptor related disorders,
 CC diseases, or pathological conditions treatable by this method include
 CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
 CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
 CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and
 CC Crohn's disease), cardiovascular conditions (stroke), chronic
 CC gastrointestinal tract inflammation, and inflammatory diseases such as
 CC inflammatory bowel diseases. Other disorders and diseases include
 CC cardiovascular pathologies including stroke, chronic inflammatory
 CC diseases such as rheumatoid arthritis, demyelinating diseases such as
 CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
 CC disorders such as allergies and poison ivy, vasospastic diseases such as
 CC angina, addiction disorders such as alcoholism, neurodegenerative
 CC disorders such as acquired immune deficiency syndrome (AIDS) related
 CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
 CC disorders such as peripheral neuropathy, oedema, stress related and
 CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
 CC effectively treat chronic conditions and other pathological states
 CC without the co-administration of substance P, and reduce the number of
 CC activated receptors while not reducing the number of quiescent NK-1
 CC receptors. Receptors not chronically stimulated are less affected,
 CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1
 CC receptor coding sequences and oligonucleotides of the invention
 XX

SO Sequence 20 BP; 6 A; 3 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 862 GTATGGAAATCACACTATG 881
 Db 1 GTATGGAAATCACACTATG 20

RESULT 120
 ABK63896
 ID ABK63896 standard; DNA; 20 BP.
 XX
 AC ABK63896;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #41.
 XX
 KM Human; neurokinin receptor-1; NK-1; dermatological disorder;
 KM

immune disorder; autoimmune disorder; cardiovascular disorder; pain; vascular disorder; airway disorder; neuropathic disorder; pain; psychiatric disorder; central nervous system disorder; inflammation; respiratory condition; ophthalmic condition; intestinal condition; demyelinating disease; small cell lung cancer; depression; hypersensitivity disorder; allergy; vasospastic disease; alcoholism; neurodegenerative disorder; acquired immune deficiency syndrome; AIDS; neuro-pathological disorder; stress; antisense; primer; ss.
 Homo sapiens.
 WO200213799-A2.
 21-FEB-2002.
 17-AUG-2001; 2001WO-IB001510.
 18-AUG-2000; 2000US-0226086P.
 (UYMC-) UNIV MCGILL.
 Henry JL, Cahill CM, Yashpal K;
 WPI; 2002-241835/29.
 Treating pathological condition involving neurokinin receptor-1, e.g. pain or inflammation, by administering oligonucleotide or a non-nucleotide disruptor compound which modulate NK-1 receptor biosynthetic pathway.
 Example 18; Page 65; 100pp; English.
 The invention relates to a method of treating a pathological condition characterised partially by involvement of neurokinin receptor-1 (NK-1) receptor, especially treating, attenuating or preventing pain or inflammatory condition. The method comprises administering to a mammal, a compound chosen from an oligonucleotide, its analogue, and a disruptor which interferes with function or production of NK-1 receptors. The method is useful for treating a pathological condition characterised by involvement of NK-1 receptor such as dermatological, immune, autoimmune, cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic, psychiatric and central nervous system disorders (e.g. anxiety, psychosis, schizophrenia), gut inflammation, arthritis, and central or peripheral aspects of chronic or acute pain, and for treating, attenuating or preventing pain or inflammation such as peripheral, chronic, acute pain or inflammation, neuropathic pain, inflammation or pain relating to psychiatric disorders and central nervous system disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia in a mammal, in particular human. NK-1 receptor related disorders, diseases, or pathological conditions treatable by this method include respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic conditions (e.g. conjunctivitis), cutaneous/dermatological conditions (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and Crohn's disease), cardiovascular conditions (stroke), chronic gastrointestinal tract inflammation, and inflammatory diseases such as inflammatory bowel diseases. Other disorders and diseases include cardiovascular pathologies including stroke, chronic inflammatory diseases such as rheumatoid arthritis, demyelinating diseases such as multiple sclerosis, small cell lung cancer, depression, hypersensitivity disorders such as allergies and poison ivy, vasospastic diseases such as angina, addiction disorders such as alcoholism, neurodegenerative disorders such as acquired immune deficiency syndrome (AIDS) related dementia, epilepsy, Alzheimer's disease, and other neuro-pathological disorders such as peripheral neuropathy, oedema, stress related and somatic disorders, and osteoarthritis. Antisense oligonucleotides effectively treat chronic conditions and other pathological states without the co-administration of substance P, and reduce the number of activated receptors while not reducing the number of quiescent NK-1 receptors. Receptors not chronically stimulated are less affected, reducing side effects of treatment. ABK6334-ABK6396 represent NK-1 receptor coding sequences and oligonucleotides of the invention
 Sequence 20 BP; 6 A; 7 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 601 TACATGCCATCATCATCC 620
 Db 1 TACATGCCATCATCATCC 20
 RESULT 121
 ABK63872
 ID ABK63872 standard; DNA; 20 BP.
 AC ABK63872;
 XX
 XX 18-JUN-2002 (first entry)
 DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #17.
 XX
 XX Human, neurokinin receptor-1; NK-1; dermatological disorder;
 KW immune disorder; autoimmune disorder; cardiovascular disorder;
 KW vascular disorder; airway disorder; neuropathic disorder; pain;
 KW psychiatric disorder; central nervous system disorder; inflammation;
 KW respiratory condition; ophthalmic condition; intestinal condition;
 KW demyelinating disease; small cell lung cancer; depression;
 KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
 KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
 KW neuro-pathological disorder; stress; antisense; primer; ss.
 Homo sapiens.
 OS
 XX
 XX WO200213799-A2.
 XX
 XX 21-FEB-2002.
 XX
 XX 17-AUG-2001; 2001WO-IB001510.
 XX
 XX 18-AUG-2000; 2000US-0226086P.
 XX
 XX (UYMC-) UNIV MCGILL.
 XX
 XX Henry JL, Cahill CM, Yashpal K;
 XX WPI; 2002-241835/29.
 XX
 XX Treating pathological condition involving neurokinin receptor-1, e.g. pain or inflammation, by administering oligonucleotide or a non-nucleotide disruptor compound which modulate NK-1 receptor biosynthetic pathway.
 XX
 XX Claim 24; Page 65; 100pp; English.
 PS
 XX The invention relates to a method of treating a pathological condition characterised partially by involvement of neurokinin receptor-1 (NK-1) receptor, especially treating, attenuating or preventing pain or inflammatory condition. The method comprises administering to a mammal, a compound chosen from an oligonucleotide, its analogue, and a disruptor which interferes with function or production of NK-1 receptors. The method is useful for treating a pathological condition characterised by involvement of NK-1 receptor such as dermatological, immune, autoimmune, cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic, psychiatric and central nervous system disorders (e.g. anxiety, psychosis, schizophrenia), gut inflammation, arthritis, and central or peripheral aspects of chronic or acute pain, and for treating, attenuating or preventing pain or inflammation such as peripheral, chronic, acute pain or inflammation, neuropathic pain, inflammation or pain relating to psychiatric disorders and central nervous system disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia in a mammal, in particular human. NK-1 receptor related disorders, diseases, or pathological conditions treatable by this method include respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic conditions (e.g. conjunctivitis), cutaneous/dermatological conditions

CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and
CC Crohn's disease), cardiovascular conditions (stroke), chronic
CC gastrointestinal tract inflammation, and inflammatory diseases such as
CC inflammatory bowel diseases. Other disorders and diseases include
CC cardiovascular pathologies including stroke, chronic inflammatory
CC diseases such as rheumatoid arthritis, demyelinating diseases such as
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
CC disorders such as allergies and poison ivy, vasospastic diseases such as
CC angina, addiction disorders such as alcoholism, neurodegenerative
CC disorders such as acquired immune deficiency syndrome (AIDS) related
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
CC disorders such as peripheral neuropathy, edema, stress related and
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
CC effectively treat chronic conditions and other pathological states
CC without the co-administration of substance P, and reduce the number of
CC activated receptors while not reducing the number of quiescent NK-1
CC receptors. Receptors not chronically stimulated are less affected,
CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1
CC receptor coding sequences and oligonucleotides of the invention
XX

SQ Sequence 20 BP; 4 A; 9 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1012 TTCTCTCTGCTCATCA 1031
Db 1 TTCTCTCTGCTCATCA 20

RESULT 122
ABK6385/c
ID ABK6385 standard; DNA; 20 BP.
AC ABK6385;
XX
DT 18-JUN-2002 (first entry)
DE Neurokinin 1 receptor (NK-1) sense oligonucleotide #6.
XX
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;
KM immune disorder; autoimmune disorder; cardiovascular disorder;
KM vascular disorder; airway disorder; neuropathic disorder; pain;
KM psychiatric disorder; central nervous system disorder; inflammation;
KM respiratory condition; ophthalmic condition; intestinal condition;
KM demyelinating disease; small cell lung cancer; depression;
KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
KM neuro-pathological disorder; stress; antisense; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200213799-A2.
XX
PD 21-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-IB001510.
XX
PR 18-AUG-2000; 2000US-0226086P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Henry JL, Cahill CM, Yaashpal K;
XX
DR WPI; 2002-241835/29.
XX
PT Treating pathological condition involving neurokinin receptor-1, e.g.
PT pain or inflammation, by administering oligonucleotide or a non-
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
PT pathway.
XX
PS Claim 24; Page 20; 100pp; English.

XX The invention relates to a method of treating a pathological condition
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)
CC receptor, especially treating, attenuating or preventing pain or
CC inflammatory condition. The method comprises administering to a mammal, a
CC compound chosen from an oligonucleotide, its analogue, and a disruptor
CC which interferes with function or production of NK-1 receptors. The
CC method is useful for treating a pathological condition characterised by
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,
CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,
CC psychiatric and central nervous system disorders (e.g. anxiety,
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or
CC peripheral aspects of chronic or acute pain, and for treating,
CC attenuating or preventing pain or inflammation such as peripheral,
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or
CC pain relating to psychiatric disorders and central nervous system
CC disorders, including hyperalgesia, allodynia, neuropathic and dysesthesia
CC in a mammal, in particular human. NK-1 receptor related disorders,
CC diseases, or pathological conditions treatable by this method include
CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and
CC Crohn's disease), cardiovascular conditions (stroke), chronic
CC gastrointestinal tract inflammation, and inflammatory diseases such as
CC inflammatory bowel diseases. Other disorders and diseases include
CC cardiovascular pathologies including stroke, chronic inflammatory
CC diseases such as rheumatoid arthritis, demyelinating diseases such as
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
CC disorders such as allergies and poison ivy, vasospastic diseases such as
CC angina, addiction disorders such as alcoholism, neurodegenerative
CC disorders such as acquired immune deficiency syndrome (AIDS) related
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
CC disorders such as peripheral neuropathy, edema, stress related and
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
CC effectively treat chronic conditions and other pathological states
CC without the co-administration of substance P, and reduce the number of
CC activated receptors while not reducing the number of quiescent NK-1
CC receptors. Receptors not chronically stimulated are less affected,
CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1
CC receptor coding sequences and oligonucleotides of the invention
XX

SQ Sequence 20 BP; 5 A; 6 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 862 GTAGTGGGATCACAATG 881
Db 20 GTAGTGGGATCACAATG 1

RESULT 123
ABT16453/c
ID ABT16453 standard; DNA; 20 BP.
XX
AC ABT16453;
XX
DT 20-MAR-2003 (first entry)
DE Human neurokinin 1 receptor gene related PCR primer SEQ ID No 34.
XX
XX Cytostatic; antineoplastic; antiinflammatory; cardiant; polymorphic site;
KM human neurokinin 1 receptor; TACRI; disease phenotype; forensics;
KM TACRI ligand mediated disease; asthma; paternity testing; cancer;
KM inflammation; heart disease; central nervous system; infection; PCR;
KM primer; ss.
XX
XX Unidentified.
OS
XX
XX EPI262565-A2.
PN
PD 04-DEC-2002.

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XX 23-MAY-2002; 2002EP-00253662.
PF (PFIZ ) PFIZER PROD INC.
XX 25-MAY-2001; 2001US-0293425P.
XX (PFIZ ) PFIZER PROD INC.
XX Affourtit JP, Nelson DL, Seymour AB, Webb SM;
PI WPI; 2003-150228/15.
XX
XX Novel nucleic acid segment from human neurokinin 1 receptor, including
PT polymorphic sites for diagnosing and treating asthma, and in forensics,
PT paternity testing, and genetic mapping of the traits.
XX
XX Example; Page 12; 27pp; English.
XX
XX The invention relates to a nucleic acid segment from the human neurokinin
CC 1 receptor (TACR1) gene of 10-100 nucleotides comprising a fragment
CC having a polymorphic site or a complement of the fragment. The TACR1
CC segment is useful for analysing a nucleic acid, by obtaining the nucleic
CC acid from an individual, and determining the base occupying any one of
CC the polymorphic sites in the segment. The nucleic acid is obtained from
CC several individuals, and the base occupying one of the polymorphic sites
CC is determined in each of the individuals, and further involves testing
CC each of the individuals for the presence of a disease phenotype, and
CC correlating the presence with the base. The TACR1 segment is useful for
CC diagnosing and treating TACR1 ligand mediated diseases, such as asthma.
CC The TACR1 segment is also useful in forensics, paternity testing,
CC correlating polymorphisms with phenotypic traits, and genetic mapping of
CC phenotypic traits. The TACR1 segment is useful in diagnosing and
CC monitoring of diseases such as cancer, inflammation, heart disease,
CC disorders of central nervous system, and susceptibility to infection to
CC microorganisms. The TACR1 segment is also useful in the manufacture of a
CC medicament for the treatment of the diseases. This polynucleotide
CC sequence represents a PCR primer of the human neurokinin 1 receptor
CC (TACR1) gene of the invention
CC
SQ Sequence 20 BP; 5 A; 9 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 GGCAACGTGTAGTATGTG 374
DB 20 GGCAACGTGTAGTATGTG 1

RESULT 124
ABT16465/c
ID ABT16465 standard; DNA; 20 BP.
XX
XX ABT16465;
AC
XX 20-MAR-2003 (first entry)
XX
XX Human neurokinin 1 receptor gene related PCR primer SEQ ID No 46.
DE
XX Cytostatic; antiasthmatic; antiinflammatory; cardiant; polymorphic site;
XX human neurokinin 1 receptor; TACR1; disease phenotype; forensics;
XX TACR1 ligand mediated disease; asthma; paternity testing; cancer;
XX inflammation; heart disease; central nervous system; infection; PCR;
XX primer; ss.
XX
XX Unidentified.
XX
XX EP1262565-A2.
XX
XX 04-DEC-2002.
XX
XX 23-MAY-2002; 2002EP-00253662.
XX
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PR 25-MAY-2001; 2001US-0293425P.
XX
XX (PFIZ ) PFIZER PROD INC.
XX Affourtit JP, Nelson DL, Seymour AB, Webb SM;
XX WPI; 2003-150228/15.
XX
XX Novel nucleic acid segment from human neurokinin 1 receptor, including
PT polymorphic sites for diagnosing and treating asthma, and in forensics,
PT paternity testing, and genetic mapping of the traits.
XX
XX Example; Page 12; 27pp; English.
XX
XX The invention relates to a nucleic acid segment from the human neurokinin
CC 1 receptor (TACR1) gene of 10-100 nucleotides comprising a fragment
CC having a polymorphic site or a complement of the fragment. The TACR1
CC segment is useful for analysing a nucleic acid, by obtaining the nucleic
CC acid from an individual, and determining the base occupying any one of
CC the polymorphic sites in the segment. The nucleic acid is obtained from
CC several individuals, and the base occupying one of the polymorphic sites
CC is determined in each of the individuals, and further involves testing
CC each of the individuals for the presence of a disease phenotype, and
CC correlating the presence with the base. The TACR1 segment is useful for
CC diagnosing and treating TACR1 ligand mediated diseases, such as asthma.
CC The TACR1 segment is also useful in forensics, paternity testing,
CC correlating polymorphisms with phenotypic traits, and genetic mapping of
CC phenotypic traits. The TACR1 segment is useful in diagnosing and
CC monitoring of diseases such as cancer, inflammation, heart disease,
CC disorders of central nervous system, and susceptibility to infection to
CC microorganisms. The TACR1 segment is also useful in the manufacture of a
CC medicament for the treatment of the diseases. This polynucleotide
CC sequence represents a PCR primer of the human neurokinin 1 receptor
CC (TACR1) gene of the invention
CC
SQ Sequence 20 BP; 6 A; 3 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1483 CCCTTCATGCATGGAATTC 1502
DB 20 CCCTTCATGCATGGAATTC 1

RESULT 125
ABT16467/c
ID ABT16467 standard; DNA; 20 BP.
XX
XX ABT16467;
AC
XX 20-MAR-2003 (first entry)
XX
XX Human neurokinin 1 receptor gene related PCR primer SEQ ID No 48.
DE
XX Cytostatic; antiasthmatic; antiinflammatory; cardiant; polymorphic site;
XX human neurokinin 1 receptor; TACR1; disease phenotype; forensics;
XX TACR1 ligand mediated disease; asthma; paternity testing; cancer;
XX inflammation; heart disease; central nervous system; infection; PCR;
XX primer; ss.
XX
XX Unidentified.
XX
XX EP1262565-A2.
XX
XX 04-DEC-2002.
XX
XX 23-MAY-2002; 2002EP-00253662.
XX
XX 25-MAY-2001; 2001US-0293425P.
XX
XX (PFIZ ) PFIZER PROD INC.
XX
```

XX Affourtit JP, Nelson DL, Seymour AB, Webb SM;
PI WPI; 2003-150228/15.
XX
XX Novel nucleic acid segment from human neurokinin 1 receptor, including
PT polymorphic sites for diagnosing and treating asthma, and in forensics,
PI paternity testing, and genetic mapping of the traits.
XX
XX Example; Page 12; 27pp; English.
XX
CC The invention relates to a nucleic acid segment from the human neurokinin
CC 1 receptor (TACR1) gene of 10-100 nucleotides comprising a fragment
CC having a polymorphic site or a complement of the fragment. The TACR1
CC segment is useful for analysing a nucleic acid, by obtaining the nucleic
CC acid from an individual, and determining the base occupying any one of
CC the polymorphic sites in the segment. The nucleic acid is obtained from
CC several individuals, and the base occupying one of the polymorphic sites
CC is determined in each of the individuals, and further involves testing
CC each of the individuals for the presence of a disease phenotype, and
CC correlating the presence with the base. The TACR1 segment is useful for
CC diagnosing and treating TACR1 ligand mediated diseases, such as asthma.
CC The TACR1 segment is also useful in forensics, paternity testing,
CC correlating polymorphisms with phenotypic traits, and genetic mapping of
CC phenotypic traits. The TACR1 segment is useful in diagnosing and
CC monitoring of diseases such as cancer, inflammation, heart disease,
CC diseases of central nervous system, and susceptibility to infection to
CC microorganisms. The TACR1 segment is also useful in the manufacture of a
CC medicament for the treatment of the diseases. This polynucleotide
CC sequence represents a PCR primer of the human neurokinin 1 receptor
CC (TACR1) gene of the invention
XX
SQ Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1746 GCGAGTGTCTCATTTACAGAT 1765
DB 20 GCGAGTGTCTCATTTACAGAT 1
XX
RESULT 126
ABT16466
ID ABT16466 standard; DNA; 20 BP.
XX
XX ABT16466;
XX
XX 20-MAR-2003 (first entry)
XX
DE Human neurokinin 1 receptor gene related PCR primer SEQ ID No 47.
XX
XX Cytostatic; antiasthmatic; antiinflammatory; cardiac; polymorphic site;
XX human neurokinin 1 receptor; TACR1; disease phenotype; forensics;
XX TACR1 ligand mediated disease; asthma; paternity testing; cancer;
XX inflammation; heart disease; central nervous system; infection; PCR;
XX primer; ss.
XX
XX Undifferentiated.
XX
XX EPI262565-A2.
XX
XX 04-DEC-2002.
XX
XX 23-MAY-2002; 2002EP-00253662.
XX
XX 25-MAY-2001; 2001US-0293425P.
XX
XX (PFI2) PRIZER PROD INC.
XX
XX Affourtit JP, Nelson DL, Seymour AB, Webb SM;

DR WPI; 2003-150228/15.
XX
XX Novel nucleic acid segment from human neurokinin 1 receptor, including
PT polymorphic sites for diagnosing and treating asthma, and in forensics,
PI paternity testing, and genetic mapping of the traits.
XX
XX Example; Page 12; 27pp; English.
XX
XX
CC The invention relates to a nucleic acid segment from the human neurokinin
CC 1 receptor (TACR1) gene of 10-100 nucleotides comprising a fragment
CC having a polymorphic site or a complement of the fragment. The TACR1
CC segment is useful for analysing a nucleic acid, by obtaining the nucleic
CC acid from an individual, and determining the base occupying any one of
CC the polymorphic sites in the segment. The nucleic acid is obtained from
CC several individuals, and the base occupying one of the polymorphic sites
CC is determined in each of the individuals, and further involves testing
CC each of the individuals for the presence of a disease phenotype, and
CC correlating the presence with the base. The TACR1 segment is useful for
CC diagnosing and treating TACR1 ligand mediated diseases, such as asthma.
CC The TACR1 segment is also useful in forensics, paternity testing,
CC correlating polymorphisms with phenotypic traits, and genetic mapping of
CC phenotypic traits. The TACR1 segment is useful in diagnosing and
CC monitoring of diseases such as cancer, inflammation, heart disease,
CC diseases of central nervous system, and susceptibility to infection to
CC microorganisms. The TACR1 segment is also useful in the manufacture of a
CC medicament for the treatment of the diseases. This polynucleotide
CC sequence represents a PCR primer of the human neurokinin 1 receptor
CC (TACR1) gene of the invention
XX
SQ Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1417 TCCAGTGTCTCTCTAGGC 1436
DB 1 TCCAGTGTCTCTCTAGGC 20
XX
RESULT 127
AED51262
ID AED51262 standard; DNA; 20 BP.
XX
XX AED51262;
XX
XX 29-DEC-2005 (first entry)
XX
XX Human tachykinin receptor 1 (TACR1) cDNA forward PCR primer.
XX
XX Screening; diagnosis; tachykinin receptor 1; TACR1;
XX cardiovascular disease; infection; dermatological disease;
XX gastrointestinal disease; cancer; neoplasm; inflammation;
XX metabolic disorder; hematological disease; respiratory disease;
XX musculoskeletal disease; neurological disease; gynecological disorder;
XX gynecology and obstetrics; genitourinary disease; cardiovascular-gen;
XX cardiac; hypotensive; antimicrobial; antibacterial; fungicide; virucide;
XX dermatological; antiparasitic; gastrointestinal-gen.; antiinflammatory;
XX cytosstatic; immunosuppressive; anorectic; antidiabetic; antianemic;
XX respiratory-gen.; antiasthmatic; muscular-gen.; osteopathic;
XX antiarthritic; neuroprotective; nootropic; antiparkinsonian;
XX gynecological; antifertility; nephrotropic; metabolic; uropathic; PCR;
XX ss; primer.
XX
XX Homo sapiens.
XX
XX W02005100986-A1.
XX
XX 27-OCT-2005.
XX
XX 02-APR-2005; 2005WO-EP003465.
XX
XX 15-APR-2004; 2004EP-00008923.
XX

PT P in body fluid of arthritis patients.
XX
XX Disclosure; Page 8; 35pp; English.
XX
CC The sequences given in AAQ297670-82, AAQ29763 and AAQ29746-48 are primers
CC which were used in the isolation of fragments of the human neurokinin-1
CC receptor (NK1R) cDNA. Human NK1R is a membrane receptor for the
CC neurotransmitter substance P. The primers were designed using regions of
CC the human NK1R cDNA and also regions of the rat NK1R which were thought
CC to be similar to human regions. Part of the human cDNA sequence was
CC derived by amplification using these primers. The remaining part of human
CC NK1R cDNA was obtained from a human cDNA library utilising portions of
CC PCR generated fragments as probes. See also AAQ29749. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 21 BP; 7 A; 2 C; 7 G; 5 T; 0 U; 0 Other;
Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 523 TGCAGTTCCACCACTTCTT 542
Db 21 TGCAGTTCCACCACTTCTT 2
RESULT 130
ABK63898
ID ABK63898 standard; DNA; 21 BP.
XX
AC ABK63898;
XX
XX 18-JUN-2002 (first entry)
XX
DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #43.
XX
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;
KW immune disorder; autoimmune disorder; cardiovascular disorder;
KW vascular disorder; airway disorder; neuropathic disorder; pain;
KW psychiatric disorder; central nervous system disorder; inflammation;
KW respiratory condition; ophthalmic condition; intestinal condition;
KW demyelinating disease; small cell lung cancer; depression;
KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
KW neuro-pathological disorder; stress; antisense; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200213799-A2.
XX
PD 21-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-IB001510.
XX
PR 18-AUG-2000; 2000US-0226086P.
XX
PA (UTMC-) UNIV MCGILL.
XX
PI Henry JL, Cahill CM, Yashpal K;
XX
XX WPI; 2002-241835/29.
XX
PT Treating pathological condition involving neurokinin receptor-1, e.g.
PT pain or inflammation, by administering oligonucleotide or a non-
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
PT pathway.
XX
PS Example 18; Page 65; 100pp; English.
XX
CC The invention relates to a method of treating a pathological condition
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)
CC receptor, especially treating, attenuating or preventing pain or
CC inflammatory condition. The method comprises administering to a mammal, a

CC compound chosen from an oligonucleotide, its analogue, and a disruptor
CC which interferes with function or production of NK-1 receptors. The
CC method is useful for treating a pathological condition characterised by
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,
CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,
CC psychiatric and central nervous system disorders (e.g. anxiety,
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or
CC peripheral aspects of chronic or acute pain, and for treating,
CC attenuating or preventing pain or inflammation such as peripheral,
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or
CC pain relating to psychiatric disorders and central nervous system
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
CC in a mammal, in particular human. NK-1 receptor related disorders,
CC diseases, or pathological conditions treatable by this method include
CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and
CC Crohn's disease), cardiovascular conditions (stroke), chronic
CC gastrointestinal tract inflammation, and inflammatory diseases such as
CC inflammatory bowel diseases. Other disorders and diseases include
CC cardiovascular pathologies including stroke, chronic inflammatory
CC diseases such as rheumatoid arthritis, demyelinating diseases such as
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
CC disorders such as allergies and poison ivy, vasospastic diseases such as
CC angina, addiction disorders such as alcoholism, neurodegenerative
CC disorders such as acquired immune deficiency syndrome (AIDS) related
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
CC disorders such as peripheral neuropathy, oedema, stress related and
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
CC effectively treat chronic conditions and other pathological states
CC without the co-administration of substance P, and reduce the number of
CC activated receptors while not reducing the number of quiescent NK-1
CC receptors. Receptors not chronically stimulated are less affected,
CC reducing side effects of treatment. ABK63824-ABK63906 represent NK-1
CC receptor coding sequences and oligonucleotides of the invention
XX
SQ Sequence 21 BP; 5 A; 7 C; 2 G; 7 T; 0 U; 0 Other;
Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 523 TGCAGTTCCACCACTTCTT 542
Db 1 TGCAGTTCCACCACTTCTT 20
RESULT 131
ABK63879
ID ABK63879 standard; DNA; 21 BP.
XX
AC ABK63879;
XX
XX 18-JUN-2002 (first entry)
XX
DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #24.
XX
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;
KW immune disorder; autoimmune disorder; cardiovascular disorder;
KW vascular disorder; airway disorder; neuropathic disorder; pain;
KW psychiatric disorder; central nervous system disorder; inflammation;
KW respiratory condition; ophthalmic condition; intestinal condition;
KW demyelinating disease; small cell lung cancer; depression;
KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
KW neuro-pathological disorder; stress; antisense; primer; ss.
XX
OS Homo sapiens.
XX
XX WO200213799-A2.
XX
PN 21-FEB-2002.
XX

PF 17-AUG-2001; 2001MO-IB001510.
 XX
 PR 18-AUG-2000; 2000US-0226086P.
 XX
 PA (UYMC-) UNIV MCGILL.
 XX
 PI Henry JL, Cahill CM, Yashpal K;
 XX
 DR WPI; 2002-241835/29.
 XX
 PT Treating pathological condition involving neurokinin receptor-1, e.g.
 PT pain or inflammation, by administering oligonucleotide or a non-
 PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
 PT pathway.
 XX
 PS Claim 24; Page 65; 100pp; English.
 XX
 PS The invention relates to a method of treating a pathological condition
 CC characterised partially by involvement of neurokinin receptor-1 (NK-1)
 CC receptor, especially treating, attenuating or preventing pain or
 CC inflammatory condition. The method comprises administering to a mammal, a
 CC compound chosen from an oligonucleotide, its analogue, and a disruptor
 CC which interferes with function or production of NK-1 receptors. The
 CC method is useful for treating a pathological condition characterised by
 CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,
 CC cardiovascular, vascular disorders (e.g. migraine), allergy, neuropathic,
 CC psychiatric and central nervous system disorders (e.g. anxiety,
 CC psychosis, schizophrenia), gut inflammation, arthritis, and central or
 CC peripheral aspects of chronic or acute pain, and for treating,
 CC attenuating or preventing pain or inflammation such as peripheral,
 CC chronic, acute pain or inflammation, neuropathic pain, inflammation or
 CC pain relating to psychiatric disorders and central nervous system
 CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
 CC in a mammal, in particular human. NK-1 receptor related disorders,
 CC diseases, or pathological conditions treatable by this method include
 CC respiratory conditions (e.g. asthma, allergic rhinitis), opthalmic
 CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
 CC (allergic dermatitis), intestinal conditions (stroke), chronic
 CC Crohn's disease), cardiovascular conditions (stroke), chronic
 CC gastrointestinal tract inflammation, and inflammatory diseases such as
 CC inflammatory bowel diseases. Other disorders and diseases include
 CC cardiovascular pathologies including stroke, chronic inflammatory
 CC diseases such as rheumatoid arthritis, demyelinating diseases such as
 CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
 CC disorders such as allergies and poison ivy, vasospastic diseases such as
 CC angina, addiction disorders such as alcoholism, neurodegenerative
 CC disorders such as acquired immune deficiency syndrome (AIDS) related
 CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
 CC disorders such as peripheral neuropathy, oedema, stress related and
 CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
 CC effectively treat chronic conditions and other pathological states
 CC without the co-administration of substance P, and reduce the number of
 CC activated receptors while not reducing the number of quiescent NK-1
 CC receptors. Receptors not chronically stimulated are less affected,
 CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1
 CC receptor coding sequences and oligonucleotides of the invention
 XX
 SQ Sequence 21 BP; 5 A; 7 C; 2 G; 7 T; 0 U; 0 Other;
 XX
 QY Query Match 1.1%; Score 20; DB 1; Length 21;
 Db Best Local Similarity 100.0%; Pred. No. 54;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 523 TGCAGTTCACCACTTCTT 542
 Db 1 TGCAGTTCACCACTTCTT 20
 RESULT 132
 ABK63860/c
 ID ABK63860 standard; DNA; 21 BP.
 XX
 AC ABK63860;

XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Neurokinin 1 receptor (NK-1) sense oligonucleotide #11.
 XX
 KW Human; neurokinin receptor-1; NK-1; dermatological disorder;
 KW immune disorder; autoimmune disorder; cardiovascular disorder;
 KW vascular disorder; allergy disorder; neuropathic disorder; pain;
 KW psychiatric disorder; central nervous system disorder; inflammation;
 KW respiratory condition; opthalmic condition; intestinal condition;
 KW demyelinating disease; small cell lung cancer; depression;
 KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
 KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
 KW neuro-pathological disorder; stress; antisense; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200213799-A2.
 XX
 PD 21-FEB-2002.
 XX
 PF 17-AUG-2001; 2001MO-IB001510.
 XX
 PR 18-AUG-2000; 2000US-0226086P.
 XX
 PA (UYMC-) UNIV MCGILL.
 XX
 PI Henry JL, Cahill CM, Yashpal K;
 XX
 DR WPI; 2002-241835/29.
 XX
 PT Treating pathological condition involving neurokinin receptor-1, e.g.
 PT pain or inflammation, by administering oligonucleotide or a non-
 PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
 PT pathway.
 XX
 PS Claim 24; Page 20; 100pp; English.
 XX
 PS The invention relates to a method of treating a pathological condition
 CC characterised partially by involvement of neurokinin receptor-1 (NK-1)
 CC receptor, especially treating, attenuating or preventing pain or
 CC inflammatory condition. The method comprises administering to a mammal, a
 CC compound chosen from an oligonucleotide, its analogue, and a disruptor
 CC which interferes with function or production of NK-1 receptors. The
 CC method is useful for treating a pathological condition characterised by
 CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,
 CC cardiovascular, vascular disorders (e.g. migraine), allergy, neuropathic,
 CC psychiatric and central nervous system disorders (e.g. anxiety,
 CC psychosis, schizophrenia), gut inflammation, arthritis, and central or
 CC peripheral aspects of chronic or acute pain, and for treating,
 CC attenuating or preventing pain or inflammation such as peripheral,
 CC chronic, acute pain or inflammation, neuropathic pain, inflammation or
 CC pain relating to psychiatric disorders and central nervous system
 CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
 CC in a mammal, in particular human. NK-1 receptor related disorders,
 CC diseases, or pathological conditions treatable by this method include
 CC respiratory conditions (e.g. asthma, allergic rhinitis), opthalmic
 CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
 CC (allergic dermatitis), intestinal conditions (stroke), chronic
 CC Crohn's disease), cardiovascular conditions (stroke), chronic
 CC gastrointestinal tract inflammation, and inflammatory diseases such as
 CC inflammatory bowel diseases. Other disorders and diseases include
 CC cardiovascular pathologies including stroke, chronic inflammatory
 CC diseases such as rheumatoid arthritis, demyelinating diseases such as
 CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
 CC disorders such as allergies and poison ivy, vasospastic diseases such as
 CC angina, addiction disorders such as alcoholism, neurodegenerative
 CC disorders such as acquired immune deficiency syndrome (AIDS) related
 CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
 CC disorders such as peripheral neuropathy, oedema, stress related and
 CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
 CC effectively treat chronic conditions and other pathological states
 CC without the co-administration of substance P, and reduce the number of

CC activated receptors while not reducing the number of quiescent NK-1
CC receptors. Receptors not chronically stimulated are less affected,
CC reducing side effects of treatment. ABK6384-ABK63906 represent NK-1
CC receptor coding sequences and oligonucleotides of the invention
XX Sequence 21 BP; 7 A; 2 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 523 TGCAGTTCACACTCTT 542
DB 21 TGCAGTTCACACTCTT 2

RESULT 133
AB081645
ID AB081645 standard; DNA; 23 BP.

AC AB081645;
XX
XX 12-DEC-2002 (first entry)

DE Oligonucleotide sense-C for the preparation of a modified NK-1 receptor.

XX Tachykinin receptor; antiinflammatory; antimigraine; antidepressant;
XX anorectic; neuroleptic; neuroprotective; tranquiliser;
XX antianginal; dermatological; antiarrhythmic; protein therapy; gene therapy;
XX neurotransmission; substance P; SP; neurokinin A; NKA; neurokinin B; NKB;
XX arthritis; pain; migraine; anxiety; schizophrenia; asthma;
XX rheumatoid arthritis; gastrointestinal disorder; gastrointestinal tract;
XX attention deficit disorder; premenstrual syndrome; mania; depression;
XX inflammation; eating disorder; obesity; cognitive dysfunction; stress;
XX movement disorder; schizophrenic disorder; sexual dysfunction;
XX Alzheimer's disease; angina; multiple sclerosis; scleroderma;
XX central nervous system disorder; NK-1v; ss.

OS Synthetic.

XX GB2370274-A.

XX 26-JUN-2002.

PF 19-DEC-2000; 2000GB-00031148.

XX 19-DEC-2000; 2000GB-00031148.

PA (WARN) WARNER LAMBERT CO.

PI Hall MD, McNulty S, Murray JH, Suman-Chauhan N;

XX WPI; 2002-638104/69.

PT Novel modified tachykinin receptors useful for removing or suppressing
PT substance P in body fluids, and treatment or prophylaxis of a condition
PT associated with substance P or other tachykinin receptor-binding ligand.
XX
XX Example 1; Page 27; 45pp; English.

XX The invention relates to a mutant tachykinin receptor in which the three
CC amino acids of the DRV sequence that occurs adjacent to the junction of
CC the TM3 domain with intracellular loop 2 are replaced with amino acids
CC whose side chains are neither lipophilic nor contain charged groups.
CC Mammalian tachykinins include substance P (SP), neurokinin A (NKA) and
CC neurokinin B (NKB). The mutant receptor of the invention is useful for
CC treatment or prevention of a condition associated with over-expression or
CC inappropriate of an endogenous tachykinin ligand, including protein and/or
CC gene therapy. It is useful as a substitute in an assay to identify and/or
CC evaluate entities that bind to the wild type tachykinin receptor, and in
CC an assay to determine the concentration of ligand in body fluids in
CC patients with arthritis, pain, migraine, anxiety, schizophrenia, asthma,
CC rheumatoid arthritis and in gastrointestinal disorders and diseases of

CC the gastrointestinal tract. Other conditions or disease states that can
CC be treated, ameliorated or prevented include, attention deficit disorder,
CC premenstrual syndrome, mania, depression, inflammation, eating disorders,
CC such as obesity, cognitive disorders, movement disorders, schizophrenic
CC disorders, sexual dysfunction, stress, Alzheimer's disease, angina,
CC multiple sclerosis, scleroderma, central nervous system (CNS) disorders
CC and other conditions where excess tachykinin peptides such as SP are
CC involved. Tachykinins have an established role in neurotransmission. The
CC current sequence represents an oligonucleotide designated sense-C, used
CC in an example from the invention for the preparation of a modified human
CC NK-1 receptor (NK-1v) by site-directed mutagenesis
XX

SO Sequence 23 BP; 3 A; 6 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 1.1%; Score 19.8; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 73;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 438 CGCGAGGCTTCATGGCTGCAT 460
DB 1 CGCGAGGCTTCATGGCTGCAT 23

RESULT 134

ID ADU41834 standard; DNA; 21 BP.

XX ADU41834;

XX 27-JAN-2005 (first entry)

DE Knock-down target sequence #7013.

XX ds; RNA production; protein production; drug development;
XX knock-down target.

XX Unidentified.

XX W02004094636-A1.

XX 04-NOV-2004.

PF 24-APR-2003; 2003WO-EP004362.

XX 24-APR-2003; 2003WO-EP004362.

PA (GALA-) GALAPAGOS GENOMICS NV.

PA (VSCB/) VAN DER SCHUREN J.

PI Arts GJF, Lambrecht MJT, Djokic K, Claesen RJ, Meaic B;

XX Griffioen S, Bergs CUL;

XX WPI; 2004-775940/76.

PT New knockdown sequences, useful in lowering the amount of RNA and/or
PT protein production in cells used in drug development process.
XX
XX Claim 11; SEQ ID NO 7062; 402pp; English.

XX The invention relates to a polynucleotide comprising an RNA sequence. The
CC polynucleotides, vector, libraries, and method are useful in lowering the
CC amount of RNA and/or protein production in cells used in drug development
CC process. The present sequence represents a knock-down target sequence.

SO Sequence 21 BP; 3 A; 6 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 1.1%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 67;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1135 AATGACAGGTTCCGTCTGGGC 1155
DB 1 ACTGACAGGTTCCGTCTGGGC 21

RESULT 135

ADU41833 standard; DNA; 21 BP.

ADU41833;

27-JAN-2005 (first entry)

Knock-down target sequence #7012.

des; RNA production; protein production; drug development; knock-down target.

Unidentified.

WO2004094636-A1.

04-NOV-2004.

24-APR-2003; 2003WO-EP004362.

24-APR-2003; 2003WO-EP004362.

(GALA-) GALAPAGOS GENOMICS NV.

(VSCN/) VAN DER SCHUREN J.

Arts GJF, Lambrecht MY, Djokic K, Clasen RJ, Mesic E;

Griffioen S, Bergs CJL;

WPI; 2004-775940/76.

New knockdown sequences, useful in lowering the amount of RNA and/or protein production in cells used in drug development process.

Claim 11; SEQ ID NO 7061; 402pp; English.

The invention relates to a polynucleotide comprising an RNA sequence. The amount of RNA and/or protein production in cells used in drug development process. The present sequence represents a knock-down target sequence.

Sequence 21 BP; 4 A; 9 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 1.1%; Score 19.4; DB 1; Length 21;

Best Local Similarity 95.2%; Pred. No. 67;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

526 AAGTTCACAACTCTTCTCC 546

1 ACGTTCACAACTCTTCTCC 21

RESULT 136

AAO67148 standard; DNA; 24 BP.

AAO67148;

25-MAR-2003 (revised)

21-MAR-1995 (first entry)

Primer for amplifying HTLV envelope coding region.

Immunisation; vaccine; therapy; prophylaxis; defective gene;

non-functional gene; template; antisense; ribozyme; bupivacaine; HTLV;

human T-cell lymphotropic virus; ss.

Synthetic.

WO9416737-A1.

04-AUG-1994.

26-JAN-1994; 94WO-US000899.

26-JAN-1993; 93US-00008342.

11-MAR-1993; 93US-00029336.

15-JUL-1993; 93US-00093235.

21-SEP-1993; 93US-00124962.

21-SEP-1993; 93US-00125012.

(WEIN/) WEINER D B.

(WILL/) WILLIAMS W V.

(WANG/) WANG B.

(CONE/) CONEY L R.

(MERV/) MERVA M U.

(ZURA/) ZURAWSKI V R.

Weiner DB, Williams WV, Wang B, Coney LR, Merva MU, Zurawski VR;

WPI; 1994-263787/32.

Method for introducing genetic material into cells - utilises

polynucleotide function enhancer and nucleic acid free of retroviral

particles, e.g. HIV immunisation.

Example 22; Page 54; 136pp; English.

Two primers (AAO67148, AAO67149) were used to amplify a DNA segment

encoding the entire envelope region from HTLV-1/TSP and /ATK isolates.

The genetic material can then be introduced into the cells of an

individual by (a) contacting the individual's cells with a polynucleotide

function enhancer (bupivacaine) and (b) administering to the cells the

nucleic acid molecule free of retroviral particles. Nucleic acid

molecules which are delivered to cells may serve as genetic templates for

proteins that function as prophylactic and/or therapeutic immunising

agents; replacement copies of defective, missing or non-functional genes;

genetic templates for therapeutic proteins; genetic templates for

antisense molecules or as genetic templates for ribozymes. The HTLV env

target protein is useful in the immunisation against and treatment of

infection by HTLV and T-cell lymphoma. (Updated on 25-MAR-2003 to correct

PN field.)

Sequence 24 BP; 5 A; 8 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 1.1%; Score 19.2; DB 1; Length 24;

Best Local Similarity 87.5%; Pred. No. 1e+02;

Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

885 CAGTGAATCCCCCGGAGACTCTC 908

1 CAGTGAATATCCCCGGAGACTCTC 24

RESULT 137

AAT00836 standard; DNA; 24 BP.

AAT00836;

16-MAY-1996 (first entry)

HTLV-1 strains TSP and ATK envelope coding region 5' primer.

Immunisation; disease; pathogen; genetic vaccine facilitator; saponin;

antionic lipid; lectin; oestrogen; alkyl, dimethylsulphoxide; urea; PCR;

retroviral particle; retrovirus; HIV; SIV; epitope; primer; envelope;

amplification; HTLV; lymphoma; ss.

Synthetic.

WO9526718-A1.

12-OCT-1995.

```

XX PF 30-MAR-1995; 95MO-US004071.
XX XX
PR 01-APR-1994; 94US-00221579.
XX XX
PA (APOL-) APOLLON INC.
XX XX
PI Carraro RA;
XX XX
DR WPI; 1995-358434/46.
XX XX
PT Introducing genetic material into cells of an individual - by contacting
PT the cells with a genetic vaccine facilitator and a nucleic acid molecule.
XX XX
PS Example 19; Page 50; 114pp; English.
XX XX
CC Immunisation of an individual against a disease or pathogen comprises
CC introducing genetic material (a genetic vaccine) into the cell of the
CC individual by contacting the cell with a genetic vaccine facilitator
CC (GVF) selected from anionic lipids, saponins, lectins, oestrogenic cpds.,
CC hydroxylated lower alkylys, dimethylsulphoxide (DMSO) or urea, and a
CC nucleic acid that is free of retroviral particles. The primers AAT00830-
CC 71 are used in the construction of the genetic vaccines based on sequences
CC of HIV, SIV or pathogenic bacterial epitopes. The primers AAT00836-7 were
CC used to amplify the human T-cell lymphoma virus (HTLV)-1 envelope protein
CC gene for construction of the plasmid pCISK/ATK-env. The env protein is
CC useful for immunisation against and treatment of HTLV infection and T
CC cell lymphoma
XX XX
SQ Sequence 24 BP; 5 A; 8 C; 6 G; 5 T; 0 U; 0 Other;
XX XX
Query Match 1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 885 CAGTGAATCCCCGGAGACTCCTC 908
Db 1 CAGTGAATCCCCGGAGACTCCTC 24
RESULT 139
ABSS9899/c
ID ABSS9899 standard; DNA; 19 BP.
XX XX
AC ABSS9899;
XX XX
DT 05-NOV-2002 (first entry)
XX XX
DE Human DNA representing a single nucleotide polymorphism #49.
XX XX
KW Aminopeptidase P; XPNP2; bradykinin receptor B1; ds; SNP; BDKRB1;
KW tachykinin receptor B1; TRACR1; C1 esterase inhibitor; C1NH; kallikrein 1;
KW KLK1; bradykinin receptor B2; BDKRB2; gene therapy;
KW angiotensin converting enzyme 2; ACE2; proase inhibitor 4; PI4;
KW polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
KW cardiovascular disease; angina pectoris; hypertension; heart failure;
KW myocardial infarction; ventricular hypertrophy; vascular disease;
KW aneurysm; embolism; thrombosis; coronary artery disease; angiodaema;
KW arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;
KW autoimmune disease; inflammatory arthritis; cancer; wound;
KW viral infection; bacterial infection; fungal infection; COPD;
KW chronic obstructive pulmonary disease; enterocolitis;
KW single-nucleotide polymorphism.
XX XX
OS Homo sapiens.
XX XX
PN MO200261131-A2.
XX XX
PD 08-AUG-2002.
XX XX
PF 03-DEC-2001; 2001WO-US047235.
XX XX
PR 04-DEC-2000; 2000US-0251015P.

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PR 23-JAN-2001; 2001US-0263678P.
PR 02-MAR-2001; 2001US-0273037P.
XX XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
PA (TSUC/) TSUCHIHASHI Z.
PA (HUI/L/) HUI L.
XX XX
PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;
PI Swanson BM, Powell JR;
XX XX
DR WPI; 2002-619265/66.
XX XX
PT New isolated nucleic acid with at least one polymorphic position, useful
PT for detecting, diagnosing and treating disorders such as angiodema,
PT cancer, viral, bacterial or fungal infection, cardiovascular and
PT autoimmune diseases.
XX XX
PS Disclosure; Page 653; 977pp; English.
XX XX
CC The invention relates to an isolated nucleic acid from a human gene
CC encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDKRB1),
CC tachykinin receptor B1 (TRACR1), C1 esterase inhibitor (C1NH), kallikrein
CC 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme
CC 2 (ACE2) or proase inhibitor 4 (PI4), comprising at least one
CC polymorphic position. Also included are (1) a probe that hybridises to a
CC polymorphic position as provided in the detailed summary of single
CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising
CC obtaining the sample from one or more individuals and determining the
CC nucleic acid sequence at one or more polymorphic positions in a gene
CC encoding a protein selected from the group above; (3) constructing (M2)
CC haplotypes using the genes comprising grouping at least two nucleic acids
CC; (4) identifying (M3) an individual at risk of developing a disorder
CC upon administration of an ACE inhibitor and/or vasopeptidase inhibitor
CC using the polymorphic data; (5) a library of nucleic acids, each of which
CC comprises one or more polymorphic positions within a gene encoding a
CC human protein selected from the group above; and (6) genotyping (M4) an
CC individual comprising obtaining a nucleic acid sample, determining the
CC nucleotide present in at least one polymorphic position, and comparing at
CC least one position with a known data set. The genes, (M1, M2, M3 and M4)
CC and compositions are useful for detecting, diagnosing, treating,
CC preventing various disorders such as angiodaema and diseases which
CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's
CC disease, trachomas, and cardiovascular diseases like angina pectoris,
CC hypertension, heart failure, myocardial infarction, ventricular
CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
CC artery disease, arteriosclerosis and/or atherosclerosis, and
CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory
CC arthritis, cancer, wounds, viral, bacterial or fungal infection, chronic
CC obstructive pulmonary disease (COPD) and enterocolitis (many other
CC diseases and disorders are listed in the specification). The
CC polymorphisms are also useful for chromosome identification. Antibodies
CC against the proteins may be utilised for immunophenotyping of cell lines
CC and biological samples. The present sequence represents or contains the
CC region surrounding a single-nucleotide polymorphism in one of the genes
CC encoding one of the proteins listed above
XX XX
SQ Sequence 19 BP; 6 A; 4 C; 4 G; 5 T; 0 U; 0 Other;
XX XX
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1626 TCATGCTGTGTGACTCAA 1644
Db 19 TCATGCTGTGTGACTCAA 1
RESULT 139
ABSS9963/c
ID ABSS9963 standard; DNA; 19 BP.
XX XX
AC ABSS9963;

```

XX 05-NOV-2002 (first entry)

XX Human DNA representing a single nucleotide polymorphism #113.

XX Antinopeptidase P; XPNBP2; bradykinin receptor B1; de; SNP; BDKRB1;

XX bradykinin receptor B1; TACR1; Cl esterase inhibitor; C1NH; kallikrein 1;

XX KUK1; bradykinin receptor B2; BDKRB2; gene therapy;

XX angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;

XX polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;

XX cardiovascular disease; angina pectoris; hypertension; heart failure;

XX myocardial infarction; ventricular hypertrophy; vascular disease;

XX aneurysm; embolism; thrombosis; coronary artery disease; angioedema;

XX arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;

XX autoimmune disease; inflammatory arthritis; cancer; wound;

XX viral infection; bacterial infection; fungal infection; COPD;

XX Chronic obstructive pulmonary disease; enterocolitis;

XX single-nucleotide polymorphism.

XX Homo sapiens.

XX WO200261131-A2.

XX 08-AUG-2002.

XX 03-DEC-2001; 2001WO-US047235.

XX 04-DEC-2000; 2000US-0251015P.

XX 23-JAN-2001; 2001US-0263678P.

XX 02-MAR-2001; 2001US-0273037P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX (TSUC/) TSUCHIHASHI Z.

XX (HUI/) HUI L.

XX Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;

XX Swanson BN, Powell JR;

XX WPI; 2002-619265/66.

XX New isolated nucleic acid with at least one polymorphic position, useful

XX for detecting, diagnosing and treating disorders such as angioedema,

XX cancer, viral, bacterial or fungal infection, cardiovascular and

XX autoimmune diseases.

XX Disclosure; Page 663; 977p; English.

XX The invention relates to an isolated nucleic acid from a human gene

XX encoding antinopeptidase P (XPNBP2), bradykinin receptor B1 (BDKRB1),

XX tachykinin receptor B1 (TACR1), Cl esterase inhibitor (C1NH), kallikrein

XX 1 (KUK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme

XX 2 (ACE2) or protease inhibitor 4 (P14), comprising at least one

XX polymorphic position. Also included are (1) a probe that hybridises to a

XX nucleotide position as provided in the detailed summary of single

XX nucleotide polymorphisms comprising additional 5' and 3' flanking genomic

XX sequence; (2) analysing (M1) at least one nucleic acid sample comprising

XX obtaining the sample from one or more individuals and determining the

XX nucleic acid sequence at one or more polymorphic positions in a gene

XX encoding a protein selected from the group above; (3) constructing (M2)

XX haplotypes using the genes comprising grouping at least two nucleic acids

XX; (4) identifying (M3) an individual at risk of developing a disorder

XX upon administration of an ACE inhibitor and/or vasopeptidase inhibitor

XX using the polymorphic data; (5) a library of nucleic acids, each of which

XX comprises one or more polymorphic positions within a gene encoding a

XX human protein selected from the group above; and (6) genotyping (M4) an

XX individual comprising obtaining a nucleic acid sample, determining the

XX nucleotide present in at least one polymorphic position, and comparing at

XX least one position with a known data set. The genes, (M1, M2, M3 and M4)

XX and compositions are useful for detecting, diagnosing, treating,

XX preventing various disorders such as angioedema and diseases which

XX involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's

XX disease, trachomas, and cardiovascular diseases like angina pectoris,

XX hypertension, heart failure, myocardial infarction, ventricular

CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary

CC artery disease, arteriosclerosis and/or atherosclerosis, and

CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory

CC arthritis, cancer, wounds, viral, bacterial or fungal infection. Chronic

CC obstructive pulmonary disease (COPD) and enterocolitis (many other

CC diseases and disorders are listed in the specification). The

CC polynucleotides are also useful for chromosome identification. Antibodies

CC against the proteins may be utilised for immunophenotyping of cell lines

CC and biological samples. The present sequence represents or contains the

CC region surrounding a single-nucleotide polymorphism in one of the genes

CC encoding one of the proteins listed above

XX

XX Sequence 19 BP; 4 A; 4 C; 7 G; 4 T; 0 U; 0 Other;

XX

XX Query Match 1.1%; Score 19; DB 1; Length 19;

XX Best Local Similarity 100.0%; Pred. No. 59;

XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

XX QY 1529 CCTCACACTGGGACTTGA 1547

XX Db 19 CCTCACACTGGGACTTGA 1

XX

XX RESULT 140

XX ABS59895

XX ID ABS59895 standard; DNA; 19 BP.

XX AC ABS59895;

XX XX

XX DT 05-NOV-2002 (first entry)

XX XX

XX Human DNA representing a single nucleotide polymorphism #45.

XX

XX Antinopeptidase P; XPNBP2; bradykinin receptor B1; de; SNP; BDKRB1;

XX tachykinin receptor B1; TACR1; Cl esterase inhibitor; C1NH; kallikrein 1;

XX KUK1; bradykinin receptor B2; BDKRB2; gene therapy;

XX angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;

XX polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;

XX cardiovascular disease; angina pectoris; hypertension; heart failure;

XX myocardial infarction; ventricular hypertrophy; vascular disease;

XX aneurysm; embolism; thrombosis; coronary artery disease; angioedema;

XX arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;

XX autoimmune disease; inflammatory arthritis; cancer; wound;

XX viral infection; bacterial infection; fungal infection; COPD;

XX Chronic obstructive pulmonary disease; enterocolitis;

XX single-nucleotide polymorphism.

XX

XX Homo sapiens.

XX WO200261131-A2.

XX 08-AUG-2002.

XX 03-DEC-2001; 2001WO-US047235.

XX 04-DEC-2000; 2000US-0251015P.

XX 23-JAN-2001; 2001US-0263678P.

XX 02-MAR-2001; 2001US-0273037P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX (TSUC/) TSUCHIHASHI Z.

XX (HUI/) HUI L.

XX Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;

XX Swanson BN, Powell JR;

XX WPI; 2002-619265/66.

XX New isolated nucleic acid with at least one polymorphic position, useful

XX for detecting, diagnosing and treating disorders such as angioedema,

XX cancer, viral, bacterial or fungal infection, cardiovascular and

XX autoimmune diseases.

PS Disclosure; Page 653; 977bp; English.

XX The invention relates to an isolated nucleic acid from a human gene
 CC encoding aminopeptidase P (XPNPEP2), bradykinin receptor B1 (BDRB1),
 CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein
 CC 1 (KLK1), bradykinin receptor B2 (BDRB2), angiotensin converting enzyme
 CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one
 CC polymorphic position. Also included are (1) a probe that hybridises to a
 CC polymorphic position as provided in the detailed summary of single
 CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
 CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising
 CC obtaining the sample from one or more individuals and determining the
 CC nucleic acid sequence at one or more polymorphic positions in a gene
 CC encoding a protein selected from the group above; (3) constructing (M2)
 CC haplotypes using the genes comprising grouping at least two nucleic acids
 CC ; (4) identifying (M3) an individual at risk of developing a disorder
 CC upon administration of an ACE inhibitor and/or vasopressinase inhibitor
 CC using the polymorphic data; (5) a library of nucleic acids, each of which
 CC comprises one or more polymorphic positions within a gene encoding a
 CC human protein selected from the group above; and (6) genotyping (M4) an
 CC individual comprising obtaining a nucleic acid sample, determining the
 CC nucleotide present in at least one polymorphic position, and comparing at
 CC least one position with a known data set. The genes, (M1, M2, M3 and M4)
 CC and compositions are useful for detecting, diagnosing, treating,
 CC preventing various disorders such as angioedema and diseases which
 CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's
 CC disease, trachomas, and cardiovascular diseases like angina pectoris,
 CC hypertension, heart failure, myocardial infarction, ventricular
 CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
 CC artery disease, arteriosclerosis and/or atherosclerosis, and
 CC hyperreninemic reactions, sepsis, autoimmune diseases, inflammatory
 CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic
 CC obstructive pulmonary disease (COPD) and enterocolitis (many other
 CC diseases and disorders are listed in the specification). The
 CC polymorphisms are also useful for chromosome identification. Antibodies
 CC against the proteins may be utilised for immunophenotyping of cell lines
 CC and biological samples. The present sequence represents or contains the
 CC region surrounding a single- nucleotide polymorphism in one of the genes
 CC encoding one of the proteins listed above

XX Sequence 19 BP; 3 A; 9 C; 1 G; 6 T; 0 U; 0 Other;

SQ Query Match 1.1%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 59;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 534 CAACCTCTTCCATCGCC 552
 Db 1 CAACCTCTTCCATCGCC 19

RESULT 141
 ABSS59901/c
 ID ABSS59901 standard; DNA; 19 BP.

XX
 AC ABSS59901;
 XX
 XX 05-NOV-2002 (first entry)
 XX
 XX Human DNA representing a single nucleotide polymorphism #51.

XX Aminopeptidase P, XPNPEP2; bradykinin receptor B1; de; SNP; BDRB1;
 KM tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH; Kallikrein 1;
 KM KLK1; bradykinin receptor B2; BDRB2; gene therapy;
 KM angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;
 KM polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
 KM cardiovascular disease; angina pectoris; hypertension; heart failure;
 KM myocardial infarction; ventricular hypertrophy; vascular disease;
 KM aneurysm; embolism; thrombosis; coronary artery disease; angioedema;
 KM arteriosclerosis; atherosclerosis; hyperreninemia; sepsis;
 KM autoimmune disease; inflammatory arthritis; cancer; wound;
 KM viral infection; bacterial infection; fungal infection; COPD;
 KM Chronic obstructive pulmonary disease; enterocolitis;

KM single-nucleotide polymorphism.

XX
 XX Homo sapiens.
 XX
 XX MO200261131-A2.
 XX
 XX 08-AUG-2002.
 XX
 XX 03-DEC-2001; 2001MO-US047235.
 XX
 XX 04-DEC-2000; 2000US-0251015P.
 XX 23-JAN-2001; 2001US-0263678P.
 XX 02-MAR-2001; 2001US-0273037P.
 XX
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX (TSUC/) TSUCHIHASHI Z.
 XX (HUI/) HUI L.
 XX
 XX Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;
 PI Swanson BN, Powell JR;
 XX WPI; 2002-619265/66.
 XX
 XX New isolated nucleic acid with at least one polymorphic position, useful
 PT for detecting, diagnosing and treating disorders such as angioedema,
 PT cancer, viral, bacterial or fungal infection, cardiovascular and
 PT autoimmune diseases.

PS Disclosure; Page 653; 977bp; English.

XX The invention relates to an isolated nucleic acid from a human gene
 CC encoding aminopeptidase P (XPNPEP2), bradykinin receptor B1 (BDRB1),
 CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein
 CC 1 (KLK1), bradykinin receptor B2 (BDRB2), angiotensin converting enzyme
 CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one
 CC polymorphic position. Also included are (1) a probe that hybridises to a
 CC polymorphic position as provided in the detailed summary of single
 CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
 CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising
 CC obtaining the sample from one or more individuals and determining the
 CC nucleic acid sequence at one or more polymorphic positions in a gene
 CC encoding a protein selected from the group above; (3) constructing (M2)
 CC haplotypes using the genes comprising grouping at least two nucleic acids
 CC ; (4) identifying (M3) an individual at risk of developing a disorder
 CC upon administration of an ACE inhibitor and/or vasopressinase inhibitor.
 CC using the polymorphic data; (5) a library of nucleic acids, each of which
 CC comprises one or more polymorphic positions within a gene encoding a
 CC human protein selected from the group above; and (6) genotyping (M4) an
 CC individual comprising obtaining a nucleic acid sample, determining the
 CC nucleotide present in at least one polymorphic position, and comparing at
 CC least one position with a known data set. The genes, (M1, M2, M3 and M4)
 CC and compositions are useful for detecting, diagnosing, treating,
 CC preventing various disorders such as angioedema and diseases which
 CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's
 CC disease, trachomas, and cardiovascular diseases like angina pectoris,
 CC hypertension, heart failure, myocardial infarction, ventricular
 CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
 CC artery disease, arteriosclerosis and/or atherosclerosis, and
 CC hyperreninemic reactions, sepsis, autoimmune diseases, inflammatory
 CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic
 CC obstructive pulmonary disease (COPD) and enterocolitis (many other
 CC diseases and disorders are listed in the specification). The
 CC polymorphisms are also useful for chromosome identification. Antibodies
 CC against the proteins may be utilised for immunophenotyping of cell lines
 CC and biological samples. The present sequence represents or contains the
 CC region surrounding a single- nucleotide polymorphism in one of the genes
 CC encoding one of the proteins listed above

XX Sequence 19 BP; 3 A; 3 C; 10 G; 3 T; 0 U; 0 Other;

SQ Query Match 1.1%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 59;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1335 CACACCTCTGCTGAGC 1333
 Db 19 CACACCTCTGCTGAGC 1
 RESULT 142
 ABS5959/c
 ID ABS5959 standard; DNA, 19 BP.
 AC ABS5959;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Human DNA representing a single nucleotide polymorphism #109.
 XX
 KW Aminopectidase P; XPNP2; bradykinin receptor B1; ds; SNP; BDKRB1;
 KW tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH; kallikrein 1;
 KW KUK1; bradykinin receptor B2; BDKRB2; gene therapy;
 KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;
 KW polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
 KW cardiovascular disease; angina pectoris; hypertension; heart failure;
 KW myocardial infarction; ventricular hypertrophy; vascular disease;
 KW aneurysm; embolism; thrombosis; coronary artery disease; angioedema;
 KW arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;
 KW autoimmune disease; inflammatory arthritis; cancer; wound;
 KW viral infection; bacterial infection; fungal infection; COPD;
 KW chronic obstructive pulmonary disease; enterocolitis;
 KW single-nucleotide polymorphism.
 XX
 OS Homo sapiens.
 XX
 PN WO200261131-A2.
 PD 08-AUG-2002.
 XX
 PF 03-DEC-2001; 2001WO-US047235.
 XX
 PR 04-DEC-2000; 2000US-0251015P.
 PR 23-JAN-2001; 2001US-0263678P.
 PR 02-MAR-2001; 2001US-0273037P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 PA (TSUC/) TSUCHIHASHI Z.
 PA (HUI/) HUI L.
 XX
 PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;
 PI Swanson BN, Powell JR;
 DR WPI; 2002-619265/66.
 XX
 PT New isolated nucleic acid with at least one polymorphic position, useful
 PT for detecting, diagnosing and treating disorders such as angioedema,
 PT cancer, viral, bacterial or fungal infection, cardiovascular and
 PT autoimmune diseases.
 PT
 PS Disclosure; Page 663; 977bp; English.
 XX
 XX The invention relates to an isolated nucleic acid from a human gene
 CC encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDKRB1),
 CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein
 CC 1 (KUK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme
 CC 2 (ACE2) or protease inhibitor 4 (P14), comprising at least one
 CC polymorphic position. Also included are (1) a probe that hybridises to a
 CC polymorphic position as provided in the detailed summary of single
 CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
 CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising
 CC obtaining the sample from one or more individuals and determining the
 CC nucleic acid sequence at one or more polymorphic positions in a gene
 CC encoding a protein selected from the group above; (3) constructing (M2)
 CC haplotypes using the genes comprising grouping at least two nucleic acids
 CC ; (4) identifying (M3) an individual at risk of developing a disorder
 CC upon administration of an ACE inhibitor and/or vasopeptidase inhibitor

CC using the polymorphic data; (5) a library of nucleic acids, each of which
 CC comprises one or more polymorphic positions within a gene encoding a
 CC human protein selected from the group above; and (6) genotyping (M4) an
 CC individual comprising obtaining a nucleic acid sample, determining the
 CC nucleotide present in at least one polymorphic position, and comparing at
 CC least one position with a known data set. The genes, (M1, M2, M3 and M4)
 CC and compositions are useful for detecting, diagnosing, treating,
 CC preventing various disorders such as angioedema and diseases which
 CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's
 CC disease, trachomas, and cardiovascular diseases, like angina pectoris,
 CC hypertension, heart failure, myocardial infarction, ventricular
 CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
 CC artery disease, arteriosclerosis and/or atherosclerosis, and
 CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory
 CC arthritis, cancer, wounds, viral, bacterial or fungal infection. Chronic
 CC obstructive pulmonary disease (COPD) and enterocolitis (many other
 CC diseases and disorders are listed in the specific identification. Antibodies
 CC polymorphisms are also useful for immunophenotyping of cell lines
 CC against the proteins may be utilised for sequence represents or contains the
 CC and biological samples. The present sequence represents or contains the
 CC region surrounding a single-nucleotide polymorphism in one of the genes
 CC encoding one of the proteins listed above
 XX
 SQ Sequence 19 BP; 7 A; 6 C; 5 G; 1 T; 0 U; 0 Other;
 Query Match 1.1%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 59;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 663 CTGTGTCATCTGGCTCCTG 681
 Db 19 CTGTGTCATCTGGCTCCTG 1
 RESULT 143
 ABR63901/c
 ID ABR63901 standard; DNA, 19 BP.
 XX
 AC ABR63901;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #46.
 XX
 KW Human; neurokinin receptor-1; NK-1; dermatological disorder;
 KW immune disorder; autoimmune disorder; cardiovascular disorder;
 KW vascular disorder; airway disorder; neuropathic disorder; pain;
 KW psychiatric disorder; central nervous system disorder; inflammation;
 KW respiratory condition; ophthalmic condition; intestinal condition;
 KW demyelinating disease; small cell lung cancer; depression;
 KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
 KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
 KW neuro-pathological disorder; stress; antisense; primer; ss.
 OS Homo sapiens.
 XX
 PN WO200213799-A2.
 PD 21-FEB-2002.
 XX
 PF 17-AUG-2001; 2001WO-1B001510.
 PR 18-AUG-2000; 2000US-0226086P.
 XX
 PA (UYMC-) UNIV MCGILL.
 PA Henry UL, Cahill CW, Yashpal K;
 DR WPI; 2002-241835/29.
 XX
 PT Treating pathological condition involving neurokinin receptor-1, e.g.
 PT pain or inflammation, by administering oligonucleotide or a non-
 PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic

PT pathway.
XX
XX Example 18; Page 65; 100pp; English.
XX
XX The invention relates to a method of treating a pathological condition
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)
CC receptor, especially treating, attenuating or preventing pain or
CC inflammatory condition. The method comprises administering to a mammal, a
CC compound chosen from an oligonucleotide, its analogue, and a disruptor
CC which interferes with function or production of NK-1 receptors. The
CC method is useful for treating a pathological condition characterised by
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,
CC cardiovascular, vascular disorders (e.g. migraine), allergy, neuropathic,
CC psychiatric and central nervous system disorders (e.g. anxiety,
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or
CC peripheral aspects of chronic or acute pain, and for treating,
CC attenuating or preventing pain or inflammation such as peripheral,
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or
CC pain relating to psychiatric disorders and central nervous system
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
CC in a mammal, in particular human. NK-1 receptor related disorders,
CC diseases, or pathological conditions treatable by this method include
CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and
CC Crohn's disease), cardiovascular conditions (stroke), chronic
CC gastrointestinal tract inflammation, and inflammatory diseases such as
CC inflammatory bowel diseases. Other disorders and diseases include
CC cardiovascular pathologies including stroke, chronic inflammatory
CC diseases such as rheumatoid arthritis, demyelinating diseases such as
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
CC disorders such as allergies and poison ivy, vasospastic diseases such as
CC angina, addiction disorders such as alcoholism, neurodegenerative
CC disorders such as acquired immune deficiency syndrome (AIDS) related
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
CC disorders such as peripheral neuropathy, oedema, stress related and
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
CC effectively treat chronic conditions and other pathological states
CC without the co-administration of substance P, and reduce the number of
CC activated receptors while not reducing the number of quiescent NK-1
CC receptors. Receptors not chronically stimulated are less affected,
CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1
CC receptor coding sequences and oligonucleotides of the invention
XX
SQ Sequence 19 BP; 6 A; 6 C; 2 G; 5 T; 0 U; 0 Other;
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 176 GTGTACGATGTAGGCTT 194
DB 19 GTGTACGATGTAGGCTT 1
RESULT 144
ABK63865/C
ID ABK63865 standard; DNA; 19 BP.
XX
AC ABK63865;
XX
DT 18-JUN-2002 (first entry)
XX
DE Neurokinin 1 receptor (NK-1) sense oligonucleotide #16.
XX
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;
KM immune disorder; autoimmune disorder; cardiovascular disorder;
KM vascular disorder; airway disorder; neuropathic disorder; pain;
KM psychiatric disorder; central nervous system disorder; inflammation;
KM respiratory condition; ophthalmic condition; intestinal condition;
KM demyelinating disease; small cell lung cancer; depression;
KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;

KW neuro-pathological disorder; stress; antisense; primer; ss.
XX
XX Homo sapiens.
OS
XX WC0200213799-A2.
XX
XX 21-FEB-2002.
PD
XX 17-AUG-2001; 2001WO-IB001510.
XX
XX 18-AUG-2000; 2000US-0226086P.
PR
XX (UWMC-) UNIV MCGILL.
PA
XX Henry JL, Cahill CM, Yashpal K;
XX WPI; 2002-241835/29.
DR
XX
XX
PT Treating pathological condition involving neurokinin receptor-1, e.g.
PT pain or inflammation, by administering oligonucleotide or a non-
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
PT pathway.
XX
XX Claim 24; Page 20; 100pp; English.
XX
XX The invention relates to a method of treating a pathological condition
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)
CC receptor, especially treating, attenuating or preventing pain or
CC inflammatory condition. The method comprises administering to a mammal, a
CC compound chosen from an oligonucleotide, its analogue, and a disruptor
CC which interferes with function or production of NK-1 receptors. The
CC method is useful for treating a pathological condition characterised by
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,
CC cardiovascular, vascular disorders (e.g. migraine), allergy, neuropathic,
CC psychiatric and central nervous system disorders (e.g. anxiety,
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or
CC peripheral aspects of chronic or acute pain, and for treating,
CC attenuating or preventing pain or inflammation such as peripheral,
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or
CC pain relating to psychiatric disorders and central nervous system
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
CC in a mammal, in particular human. NK-1 receptor related disorders,
CC diseases, or pathological conditions treatable by this method include
CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and
CC Crohn's disease), cardiovascular conditions (stroke), chronic
CC gastrointestinal tract inflammation, and inflammatory diseases such as
CC inflammatory bowel diseases. Other disorders and diseases include
CC cardiovascular pathologies including stroke, chronic inflammatory
CC diseases such as rheumatoid arthritis, demyelinating diseases such as
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
CC disorders such as allergies and poison ivy, vasospastic diseases such as
CC angina, addiction disorders such as alcoholism, neurodegenerative
CC disorders such as acquired immune deficiency syndrome (AIDS) related
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
CC disorders such as peripheral neuropathy, oedema, stress related and
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
CC effectively treat chronic conditions and other pathological states
CC without the co-administration of substance P, and reduce the number of
CC activated receptors while not reducing the number of quiescent NK-1
CC receptors. Receptors not chronically stimulated are less affected,
CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1
CC receptor coding sequences and oligonucleotides of the invention
XX
SQ Sequence 19 BP; 5 A; 7 C; 1 G; 6 T; 0 U; 0 Other;
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1548 AAAAGGTCAGTAGGCTT 1566
|||||

Db 19 AAAAGGTACATAGGCTT 1

RESULT 145
ABK63882/c
ID ABK63882 standard; DNA; 19 BP.
XX
XX ABK63882;
AC
AC 18-JUN-2002 (first entry)
DT
DT
DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #27.
XX
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;
KW human disorder; autoimmune disorder; cardiovascular disorder;
KW vascular disorder; airway disorder; neuropathic disorder; pain;
KW psychiatric disorder; central nervous system disorder; inflammation;
KW respiratory condition; ophthalmic condition; intestinal condition;
KW demyelinating disease; small cell lung cancer; depression;
KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
KW neuro-pathological disorder; stress; antisense; primer; ss.
XX
XX Homo sapiens.
OS
XX WO200213799-A2.
XX
XX 21-FEB-2002.
PD
XX 17-AUG-2001; 2001WO-1B001510.
XX
XX 18-AUG-2000; 2000US-0226086P.
PR
XX (UWMC-) UNIV MCGILL.
XX
XX Henry JL, Cahill CM, Yashpal K;
PI
XX WPI; 2002-241835/29.
DR
XX Treating pathological condition involving neurokinin receptor-1, e.g.
PT pain or inflammation, by administering oligonucleotide or a non-
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
PT pathway.
XX
XX Claim 24; Page 65; 100pp; English.
PS
XX The invention relates to a method of treating a pathological condition
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)
CC receptor, especially treating, attenuating or preventing pain or
CC inflammatory condition. The method comprises administering to a mammal, a
CC compound chosen from an oligonucleotide, its analogue, and a disruptor
CC which interferes with function or production of NK-1 receptors. The
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,
CC cardiovascular, vascular disorders (e.g. migraine, allergy, neuropathic,
CC psychiatric and central nervous system disorders (e.g. anxiety,
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or
CC peripheral aspects of chronic or acute pain, and for treating,
CC attenuating or preventing pain or inflammation such as peripheral
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or
CC pain relating to psychiatric disorders and central nervous system
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
CC in a mammal, in particular human, NK-1 receptor related disorders,
CC diseases, or pathological conditions treatable by this method include
CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and
CC Crohn's disease), cardiovascular conditions (stroke), chronic
CC gastrointestinal tract inflammation, and inflammatory diseases such as
CC cardiovascular pathologies including stroke, chronic inflammatory
CC diseases such as rheumatoid arthritis, demyelinating diseases such as
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity

disorders such as allergies and poison ivy, vasospastic diseases such as
CC angina, addiction disorders such as alcoholism, neurodegenerative
CC disorders such as acquired immune deficiency syndrome (AIDS) related
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
CC disorders, such as peripheral neuropathy, oedema, stress related and
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
CC effectively treat chronic conditions and other pathological states
CC without the co-administration of substance P, and reduce the number of
CC activated receptors while not reducing the number of quiescent NK-1
CC receptors. Receptors not chronically stimulated are less affected,
CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1
CC receptor coding sequences and oligonucleotides of the invention
CC
XX
SQ Sequence 19 BP; 6 A; 6 C; 2 G; 5 T; 0 U; 0 Other;
Query Match 1.1%; Score 19; DB 1; Length 19;
Best local Similarity 100.0%; Pred. No. 59;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 176 GTGTACAGTATAGGCTT 194
Db 19 GTGTACAGTATAGGCTT 1
RESULT 146
ABK63863
ID ABK63863 standard; DNA; 19 BP.
XX
XX ABK63863;
AC
XX 18-JUN-2002 (first entry)
DT
XX
DE Neurokinin 1 receptor (NK-1) sense oligonucleotide #14.
XX
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;
KW human disorder; autoimmune disorder; cardiovascular disorder;
KW immune disorder; airway disorder; neuropathic disorder; pain;
KW vascular disorder; central nervous system disorder; inflammation;
KW psychiatric disorder; ophthalmic condition; intestinal condition;
KW respiratory condition; small cell lung cancer; depression;
KW demyelinating disease; allergy; vasospastic disease; alcoholism;
KW hypersensitivity disorder; acquired immune deficiency syndrome; AIDS;
KW neurodegenerative disorder; stress; antisense; primer; ss.
KW neuro-pathological disorder; stress; antisense; primer; ss.
XX
XX Homo sapiens.
OS
XX WO200213799-A2.
XX
XX 21-FEB-2002.
PD
XX 17-AUG-2001; 2001WO-1B001510.
XX
XX 18-AUG-2000; 2000US-0226086P.
PR
XX (UWMC-) UNIV MCGILL.
XX
XX Henry JL, Cahill CM, Yashpal K;
PI
XX WPI; 2002-241835/29.
DR
XX Treating pathological condition involving neurokinin receptor-1, e.g.
PT pain or inflammation, by administering oligonucleotide or a non-
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
PT pathway.
XX
XX Claim 24; Page 20; 100pp; English.
PS
XX The invention relates to a method of treating a pathological condition
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)
CC receptor, especially treating, attenuating or preventing pain or
CC inflammatory condition. The method comprises administering to a mammal, a
CC compound chosen from an oligonucleotide, its analogue, and a disruptor
CC which interferes with function or production of NK-1 receptors. The

CC method is useful for treating a pathological condition characterised by
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,
CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,
CC psychiatric and central nervous system disorders (e.g. anxiety,
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or
CC peripheral aspects of chronic or acute pain, and for treating,
CC attenuating or preventing pain or inflammation such as peripheral,
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or
CC pain relating to psychiatric disorders and central nervous system
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
CC in a mammal, in particular human. NK-1 receptor related disorders,
CC diseases, or pathological conditions treatable by this method include
CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and
CC Crohn's disease), cardiovascular conditions (stroke), chronic
CC gastrointestinal tract inflammation, and inflammatory diseases such as
CC inflammatory bowel diseases. Other disorders and diseases include
CC cardiovascular pathologies including stroke, chronic inflammatory
CC diseases such as rheumatoid arthritis, demyelinating diseases such as
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
CC disorders such as allergies and poison ivy, vasospastic diseases such as
CC angina, addiction disorders such as alcoholism, neurodegenerative
CC disorders such as acquired immune deficiency syndrome (AIDS) related
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
CC disorders such as peripheral neuropathy, oedema, stress related and
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
CC effectively treat chronic conditions and other pathological states
CC without the co-administration of substance P, and reduce the number of
CC activated receptors while not reducing the number of quiescent NK-1
CC receptors. Receptors not chronically stimulated are less affected,
CC reducing side effects of treatment. ABR63834-ABR63906 represent NK-1
CC receptor coding sequences and oligonucleotides of the invention

XX
SQ Sequence 19 BP; 5 A; 2 C; 6 G; 6 T; 0 U; 0 Other;

XX
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 GTGTACGATGATGAGCTT 194
|||||
DB 1 GTGTACGATGATGAGCTT 19

RESULT 147
ABR63903
ID ABR63903 standard; DNA; 19 BP.
XX
AC ABR63903;
XX
DT 18-JUN-2002 (first entry)
XX
DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #48.
XX
KM Human; neurokinin receptor-1; NK-1; dermatological disorder;
KM immune disorder; autoimmune disorder; cardiovascular disorder;
KM vascular disorder; airway disorder; neuropathic disorder; pain;
KM psychiatric disorder; central nervous system disorder; inflammation;
KM respiratory condition; ophthalmic condition; intestinal condition;
KM demyelinating disease; small cell lung cancer; depression;
KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
KM neuro-pathological disorder; stress; antisense; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200213799-A2.
XX
PD 21-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-IB001510.
XX

PR 18-AUG-2000; 2000US-0226086P.
XX
XX (UTMC-) UNIV MCGILL.
XX
XX Henry JL, Cahill CM, Yaehpal K;
XX
XX WPI; 2002-241835/29.
XX
PT Treating pathological condition involving neurokinin receptor-1, e.g.
PT pain or inflammation, by administering oligonucleotide or a non-
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
PT pathway.

PS Example 18; Page 66; 100pp; English.

XX
XX The invention relates to a method of treating a pathological condition
XX characterised partially by involvement of neurokinin receptor-1 (NK-1)
XX receptor, especially treating, attenuating or preventing pain or
XX inflammatory condition. The method comprises administering to a mammal, a
XX compound chosen from an oligonucleotide, its analogue, and a disruptor
XX which interferes with function or production of NK-1 receptors. The
XX method is useful for treating a pathological condition characterised by
XX involvement of NK-1 receptor such as dermatological, immune, autoimmune,
XX cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,
XX psychiatric and central nervous system disorders (e.g. anxiety,
XX psychosis, schizophrenia), gut inflammation, arthritis, and central or
XX peripheral aspects of chronic or acute pain, and for treating,
XX attenuating or preventing pain or inflammation such as peripheral,
XX chronic, acute pain or inflammation, neuropathic pain, inflammation or
XX pain relating to psychiatric disorders and central nervous system
XX disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
XX in a mammal, in particular human. NK-1 receptor related disorders,
XX diseases, or pathological conditions treatable by this method include
XX respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
XX conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
XX (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and
XX Crohn's disease), cardiovascular conditions (stroke), chronic
XX gastrointestinal tract inflammation, and inflammatory diseases such as
XX inflammatory bowel diseases. Other disorders and diseases include
XX cardiovascular pathologies including stroke, chronic inflammatory
XX diseases such as rheumatoid arthritis, demyelinating diseases such as
XX multiple sclerosis, small cell lung cancer, depression, hypersensitivity
XX disorders such as allergies and poison ivy, vasospastic diseases such as
XX angina, addiction disorders such as alcoholism, neurodegenerative
XX disorders such as acquired immune deficiency syndrome (AIDS) related
XX dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
XX disorders such as peripheral neuropathy, oedema, stress related and
XX somatic disorders, and osteoarthritis. Antisense oligonucleotides
XX effectively treat chronic conditions and other pathological states
XX without the co-administration of substance P, and reduce the number of
XX activated receptors while not reducing the number of quiescent NK-1
XX receptors. Receptors not chronically stimulated are less affected,
XX reducing side effects of treatment. ABR63834-ABR63906 represent NK-1
XX receptor coding sequences and oligonucleotides of the invention

SO Sequence 19 BP; 6 A; 1 C; 7 G; 5 T; 0 U; 0 Other;

QY
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1548 AAAAGGTCAGTATGAGCTT 1566
|||||
DB 1 AAAAGGTCAGTATGAGCTT 19

RESULT 148
ABR63884
ID ABR63884 standard; DNA; 19 BP.
XX
XX ABR63884;
XX
DT 18-JUN-2002 (first entry)

XX Neurokinin 1 receptor (NK-1) antisense oligonucleotide #29.
DE
XX
XX Human, neurokinin receptor-1; NK-1; dermatological disorder;
KM immune disorder; autoimmune disorder; cardiovascular disorder;
KM vascular disorder; airway disorder; neuropathic disorder; pain;
KM psychiatric disorder; central nervous system disorder; inflammation;
KM respiratory condition; ophthalmic condition; intestinal condition;
KM demyelinating disease; small cell lung cancer; depression;
KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
KM neuro-pathological disorder; stress; antisense; primer; ss.
XX
XX Homo sapiens.
OS
XX WO200213799-A2.
PN
XX 21-FEB-2002.
PD
XX 17-AUG-2001; 2001WO-IB001510.
XX
XX 18-AUG-2000; 2000US-0226086P.
XX
XX (UWMC-) UNIV MCGILL.
XX
XX Henry JL, Cahill CM, Yashpal K;
PI
XX WPI; 2002-241835/29.
XX
XX Treating pathological condition involving neurokinin receptor-1, e.g.
PT pain or inflammation, by administering oligonucleotide or a non-
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
PT pathway.
XX
XX Claim 24; Page 65; 100pp; English.
PS
XX The invention relates to a method of treating a pathological condition
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)
CC receptor, especially treating, attenuating or preventing pain or
CC inflammatory condition. The method comprises administering to a mammal, a
CC compound chosen from an oligonucleotide, its analogue, and a disruptor
CC which interferes with function or production of NK-1 receptors. The
CC method is useful for treating a pathological condition characterised by
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,
CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,
CC psychiatric and central nervous system disorders (e.g. anxiety,
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or
CC peripheral aspects of chronic or acute pain, and for treating,
CC attenuating or preventing pain or inflammation such as peripheral,
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or
CC pain relating to psychiatric disorders and central nervous system
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
CC in a mammal, in particular human. NK-1 receptor related disorders,
CC diseases, or pathological conditions treatable by this method include
CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
CC (allergic dermatitis), intestinal conditions (stroke), chronic
CC (Crohn's disease), cardiovascular conditions (stroke), chronic
CC gastrointestinal tract inflammation, and inflammatory diseases such as
CC inflammatory bowel diseases. Other disorders and diseases include
CC cardiovascular pathologies including stroke, chronic inflammatory
CC diseases such as rheumatoid arthritis, demyelinating diseases such as
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
CC disorders such as allergies and poison ivy, vasospastic diseases such as
CC angina, addiction disorders such as alcoholism, neurodegenerative
CC disorders such as acquired immune deficiency syndrome (AIDS) related
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
CC disorders such as peripheral neuropathy, oedema, stress related and
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
CC effectively treat chronic conditions and other pathological states
CC without the co-administration of substance P, and reduce the number of
CC activated receptors while not reducing the number of quiescent NK-1
CC receptors. Receptors not chronically stimulated are less affected.

CC reducing side effects of treatment. ABE63834-ABE63906 represent NK-1
CC receptor coding sequences and oligonucleotides of the invention
XX
XX Sequence 19 BP; 6 A; 1 C; 7 G; 5 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.1%; Score 19; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 59;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1548 AAAAGGTCAGTATGGTT 1566
DB 1 AAAAGGTCAGTATGGTT 19
RESULT 149
ABE29146
ID ABE29146 standard; DNA; 19 BP.
XX
XX ABE29146;
AC
XX 22-SEP-2005 (first entry)
DT
XX
XX Human siRNA molecule #52.
DE
XX Cell differentiation; osteoblast; bone; short interfering RNA; siRNA;
KM gene silencing; RNA interference; osteoporosis; hypercalcaemia;
KM multiple myeloma; hyperparathyroidism; hyperthyroidism; osteopathic;
KM endocrine-gen.; antihypertoid; cardiovascular-gen.; CNS-Gen.;
KM gastrointestinal-gen.; cytostatic; ss.
XX
XX Homo sapiens.
OS
XX WO2005063983-A1.
PN
XX 14-JUL-2005.
XX
XX 29-DEC-2003; 2003WO-EP014994.
XX
XX 29-DEC-2003; 2003WO-EP014994.
XX
XX (GALA-) GALAPAGOS GENOMICS NV.
XX
XX Van Rompaey LJC, Tonne PPM, Brown RJ;
PI
XX WPI; 2005-522575/53.
XX
XX Inducing differentiation of undifferentiated mammalian cells into
PT osteoblasts, for treating e.g. osteoporosis, by contacting the cell with
PT an expression or translation inhibitory agent for a polyribonucleotide
PT encoding a polypeptide.
XX
XX Claim 9; SEQ ID NO 52; 88pp; English.
PS
XX The invention relates to a method of inducing differentiation of
CC undifferentiated mammalian cells into osteoblasts comprising inhibiting
CC the biological activity of a polypeptide, its fragments and/or
CC derivatives, comprising contacting the cell with an expression or
CC translation inhibitory agent that inhibits the expression or translation
CC in the cell of a polyribonucleotide encoding the polypeptide. The
CC invention also relates to a method of identifying a compound that induces
CC differentiation of undifferentiated mammalian cells into osteoblasts, a
CC vector comprising a nucleotide sequence of the invention, in vitro
CC production of bone tissue, osteoblast cells obtainable by the method and
CC a method of diagnosing a pathological condition involving a systemic or
CC local decrease in mean bone density or a susceptibility to the condition
CC in a subject. In the method above, the expression inhibitory agent is
CC selected from antisense RNA, a nucleic acid expressing the antisense RNA,
CC a ribozyme that cleaves the polyribonucleotide, an antisense
CC oligodeoxynucleotide, a small interfering RNA (siRNA) that is
CC sufficiently homologous to a portion of the polyribonucleotide such that
CC the siRNA is capable of inhibiting the polyribonucleotide that would
CC otherwise cause the production of the polypeptide, and an antibody
CC reactive to the polypeptide. The osteoblast cells are useful for in vitro

CC production of bone tissue. The polynucleotide or the vector is useful as
 CC a medicament or for manufacturing a medicament for the treatment of a
 CC disease involving a systemic or local decrease in mean bone density,
 CC selected from osteoporosis, hypercalcaemia, multiple myeloma,
 CC hyperparathyroidism and hyperthyroidism. The method is useful for
 CC inducing differentiation of undifferentiated mammalian cells into
 CC osteoblasts. This sequence represents a human siRNA molecule of the
 CC invention.

XX Sequence 19 BP; 2 A; 5 C; 7 G; 5 T; 0 U; 0 Other;
 SQ

Query Match 1.1%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 59;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1137 TGACAGGTTCCGCTGGGC 1155
 Db 1 TGACAGGTTCCGCTGGGC 19

RESULT 150
 AEB54827
 ID AEB54827 standard; DNA; 19 BP.
 AC AEB54827;
 XX
 XX 22-SEP-2005 (first entry)
 DT
 DE siRNA targeting human TACR1 gene SEQ ID 53.
 XX
 KM Osteoblast; differentiating; bone; gene silencing; RNA interference;
 KM siRNA; short interfering RNA; ss; osteoporosis; osteopathic;
 KM muscular-gen.; cytostatic; antiarthritis; antirheumatic;
 KM rheumatoid arthritis; periodontal disease; Paget's disease; bone disease;
 XX rheumatoid arthritis; periodontal disease; rickets; osteogenesis.
 XX Homo sapiens.
 OS
 XX
 PN WO2005063976-A2.
 XX
 PD 14-JUL-2005.
 XX
 PF 29-DEC-2004; 2004WO-EP014885.
 XX
 PR 29-DEC-2003; 2003WO-EP014994.
 XX
 XX (GALA-) GALAGAPOS GENOMICS NV.
 PA
 PI Van Rompaey LJC, Tomme PHM, Brown RJ;
 XX
 XX WPI; 2005-541824/55.
 DR
 XX
 XX
 PT Inducing differentiation of undifferentiated mammalian cells into
 PT osteoblasts, comprises contacting undifferentiated cells with inhibitors
 PT of polypeptides of isolated knock-down constructs and corresponding
 PT target gene sequences.

PS Claim 8; SEQ ID NO 53; 98bp; English.
 XX
 XX The invention relates to inducing differentiation of undifferentiated
 CC mammalian cells into osteoblasts, comprising contacting the
 CC undifferentiated cells with an inhibitor of any of the 220 polypeptides
 CC given in the specification (table 4 for overview of isolated knock-down
 CC constructs and corresponding target gene sequences), their fragments
 CC and/or derivatives. Also included are identifying a compound that induces
 CC differentiation of undifferentiated mammalian cells into osteoblasts
 CC (comprising contacting one or more compounds with a polypeptide listed in
 CC table 4 of the specification, encoded by any of the genes listed in table
 CC 4 of the specification, and/or their fragments and/or derivatives,
 CC determining the binding affinity of the compound to the polypeptide,
 CC contacting a population of undifferentiated mammalian cells with the
 CC compound that exhibits a binding affinity of at least 10 micromolar and
 CC identifying the compound that induces the differentiation of the

CC undifferentiated mammalian cells), identifying a compound or mixture of
 CC compounds that induces differentiation of undifferentiated mammalian
 CC cells into osteoblasts, a polynucleotide comprising a sequence of 17-23
 CC nucleotides homologous to a nucleotide sequence of the target genes
 CC listed in table 4 of the specification, a vector comprising a
 CC polynucleotide comprising a sequence of 17-23 nucleotides, in vitro
 CC production of bone tissue (comprising applying undifferentiated mammalian
 CC cells on a substrate to form a cellular substrate, introducing a
 CC polynucleotide comprising a sequence of 17-23 nucleotides or a vector
 CC comprising the polynucleotide to differentiate the undifferentiated cells
 CC into osteoblasts, to produce a continuous bone matrix), diagnosing a
 CC pathological condition involving a systemic or local decrease in mean
 CC bone density (or a susceptibility to the condition) in a subject (
 CC comprising determining the level of expression of a polynucleotide
 CC encoded by any of the target genes (listed in table 4 of the
 CC specification) in a biological sample and comparing the level of
 CC expression with the level of expression of the polynucleotides in a
 CC sample derived from a healthy subject, and diagnosing a pathological
 CC condition involving a systemic or local decrease in mean bone density (or
 CC a susceptibility to the condition) comprising determining the amount of
 CC polypeptide encoded by the genes. The method is useful for inducing
 CC differentiation of undifferentiated mammalian cells into osteoblasts. The
 CC vector comprising the polynucleotide is useful in medicaments for the
 CC treatment of diseases involving a systemic or local decrease in mean bone
 CC density. The method is useful for in vitro production of bone tissue and
 CC osteoblast cells, and for diagnosing a pathological condition involving a
 CC systemic or local decrease in mean bone density or a susceptibility to
 CC the condition (e.g. osteoporosis, musculoskeletal disease, Paget's
 CC disease, bone disease, rheumatoid arthritis, periodontal disease,
 CC Crohn's syndrome, rickets, opsismodysplasia, pyonodysostosis, Toulouse-
 CC Lautrec syndrome and osteogenesis). The present sequence is a siRNA
 CC (short interfering RNA) that targets the mRNA of a gene listed in table 4
 CC or 5 of the specification (genes which, when their expression is reduced,
 CC promote differentiation into osteoblasts). NOTE: The present sequence is
 CC described as an siRNA but appears as a DNA sequence.

XX
 SQ Sequence 19 BP; 2 A; 5 C; 7 G; 5 T; 0 U; 0 Other;
 QY
 Query Match 1.1%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 59;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1137 TGACAGGTTCCGCTGGGC 1155
 Db 1 TGACAGGTTCCGCTGGGC 19

RESULT 151
 AED51263/c
 ID AED51263 standard; DNA; 19 BP.
 AC AED51263;
 XX
 XX 29-DEC-2005 (first entry)
 DT
 DE Human tachykinin receptor 1 (TACR1) cDNA reverse PCR primer.
 XX
 XX Screening; diagnosis; tachykinin receptor 1; TACR1;
 KM cardiovascular disease; infection; dermatological disease;
 KM gastrointestinal disease; cancer; neoplasm; inflammation;
 KM metabolic disorder; hematological disease; respiratory disease;
 KM musculoskeletal disease; neurological disease; gynecological disorder;
 KM gynecology and obstetrics; genitourinary disease; cardiovascular-gen.;
 KM glandant; hypotensive; antimicrobial; antibacterial; fungicide; virucide;
 KM dermatological; antiproliferative; gastrointestinal-gen.; antirheumatic;
 KM cytostatic; immunosuppressive; anorectic; antidiabetic; antiinfective;
 KM respiratory-gen.; antiaspheric; muscular-gen.; osteopathic;
 KM antirheumatic; neuromuscular; nociceptive; antiparkinsonian;
 KM gynecological; antifertility; nephrotropic; metabolic; uropathic; PCR;
 KM ss; primer.
 XX
 XX Homo sapiens.
 OS

PN W02005100986-A1.
 XX 27-OCT-2005.
 PD
 XX
 PF 02-APR-2005; 2005WO-EP003465.
 XX
 PR 15-APR-2004; 2004EP-00008923.
 XX
 PA (PARB) BAYER HEALTHCARE AG.
 XX
 PI Golz S, Brueggemeier U, Geerts A;
 XX WPI; 2005-758663/77.
 DR
 XX Screening for therapeutic agents, useful for treating a disease, e.g.
 XX cardiovascular, infections, dermatological, cancer, inflammation, PT
 XX respiratory, or neurological, comprises contacting a test compound with a
 XX tachykinin receptor 1.
 PS
 XX Example 2; SEQ ID NO 4; 118bp; English.
 CC The invention relates to a method of screening for therapeutic agents
 CC useful for treating a disease, comprising contacting a test compound with
 CC a tachykinin receptor 1 (TACR1) polypeptide or polynucleotide, detecting
 CC binding of the polypeptide or polynucleotide, determining the activity of
 CC TACR1 at a certain concentration of the test compound, in the absence of
 CC the compound or in the presence of a known regulator of the TACR1
 CC polypeptide. The invention also relates to a method of diagnosing a
 CC disease in a mammal comprising determining the amount of a TACR1
 CC polynucleotide in a sample taken from the mammal and/or diseased mammals, a
 CC amount of TACR1 polynucleotide in healthy and/or diseased mammals, a
 CC pharmaceutical composition for treating diseases in a mammal comprising a
 CC TACR1 polynucleotide or polypeptide or a therapeutic agent which binds to
 CC or regulates the activity of a TACR1 polypeptide, and preparing a
 CC pharmaceutical composition useful for treating diseases in a mammal. The
 CC disease is chosen from cardiovascular diseases, infections, cancer, inflammation,
 CC dermatological diseases, gastrointestinal diseases, cancer, inflammation,
 CC metabolic disorders, hematological diseases, respiratory diseases,
 CC musculoskeletal diseases, neurological diseases, gynecological disorders
 CC and genitourinary diseases. This sequence represents a PCR primer used in
 CC expression profiling of the human TACR1 cDNA of the invention.
 CC
 XX Sequence 19 BP; 5 A; 6 C; 5 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 1.1%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 59;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 322 GCCTACACGGTCATTGTGG 340
 DB 19 GCCTACACGGTCATTGTGG 1
 RESULT 152
 AEE77699 standard; DNA; 20 BP.
 ID AEE77699;
 AC AEE77699;
 XX
 DT 09-FEB-2006 (first entry)
 XX
 DE Human dopamine receptor D2 (DRD2) DNA oligonucleotide SEQ ID NO:1320.
 XX
 KM Diagnosis; therapeutic; neurological disease; psychiatric disorder;
 KM neuropsychologic disorder; dopamine receptor D2; DRD2; ss.
 XX
 OS Homo sapiens.
 XX W02005118843-A1.
 PN
 XX 15-DEC-2005.
 PD
 XX 01-JUN-2005; 2005WO-AU000775.
 PF

XX 01-JUN-2004; 2004AU-00902919.
 XX
 XX (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
 XX
 PA Morris CP, Van Daal A, Swagell CD, Lawford BR, Young RM;
 XX WPI; 2006-047555/05.
 DR
 XX Identifying genetic profile associated with a neurological, psychiatric,
 XX or psychological condition, comprises screening individuals for a PT
 XX polymorphism in a genetic locus comprising the dopamine receptor D2 PT
 XX (DRD2) gene.
 PT
 XX Claim 31; SEQ ID NO 1320; 634bp; English.
 PS
 XX The invention relates to a method of identifying a genetic profile
 XX associated with a neurological, psychiatric or psychological condition,
 XX phenotype or state including a sub-threshold neurological, psychiatric or
 XX psychological condition, phenotype or state in an individual, comprising
 XX screening individuals for a polymorphism in a genetic locus comprising
 XX the dopamine receptor D2 (DRD2) gene. The invention also relates to a
 XX genetic mutation providing a genetic marker for a neurological,
 XX psychiatric, or psychological condition, state or phenotype in an
 XX individual, where the presence of a 957C polymorphism is indicative of a
 XX predisposition to developing a neurological, psychiatric or psychological
 XX condition, phenotype or state. The compositions and methods are useful
 XX for identifying a genetic profile associated with a neurological,
 XX psychiatric or psychological condition. The method enables clinicians to
 XX make a genetic-based diagnosis of a neurological, psychiatric or
 XX psychological condition and can thereby implement treatment or
 XX preventative or symptom-ameliorating protocols to reduce the adverse
 XX consequences of the condition. This sequence represents a human dopamine
 XX receptor D2 (DRD2) DNA oligonucleotide used in the scope of the
 XX invention.
 SQ
 Query Match 1.1%; Score 19; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 984 CATCTGCTGGCTGCCCTTC 1002
 DB 2 CATCTGCTGGCTGCCCTTC 20
 RESULT 153
 AEE77700 standard; DNA; 20 BP.
 ID AEE77700;
 AC AEE77700;
 XX
 DT 09-FEB-2006 (first entry)
 XX
 DE Human dopamine receptor D2 (DRD2) DNA oligonucleotide SEQ ID NO:1321.
 XX
 KM Diagnosis; therapeutic; neurological disease; psychiatric disorder;
 KM neuropsychologic disorder; dopamine receptor D2; DRD2; ss.
 XX
 OS Homo sapiens.
 XX W02005118843-A1.
 PN
 XX 15-DEC-2005.
 PD
 XX 01-JUN-2005; 2005WO-AU000775.
 PF
 XX 01-JUN-2004; 2004AU-00902919.
 PR
 XX (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
 PA Morris CP, Van Daal A, Swagell CD, Lawford BR, Young RM;
 XX

XX WPI; 2006-047555/05.
DR
XX
PT Identifying genetic profile associated with a neurological, psychiatric,
PT or psychological condition, comprises screening individuals for a
PT polymorphism in a genetic locus comprising the dopamine receptor D2
PT (DRD2) gene.
XX
PS Claim 31; SEQ ID NO 1321; 634pp; English.
XX
CC The invention relates to a method of identifying a genetic profile
CC associated with a neurological, psychiatric or psychological condition,
CC phenotype or state including a sub-threshold neurological, psychiatric or
CC psychological condition, phenotype or state in an individual, comprising
CC screening individuals for a polymorphism in a genetic locus comprising
CC the dopamine receptor D2 (DRD2) gene. The invention also relates to a
CC genetic mutation providing a genetic marker for a neurological,
CC psychiatric, or psychological condition, state or phenotype in an
CC individual, where the presence of a 957C polymorphism is indicative of a
CC predisposition to developing a neurological, psychiatric or psychological
CC condition, phenotype or state. The compositions and methods are useful
CC for identifying a genetic profile associated with a neurological,
CC psychiatric or psychological condition. The method enables clinicians to
CC make a genetic-based diagnosis of a neurological, psychiatric or
CC psychological condition and can thereby implement treatment or
CC preventative or symptom-ameliorating protocols to reduce the adverse
CC consequences of the condition. This sequence represents a human dopamine
CC receptor D2 (DRD2) DNA oligonucleotide used in the scope of the
CC invention.
XX
SQ Sequence 20 BP; 1 A; 8 C; 4 G; 7 T; 0 U; 0 Other;
XX
QY Query Match 1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Db 984 CATCTGCTGCTGCCCTTC 1002
1 CATCTGCTGCTGCCCTTC 19
XX
RESULT 154
AAQ47254
ID AAQ47254 standard; DNA; 20 BP.
XX
AC AAQ47254;
XX
DT 25-MAR-2003 (revised)
DT 25-JAN-1994 (first entry)
XX
XX PCR primer for amplifying tachykinin receptor specific mRNA from human
DE leukocytes.
XX
XX Polynucleotide; synthesis; solid support; ss.
XX
XX Synthetic.
XX
XX WO9315228-A1.
XX
XX 05-AUG-1993.
XX
XX 29-JAN-1993; 93WO-US001040.
XX
XX 29-JAN-1992; 92US-00827975.
XX
XX (HITB) HITACHI CHEM CO LTD.
XX (HITB) HITACHI CHEM RES CENT INC.
XX
XX Keller C, Mitsuhashi M, Akitaya T;
XX
XX WPI; 1993-258700/32.
XX
PT Prodn. of double stranded cDNA immobilised support - by binding

PT polynucleotide with sequence complementary to poly-adenylic acid tail of
PT mRNA to insol. support.
XX
XX Example 3; Page 26; 54pp; English.
XX
XX A polynucleotide is immobilised on an insoluble solid support and used to
CC synthesise de-cDNA, ss-cDNA and both sense and antisense mRNA. The
CC advantage of this system is that RNA bound to the solid support need not
CC be precipitated when changing solutions. Two primers were used to amplify
CC tachykinin receptor specific mRNA after its synthesis using the above
CC method (AAQ47254, AAQ47255). (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 U; 0 Other;
XX
QY Query Match 1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 84;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
Db 562 GCCAGTCTTACTTCATGAC 581
1 GCCAGCATCTTACTTCATGAC 20
XX
RESULT 155
AAQ55048
ID AAQ55048 standard; DNA; 20 BP.
XX
AC AAQ55048;
XX
XX 25-MAR-2003 (revised)
DT 18-JUL-1994 (first entry)
XX
XX Sequence of PCR primer no.11, which binds to transmembrane domain 6 of
DE peptide ligand receptors.
XX
XX PCR; oligo; primer; peptide ligand receptor; ss.
XX
XX Synthetic.
XX
XX EP578962-A2.
XX
XX 19-JAN-1994.
XX
XX 04-JUN-1993; 93EP-00108984.
XX
XX 17-JUL-1992; 92US-00915966.
XX
XX (AMCY) AMERICAN CYANAMID CO.
XX
XX Hadcock JR, Ozenberger BA, Pausch MH;
PI
DR WPI; 1994-017562/03.
XX
XX Isolation and identifying new receptor DNA - pref. G-protein linked
PT receptors, using PCR with new receptor specific primers.
XX
XX Claim 2; Fig 2A; 17pp; English.
XX
XX Consensus sequences are identified from nine rat gene receptors. The
CC receptors are for somatostatin, substance K, substance P, neuropeptide Y,
CC thyrotropin, HH/CG and others designated mas, mrg and rta. Four regions
CC of nucleotide sequence are found to exhibit a degree of conservation
CC significant enough to design degenerate oligo primers for PCR (see
CC AAQ55045-49). Five oligos are designed with 4- to 64-fold direct
CC degeneracy plus 5'-23% inosines. The oligos are designed to anneal
CC sequences in G protein-linked peptide receptor genes. They are used as
CC six different primer pairs for PCR using rat genomic DNA as template. All
CC six reactions produce DNA fragments of the expected size. Nucleotide
CC sequences of two of these fragments are given in AAQ55054 and AAQ55055.
XX
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 20 BP; 1 A; 5 C; 5 G; 6 T; 0 U; 3 Other;

Query Match 1.0%; Score 18.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 90;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 979 TTGCGCATCTGCTGCTGCC 998
1 TTYGYCATCTGCTGCTGCC 20
Db

RESULT 156
AAQ30793
ID AAQ30793 standard; DNA; 18 BP.
XX
AC AAQ30793;
XX
DT 25-MAR-2003 (revised)
DT 22-MAR-1993 (first entry)
XX
DE Oligo probe hsp65 to human NKIR sf C-terminal region.
XX
KW Neurokinin-1 receptor short form; arthritis; Substance P;
XX anchored polymerase chain reaction; rat NKIR; ss.
OS Synthetic.
XX
PN EP514207-A2.
XX
PD 19-NOV-1992.
XX
PF 15-MAY-1992; 92EP-00304432.
XX
PR 17-MAY-1991; 91US-00701930.
PR 17-MAY-1991; 91US-00701935.
PR 17-MAY-1991; 91US-00701937.
XX
PA (MERI) MERCK & CO INC.
PI Strader CD, Fong TM;
PI WPI; 1992-384034/47.
XX
DR
XX
PT New human neurokinin-1 receptor short form protein - useful for
PT identifying and determining substance P antagonists in arthritic
PT patients.
XX
PS Example 1; Page 8; 36pp; English.
XX
CC Double-stranded cDNA was prepared from human glioblastoma mRNA and large-
CC size cDNA was ligated to EcoRI linkers. Linker-ligated cDNA was then
CC ligated to the calf intestinal phosphatase-treated EcoRI site of the
CC vector Bluescript SK+. The ligated plasmid DNA was used as template in a
CC primary PCR amplification with human primers hsp65l and hsp652
CC (AAQ30789 and AAQ30790) and the vector-specific primer t3 (from
CC "Stratagene"). The primary PCR product was used as template for secondary
CC PCR with the human primer hsp653 (AAQ30791) and t3. The product of this
CC reaction was amplified in a tertiary PCR amplification with hsp654
CC (AAQ30792) and vector-specific primer SK (also from "Stratagene"). A
CC 400bp DNA fragment was detected which hybridised to human oligoprobe
CC hsp655 (AAQ30793). This fragment was subcloned and sequenced. It was
CC found to encode the C-terminal region of human NKIR sf and also contains
CC 3'UTR. (Updated on 25-MAR-2003 to correct PN field.)
CC
CC
SQ Sequence 18 BP; 5 A; 4 C; 3 G; 6 T; 0 U; 0 Other;
SQ

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1038 TCTTACTGGAAGAGTT 1055
1 TCTTACTGGAAGAGTT 18
Db

RESULT 157
AAQ29682
ID AAQ29682 standard; DNA; 18 BP.
XX
AC AAQ29682;
XX
DT 25-MAR-2003 (revised)
DT 15-MAR-1993 (first entry)
XX
DE hsp655 primer 950-967.
XX
KW Human; neurokinin-1 receptor; NKIR; membrane receptor; substance P;
KW neurotransmitter; polymerase chain reaction; PCR; rat NKIR; primer;
KW amplify; probe; ss.
XX
OS Homo sapiens.
XX
PN EP510878-A1.
XX
PD 28-OCT-1992.
XX
PF 16-APR-1992; 92EP-00303457.
XX
PR 25-APR-1991; 91US-00691197.
PR 25-APR-1991; 91US-00691198.
PR 25-APR-1991; 91US-00691200.
XX
PA (MERI) MERCK & CO INC.
PI Fong TM, Strader CD;
PI WPI; 1992-359073/44.
XX
DR
XX
PT New recombinant human neurokinin-1 receptor - used to detect and evaluate
PT substances that bind to substance P receptor, and to determine substance
PT P in body fluid of arthritis patients.
XX
PS Disclosure; Page 8; 35pp; English.
XX

XX The sequences given in AAQ29670-82, AAQ29783 and AAQ29746-48 are primers
CC which were used in the isolation of fragments of the human neurokinin-1
CC receptor (NKIR) cDNA. Human NKIR is a membrane receptor for the
CC neurotransmitter substance P. The primers were designed using regions of
CC the human NKIR cDNA and also regions of the rat NKIR which were thought
CC to be similar to human regions. Part of the human cDNA sequence was
CC derived by amplification using these primers. The remaining part of human
CC NKIR cDNA was obtained from a human cDNA library utilising portions of
CC PCR generated fragments as probes. See also AAQ29749. (Updated on 25-MAR-
CC 2003 to correct PN field.)
CC
SQ Sequence 18 BP; 5 A; 4 C; 3 G; 6 T; 0 U; 0 Other;
SQ

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1038 TCTTACTGGAAGAGTT 1055
1 TCTTACTGGAAGAGTT 18
Db

RESULT 158
AAT7648/C
ID AAT76448 standard; DNA; 18 BP.
XX
AC AAT76448;
XX
DT 16-SEP-1997 (first entry)
XX
DE Substance P receptor antisense oligonucleotide.
XX
KW Asthma; airway epithelium; adenosine free; cystic fibrosis;
KW

KM chronic obstructive pulmonary disease; bronchitis; ss.
XX Synthetic.
OS
XX MO9640162-A1.
PN
XX 19-DEC-1996.
PD
XX
PF 06-JUN-1996; 96MO-US009306.
XX
XX 07-JUN-1995; 95US-00474497.
PR
XX (UYEC-) UNIV EAST CAROLINA.
PA
XX Nyce JW, Metzger WJ;
PI
XX WPI; 1997-051871/05.
DR
XX
PT Treatment of airway diseases such as asthma - by topically applying
PT adenosine-free antisense oligonucleotide to airway epithelium of
PT subject.
XX
XX Example 5; Page 40; 71pp; English.
PS
XX A method for treating airway disease in a subject has been produced,
CC which involves the topical administration of an essentially adenosine
CC free antisense oligonucleotide (ON) to the airway epithelium of the
CC subject. The present sequence is an antisense oligonucleotide specific
CC for the substance P receptor. The method can be used to treat airway
CC diseases such as cystic fibrosis, asthma, chronic obstructive pulmonary
CC disease, bronchitis and other airway diseases characterised by an
CC inflammatory response. By eliminating adenosine from the antisense ON,
CC its liberation upon antisense degradation is prevented, thereby
CC preventing adenosine-induced bronchoconstriction in patients with hyper-
CC reactive airways
XX
SQ Sequence 18 BP; 0 A; 3 C; 8 G; 7 T; 0 U; 0 Other;
XX
Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 638 CAGCCACAGCCACCAAG 655
DB 18 CAGCCACAGCCACCAAG 1
XX
RESULT 159
AA54239/C
ID AA54239 standard; DNA; 18 BP.
XX
AC AA54239;
XX
DT 05-JUL-1999 (first entry)
XX
DE Substance P receptor antisense oligonucleotide fragment.
XX
KM Antisense oligonucleotide; multiple target; antisense treatment;
KM impaired respiration; inflammation; lung disease;
KM pulmonary vasoconstriction; inflammation; allergic rhinitis;
KM acute asthma; allergy; asthma; impeded respiration;
KM respiratory distress syndrome; pain; cystic fibrosis;
KM pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KM chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KM colon cancer; breast cancer; lung cancer; pancreatic cancer;
KM hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KM prostate cancer; ss.
XX
XX Synthetic.
OS
XX MO9913886-A1.
PN
XX 25-MAR-1999.
PD

XX
PF 17-SEP-1998; 98MO-US019419.
XX
XX 17-SEP-1997; 97US-0059160P.
PR
XX 09-JUN-1998; 98US-00093972.
XX
XX (UYEC-) UNIV EAST CAROLINA.
PA
XX Nyce JW;
PI
XX WPI; 1999-229400/19.
DR
XX
XX New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT vasoconstriction.
PT
XX Disclosure; Page 59; 120pp; English.
PS
XX
XX The specification describes antisense oligonucleotides (AA52869-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target genes, gene initiation
CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-
CC end and the juxta-section between coding and non-coding regions and all
CC segments of RNAs encoding proteins associated with one or more diseases,
CC conditions or mixtures. The antisense oligonucleotides may be derived
CC from sequences AA55272-74. These multiple target oligonucleotides
CC (specifically AA55180-271) can be used for the antisense treatment of
CC diseases and conditions. Typical diseases and conditions are those
CC associated with impaired respiration and inflammation, including lung
CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
CC acute asthma, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
CC disease (COPD), and cancers such as leukemia, lymphomas, carcinomas e.g.
CC colon cancer, breast cancer, lung cancer, pancreatic cancer,
CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
CC well as all types of cancers which may metastasize or have metastasized
CC to the lungs, including breast and prostate cancer
XX
SQ Sequence 18 BP; 0 A; 3 C; 8 G; 7 T; 0 U; 0 Other;
XX
Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 638 CAGCCACAGCCACCAAG 655
DB 18 CAGCCACAGCCACCAAG 1
XX
RESULT 160
AA33683/C
ID AA33683 standard; DNA; 18 BP.
XX
AC AA33683;
XX
DT 28-JUL-2000 (first entry)
XX
DE Low adenosine antisense oligonucleotide SEQ ID NO:1372.
XX
XX Human, adenosine receptor; low adenosine antisense oligonucleotide;
KM phosphorothioate; impaired respiration; inflammation; allergy;
KM allergic diseases; bronchoconstriction; inhibitor; antiinflammatory;
KM antiallergic; antisthmatic; cytosstatic; analgesic; impaired airway;
KM lung disease; ischemic condition; pulmonary vasoconstriction; asthma;
KM respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KM pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KM cancer; leukemia; lymphoma; carcinoma; metastasis; ss.
XX
XX Homo sapiens.
OS
XX MO200009525-A2.
PN
XX 24-FEB-2000.
PD

XX 03-AUG-1999; 99WO-US017712.
XX PF
XX 03-AUG-1998; 98US-0095212P.
XX PR
XX (UYEC-) UNIV EAST CAROLINA.
XX PA
XX MYCE JW;
XX PI
XX WPI; 2000-205971/18.
XX DR
XX New antisense oligonucleotides useful for treating e.g. pulmonary
XX PT vasoconstriction, inflammation, allergies, asthma, hypertension,
XX PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
XX PT cancers.
XX PS
XX Claim 18; Page 436; 1343pp; English.
XX
XX The present invention describes a new composition comprising an antisense
XX CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
XX CC nucleic acids involved in bronchoconstriction, allergies, and/or
XX CC inflammation. The ON can have antiinflammatory, antiallergic,
XX CC antiasthmatic, cytostatic and analgesic activities. The compositions are
XX CC useful for the treatment of diseases associated with inflammation
XX CC impaired airways, including lung disease and diseases whose secondary
XX CC effects afflict the lungs of a subject. They can be used for treating
XX CC e.g. ischemic conditions, pulmonary vasoconstriction, allergies, asthma,
XX CC e.g. ischemic conditions, respiratory distress syndrome, pain, cystic
XX CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
XX CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
XX CC carcinomas, and cancers which may metastasize to the lungs, including
XX CC breast and prostate cancer. The reduction of the adenine content of the
XX CC ON reduces side effects. The A-containing ONs break down with the
XX CC release of deoxyadenosine which activates adenosine receptors causing the
XX CC bronchoconstriction and inflammation. AAA32313 to AAA5312 represent the
XX CC nucleotide sequences given in the sequence listing from the present
XX CC invention, which correspond to SEQ ID NO:1 to 185, and then the last 185
XX CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
XX CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
XX CC AAA33992) are specifically claimed ONs from the present invention. N.B.
XX CC Sequences given in the disclosure of the present invention do not match
XX CC up with their corresponding SEQ ID NO: sequences given in the sequence
XX CC listing
XX
XX Sequence 18 BP; 0 A; 3 C; 8 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 18; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 74;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 638 CAGCCACAGCCACCAAG 655
XX DB 18 CAGCCACAGCCACCAAG 1
XX
XX RESULT 161
XX AAF19805/C
XX ID AAF19805 standard; DNA; 18 BP.
XX AC
XX AAF19805;
XX
XX 14-MAR-2001 (first entry)
XX
XX Human substance P receptor polynucleotide fragment #1372.
XX
XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
XX KW human; airway disorder; bronchoconstriction; lung inflammation;
XX KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
XX KW immunosuppressive; antiasthmatic; hypotensive; cytostatic;
XX KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;

KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
XX Homo sapiens.
XX OS
XX WO200062736-A2.
XX FN
XX 26-OCT-2000.
XX PD
XX 24-MAR-2000; 2000WO-US008020.
XX PF
XX 06-APR-1999; 99US-0127958P.
XX PR
XX (UYEC-) UNIV EAST CAROLINA.
XX PA (NYCE/) NYCE J W.
XX
XX MYCE JW;
XX PI
XX WPI; 2000-679539/66.
XX DR
XX Low adenosine (A) content antisense oligonucleotides which do not trigger
XX PT adenosine receptors during metabolism, useful e.g. for treating cancers
XX PT and respiratory obstructions.
XX
XX Claim 14; Page 245; 1592pp; English.
XX
XX The present invention describes low adenosine (A) content antisense
XX CC oligonucleotides and compositions (I) comprising them. In the antisense
XX CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
XX CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
XX CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
XX CC The antisense oligonucleotides and (I) can be used to down-regulate the
XX CC expression and/or activity of target polypeptides associated with
XX CC lung/respiratory disorders and malignancies, such as stimulating and
XX CC activating peptide factors and transmitters, transcription factors,
XX CC immunoglobulins and antibodies, antibody receptors, cytokines and
XX CC chemokines, endogenously produced specific and non-specific enzymes,
XX CC and binding proteins, adhesion molecules and their receptors, cytokine and
XX CC chemokine receptors, adenosine receptors, bradykinin receptors, central
XX CC nervous system (CNS) and peripheral nervous and non-nervous system
XX CC receptors, CNS and peripheral nervous and non-nervous system
XX CC transmitters, defensive, growth factors, vascotonic peptides and
XX CC receptors, binding proteins and malignancy associated proteins. The
XX CC antisense oligonucleotides may be used in this way to treat disorders
XX CC including respiratory obstruction (especially pulmonary obstruction
XX CC and/or bronchoconstriction) and/or lung inflammation, allergies and/or
XX CC surfactant hypoproduction which are associated with a disease or
XX CC condition selected from pulmonary vasoconstriction, inflammation,
XX CC allergies, asthma, impeded respiration, respiratory distress syndrome
XX CC (RDS), pain, cystic fibrosis (Cf), allergic rhinitis (AR), pulmonary
XX CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
XX CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
XX CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
XX CC fragments and antisense oligonucleotides used in the exemplification of
XX CC the present invention
XX
XX Sequence 18 BP; 0 A; 3 C; 8 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 18; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 74;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 638 CAGCCACAGCCACCAAG 655
XX DB 18 CAGCCACAGCCACCAAG 1
XX
XX RESULT 162
XX ABS61000
XX ID ABS61000 standard; DNA; 18 BP.
XX AC
XX ABS61000;
XX
XX

DT 18-JUN-2002 (first entry)
 XX Neurokinin 1 receptor (NK-1) antisense oligonucleotide #50.
 XX
 KW Human; neurokinin receptor-1; NK-1; dermatological disorder;
 KW immune disorder; autoimmune disorder; cardiovascular disorder;
 KW vascular disorder; airway disorder; neuropathic disorder; pain;
 KW psychiatric disorder; central nervous system disorder; inflammation;
 KW respiratory condition; ocular condition; intestinal condition;
 KW demyelinating disease; small cell lung cancer; depression;
 KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
 KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
 KW neuro-pathological disorder; stress; antisense; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO200213799-A2.
 XX
 PD 21-FEB-2002.
 XX
 PE 17-AUG-2001; 2001WO-1B001510.
 XX
 PR 18-AUG-2000; 2000US-0226086P.
 XX
 PA (UYMC-) UNIV MCGILL.
 XX
 PI Henry JL, Cahill CM, Yashpal K;
 XX
 DR WPI; 2002-241835/29.
 XX
 PT Treating pathological condition involving neurokinin receptor-1, e.g.
 PT pain or inflammation, by administering oligonucleotide or a non-
 PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
 PT pathway.
 XX
 PS Example 18; Page 66; 100pp; English.
 XX
 CC The invention relates to a method of treating a pathological condition
 CC characterised partially by involvement of neurokinin receptor-1 (NK-1)
 CC receptor, especially treating, attenuating or preventing pain or
 CC inflammatory condition. The method comprises administering to a mammal, a
 CC compound chosen from an oligonucleotide, its analogue, and a disruptor
 CC which interferes with function or production of NK-1 receptors. The
 CC method is useful for treating a pathological condition characterised by
 CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,
 CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,
 CC psychiatric and central nervous system disorders (e.g. anxiety,
 CC psychosis, schizophrenia), gut inflammation, arthritis, and central or
 CC peripheral aspects of chronic or acute pain, and for treating,
 CC attenuating or preventing pain or inflammation such as peripheral,
 CC chronic, acute pain or inflammation, neuropathic pain, inflammation or
 CC pain relating to psychiatric disorders and central nervous system
 CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
 CC in a mammal, in particular human. NK-1 receptor related disorders,
 CC diseases, or pathological conditions treatable by this method include
 CC respiratory conditions (e.g. asthma, allergic rhinitis), ocular
 CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
 CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and
 CC Crohn's disease), cardiovascular conditions (stroke), chronic
 CC gastrointestinal tract inflammation, and inflammatory diseases such as
 CC inflammatory bowel diseases. Other disorders and diseases include
 CC cardiovascular pathologies including stroke, chronic inflammatory
 CC diseases such as rheumatoid arthritis, demyelinating diseases such as
 CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
 CC disorders such as allergies and poison ivy, vasospastic diseases such as
 CC angina, addiction disorders such as alcoholism, neurodegenerative
 CC disorders such as acquired immune deficiency syndrome (AIDS) related
 CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
 CC disorders such as peripheral neuropathy, oedema, stress related and
 CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
 CC effectively treat chronic conditions and other pathological states
 CC without the co-administration of substance P, and reduce the number of
 CC activated receptors while not reducing the number of quiescent NK-1

CC receptors. Receptors not chronically stimulated are less affected.
 CC reducing side effects of treatment. ABK63874-ABK63906 represent NK-1
 CC receptor coding sequences and oligonucleotides of the invention
 XX
 SQ Sequence 18 BP; 6 A; 3 C; 4 G; 5 T; 0 U; 0 Other;
 CC
 CC Query Match 1.0%; Score 18; DB 1; Length 18;
 CC Best Local Similarity 100.0%; Pred. No. 74;
 CC Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC 1038 TCTTACCTGAGAGATT 1055
 CC |||||
 CC Db 18 TCTTACCTGAGAGATT 1
 CC
 CC RESULT 166
 CC ABK63867
 CC ID ABK63867 standard; DNA; 18 BP.
 CC XX
 CC AC ABK63867;
 CC XX
 CC DT 18-JUN-2002 (first entry)
 CC XX
 CC DE Neurokinin 1 receptor (NK-1) sense oligonucleotide #18.
 CC XX
 KW Human; neurokinin receptor-1; NK-1; dermatological disorder;
 KW immune disorder; autoimmune disorder; cardiovascular disorder;
 KW vascular disorder; airway disorder; neuropathic disorder; pain;
 KW psychiatric disorder; central nervous system disorder; inflammation;
 KW respiratory condition; ocular condition; intestinal condition;
 KW demyelinating disease; small cell lung cancer; depression;
 KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
 KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
 KW neuro-pathological disorder; stress; antisense; primer; ss.
 KW
 XX
 OS Homo sapiens.
 XX
 PN MO200213799-A2.
 XX
 PD 21-FEB-2002.
 XX
 PE 17-AUG-2001; 2001WO-1B001510.
 XX
 PR 18-AUG-2000; 2000US-0226086P.
 XX
 PA (UYMC-) UNIV MCGILL.
 XX
 PI Henry JL, Cahill CM, Yashpal K;
 XX
 DR WPI; 2002-241835/29.
 XX
 PT Treating pathological condition involving neurokinin receptor-1, e.g.
 PT pain or inflammation, by administering oligonucleotide or a non-
 PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
 PT pathway.
 XX
 PS Claim 24; Page 20; 100pp; English.
 XX
 CC The invention relates to a method of treating a pathological condition
 CC characterised partially by involvement of neurokinin receptor-1 (NK-1)
 CC receptor, especially treating, attenuating or preventing pain or
 CC inflammatory condition. The method comprises administering to a mammal, a
 CC compound chosen from an oligonucleotide, its analogue, and a disruptor
 CC which interferes with function or production of NK-1 receptors. The
 CC method is useful for treating a pathological condition characterised by
 CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,
 CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,
 CC psychiatric and central nervous system disorders (e.g. anxiety,
 CC psychosis, schizophrenia), gut inflammation, arthritis, and central or
 CC peripheral aspects of chronic or acute pain, and for treating,
 CC attenuating or preventing pain or inflammation such as peripheral,
 CC chronic, acute pain or inflammation, neuropathic pain, inflammation or
 CC pain relating to psychiatric disorders and central nervous system

disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
 CC in a mammal, in particular human. NK-1 receptor related disorders,
 CC diseases, or pathological conditions treatable by this method include
 CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
 CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
 CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and
 CC Crohn's disease), cardiovascular conditions (stroke), chronic
 CC gastrointestinal tract inflammation, and inflammatory diseases such as
 CC inflammatory bowel diseases. Other disorders and diseases include
 CC cardiovascular pathologies including stroke, chronic inflammatory
 CC diseases such as rheumatoid arthritis, demyelinating diseases such as
 CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
 CC disorders such as allergies and poison ivy, vasospastic diseases such as
 CC angina, addiction disorders such as alcoholism, neurodegenerative
 CC disorders such as acquired immune deficiency syndrome (AIDS) related
 CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
 CC disorders such as peripheral neuropathy, oedema, stress related and
 CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
 CC effectively treat chronic conditions and other pathological states
 CC without the co-administration of substance P, and reduce the number of
 CC activated receptors while not reducing the number of quiescent NK-1
 CC receptors. Receptors not chronically stimulated are less affected.
 CC reducing side effects of treatment. ABK6384-ABK63906 represent NK-1
 CC receptor coding sequences and oligonucleotides of the invention

Sequence 18 BP; 5 A; 4 C; 3 G; 6 T; 0 U; 0 Other;
 Query Match 1.0%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1038 TCTTACTGAGAGAGTT 1055
 1 TCTTACTGAGAGAGTT 18

RESULT 167
 ABT16451/c
 ID ABT16451 standard; DNA; 18 BP.

AC ABT16451;
 XX 20-MAR-2003 (first entry)
 DT Human neurokinin 1 receptor gene related PCR primer SEQ ID No 32.

XX Cytostatic; antispasmodic; antiinflammatory; cardiant; polymorphic site;
 KW human neurokinin 1 receptor; TACR1; disease phenotype; forensics;
 KW TACR1 ligand mediated disease; asthma; paternity testing; cancer;
 KW inflammation; heart disease; central nervous system; infection; PCR;
 KW primer; ss.

OS Unidentified.

PN BP1262565-A2.

PD 04-DEC-2002.

PF 23-MAY-2002; 2002EP-00253662.

PR 25-MAY-2001; 2001US-0293425P.

PA (PFIZ) PFIZER PROD INC.

PI Affourtit JP, Nelson DL, Seymour AB, Webb SM;

DR WPI; 2003-150228/15.

PT Novel nucleic acid segment from human neurokinin 1 receptor, including
 PT polymorphic sites for diagnosing and treating asthma, and in forensics,
 PT paternity testing, and genetic mapping of the traits.

PS Example; Page 12; 27pp; English.

XX The invention relates to a nucleic acid segment from the human neurokinin
 CC 1 receptor (TACR1) gene of 10-100 nucleotides comprising a fragment
 CC having a polymorphic site or a complement of the fragment. The TACR1
 CC segment is useful for analysing a nucleic acid, by obtaining any one of
 CC acid from an individual, and determining the base occupying any one of
 CC the polymorphic sites in the segment. The nucleic acid is obtained from
 CC several individuals, and the base occupying one of the polymorphic sites
 CC is determined in each of the individuals, and further involves testing
 CC each of the individuals for the presence of a disease phenotype, and
 CC correlating the presence with the base. The TACR1 segment is useful for
 CC diagnosing and treating TACR1 ligand mediated diseases, such as asthma.
 CC The TACR1 segment is also useful in forensics, paternity testing,
 CC correlating polymorphisms with phenotypic traits, and genetic mapping of
 CC phenotypic traits. The TACR1 segment is useful in diagnosing and
 CC monitoring of diseases such as cancer, inflammation, heart disease,
 CC diseases of central nervous system, and susceptibility to infection to
 CC microorganisms. The TACR1 segment is also useful in the manufacture of a
 CC medicament for the treatment of the diseases. This polynucleotide
 CC sequence represents a PCR primer of the human neurokinin 1 receptor
 CC (TACR1) gene of the invention

Sequence 18 BP; 5 A; 3 C; 6 G; 4 T; 0 U; 0 Other;
 Query Match 1.0%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 CGCCAGTTCAGCTTCCA 75
 18 CGCCAGTTCAGCTTCCA 1

RESULT 168
 ABZ95499/c
 ID ABZ95499 standard; DNA; 18 BP.

AC ABZ95499;
 XX 17-OCT-2003 (first entry)
 DT Human substance P receptor antisense fragment no.1363.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquitine; antiinflammatory; antiallergic;
 KW antispasmodic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

OS Homo sapiens.

PN WO200285308-A2.

PD 31-OCT-2002.

PF 23-APR-2002; 2002WO-US013135.

PR 24-APR-2001; 2001US-0286137P.

PA (EPIG-) EPIGENESIS PHARM INC.

PI NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;

DR WPI; 2003-229219/22.

PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquitine.

PS Disclosure; SEQ ID NO 10741; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to, adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 18 BP; 0 A; 3 C; 8 G; 7 T; 0 U; 0 Other;
Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 638 CAGCCACAGCCACCAAG 655
18 CAGCCACAGCCACCAAG 1

Db

RESULT 169
ABD19638/C
ID ABD19638 standard; DNA; 18 BP.
XX
AC ABD19638;
XX
DT 29-JUN-2004 (first entry)
XX
DE Human substance P receptor DNA fragment 1363.
XX
XX Human: antisense; bronchoconstriction; allergy; hyposecretion; pain;
KM respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KM surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KM analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KM beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KM respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KM emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KM pulmonary transplantation rejection; ds.
XX
XX Homo sapiens.
OS
XX W020285309-A2.
PN
XX 31-OCT-2002.
PD
XX 23-APR-2002; 2002WO-US013143.
PF
XX 24-APR-2001; 2001US-0286036P.
PR
XX (EPIC-) EPIDEMESIS PHARM INC.
PA
XX Myce JW, Li Y, Sandrasagra A, Katz E, Fabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S,
XX
XX WPI; 2003-093058/08.
DR
XX
XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.

XX Claim 15; SEQ ID NO 10741; 763pp; English.
PS
XX This invention describes a novel composition (a) a first active agent,
XX comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, allergies and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX

SQ Sequence 18 BP; 0 A; 3 C; 8 G; 7 T; 0 U; 0 Other;
Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 638 CAGCCACAGCCACCAAG 655
18 CAGCCACAGCCACCAAG 1

Db

RESULT 170
AEE77698
ID AEE77698 standard; DNA; 20 BP.
XX
AC AEE77698;
XX
XX 09-FEB-2006 (first entry)
DT
XX
XX Human dopamine receptor D2 (DRD2) DNA oligonucleotide SEQ ID NO:1319.
DE
XX
XX Diagnosis; therapeutic; neurological disease; psychiatric disorder;
KM neuropsychologic disorder; dopamine receptor D2; DRD2; ss.
KM
XX
XX Homo sapiens.
OS
XX W02005118843-A1.
PN
XX 15-DEC-2005.
PD
XX 01-JUN-2005; 2005WO-AU000775.
PF
XX 01-JUN-2004; 2004AU-00902919.
PR
XX (UYGU-) UNIV QUEENSLAND TECHNOLOGY.
PA
XX Morris CP, Van Daal A, Swagell CD, Lawford BR, Young RM;
PI
XX WPI; 2006-047555/05.
DR
XX

XX Identifying genetic profile associated with a neurological, psychiatric,
PT or psychological condition, comprises screening individuals for a
PT polymorphism in a genetic locus comprising the dopamine receptor D2
PT (DRD2) gene.
XX
XX
PS Claim 31; SEQ ID NO 1319; 634bp; English.
XX
XX The invention relates to a method of identifying a genetic profile
CC associated with a neurological, psychiatric or psychological condition,
CC phenotype or state including a sub-threshold neurological, psychiatric or
CC psychological condition, phenotype or state in an individual, comprising
CC screening individuals for a polymorphism in a genetic locus comprising
CC the dopamine receptor D2 (DRD2) gene. The invention also relates to a
CC genetic mutation providing a genetic marker for a neurological,
CC psychiatric, or psychological condition, state or phenotype in an
CC individual, where the presence of a 957c polymorphism is indicative of a
CC predisposition to developing a neurological, psychiatric or psychological
CC condition, phenotype or state. The compositions and methods are useful
CC for identifying a genetic profile associated with a neurological,
CC psychiatric or psychological condition. The method enables clinicians to
CC make a genetic-based diagnosis of a neurological, psychiatric or
CC psychological condition and can thereby implement treatment or
CC preventative or symptom-ameliorating protocols to reduce the adverse
CC consequences of the condition. This sequence represents a human dopamine
CC receptor D2 (DRD2) DNA oligonucleotide used in the scope of the
CC invention.
XX
SQ Sequence 20 BP; 2 A; 7 C; 4 G; 7 T; 0 U; 0 Other;
XX
Query Match 1.0%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 984 CATCTGCTGCTGCCCTT 1001
DB 3 CATCTGCTGCTGCCCTT 20
XX
RESULT 171
AEE77701 AEE77701 standard; DNA; 20 BP.
XX
AC AEE77701;
XX
DT 09-FEB-2006 (first entry)
XX
XX Human dopamine receptor D2 (DRD2) DNA oligonucleotide SEQ ID NO:1322.
XX
XX Diagnosis; therapeutic; neurological disease; psychiatric disorder;
XX neuropsychologic disorder; dopamine receptor D2; DRD2; ss.
XX
XX Homo sapiens.
XX
XX WO2005118843-A1.
XX
XX 15-DEC-2005.
XX
XX 01-JUN-2005; 2005WO-AU000775.
XX
XX 01-JUN-2004; 2004AU-00902919.
XX
XX (UYOU-) UNIV QUEENSLAND TECHNOLOGY.
XX
XX Morris CP, Van Daal A, Swagell CD, Lawford BR, Young RM;
XX
XX MPI; 2006-047555/05.
XX
XX Identifying genetic profile associated with a neurological, psychiatric,
PT or psychological condition, comprises screening individuals for a
PT polymorphism in a genetic locus comprising the dopamine receptor D2
PT (DRD2) gene.
XX

PS Claim 31; SEQ ID NO 1322; 634bp; English.
XX
XX The invention relates to a method of identifying a genetic profile
CC associated with a neurological, psychiatric or psychological condition,
CC phenotype or state including a sub-threshold neurological, psychiatric or
CC psychological condition, phenotype or state in an individual, comprising
CC screening individuals for a polymorphism in a genetic locus comprising
CC the dopamine receptor D2 (DRD2) gene. The invention also relates to a
CC genetic mutation providing a genetic marker for a neurological,
CC psychiatric, or psychological condition, state or phenotype in an
CC individual, where the presence of a 957c polymorphism is indicative of a
CC predisposition to developing a neurological, psychiatric or psychological
CC condition, phenotype or state. The compositions and methods are useful
CC for identifying a genetic profile associated with a neurological,
CC psychiatric or psychological condition. The method enables clinicians to
CC make a genetic-based diagnosis of a neurological, psychiatric or
CC psychological condition and can thereby implement treatment or
CC preventative or symptom-ameliorating protocols to reduce the adverse
CC consequences of the condition. This sequence represents a human dopamine
CC receptor D2 (DRD2) DNA oligonucleotide used in the scope of the
CC invention.
XX
SQ Sequence 20 BP; 1 A; 7 C; 4 G; 8 T; 0 U; 0 Other;
XX
Query Match 1.0%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 985 ATCTGCTGCTGCCCTTC 1002
DB 1 ATCTGCTGCTGCCCTTC 18
XX
RESULT 172
ABS61085 ABS61085 standard; DNA; 22 BP.
XX
AC ABS61085;
XX
DT 05-NOV-2002 (first entry)
XX
XX Human automated genomic bit analysis (GBA) PCR primer #62.
XX
DE Human; ss; aminopeptidase P; XPNP2; bradykinin receptor B1; primer;
XX
XX BDKRB1; tachykinin receptor B1; TACR1; Cl esterase inhibitor; CLNH;
XX
XX kallikrein 1; KLK1; bradykinin receptor B2; BDKRB2; gene therapy;
XX
XX angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;
XX
XX polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
XX
XX cardiovascular disease; ventricular hypertrophy; vascular disease;
XX
XX myocardial infarction; angina pectoris; hypertension; angioedema;
XX
XX aneurysm; embolism; thrombosis; coronary artery disease; sepsis;
XX
XX arteriosclerosis; atherosclerosis; hypersensitivity; wound; genotyping;
XX
XX autoimmune disease; inflammatory arthritis; cancer; viral infection;
XX
XX viral infection; bacterial infection; fungal infection; COPD; GBA;
XX
XX chronic obstructive pulmonary disease; enterocolitis;
XX
XX automated genetic bit analysis.
XX
XX Homo sapiens.
XX
XX WO200261131-A2.
XX
XX 08-AUG-2002.
XX
XX 03-DEC-2001; 2001WO-US047235.
XX
XX 04-DEC-2000; 2000US-0251015P.
XX
XX 23-JAN-2001; 2001US-0263678P.
XX
XX 02-MAR-2001; 2001US-0273037P.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
XX (TSUC/) TSUCHIHASHI Z.
XX
XX (HUI/) HUI L.

PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH,
PI Swanson BN, Powell JR,
XX
DR WPI: 2002-619265/66.
XX
XX New isolated nucleic acid with at least one polymorphic position, useful
PT for detecting, diagnosing and treating disorders such as angioedema,
PT cancer, viral, bacterial or fungal infection, cardiovascular and
PT autoimmune diseases.

Example 3; Page 931; 977pp; English.

The invention relates to an isolated nucleic acid from a human gene encoding aminopeptidase P (XPNPEP2), bradykinin receptor B1 (BDKBR1), tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein 1 (KLK1), bradykinin receptor B2 (BDKBR2), angiotensin converting enzyme 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one polymorphic position. Also included are (1) a probe that hybridises to a polymorphic position as provided in the detailed summary of single nucleotide polymorphisms comprising additional 5' and 3' flanking genomic sequence; (2) analysing (M1) at least one nucleic acid sample comprising obtaining the sample from one or more individuals and determining the nucleic acid sequence at one or more polymorphic positions in a gene encoding a protein selected from the group above; (3) constructing (M2) haplotypes using the genes comprising grouping at least two nucleic acids; (4) identifying (M3) an individual at risk of developing a disorder upon administration of an ACE inhibitor and/or vasopressinase inhibitor using the polymorphic data; (5) a library of nucleic acids, each of which comprises one or more polymorphic positions within a gene encoding a human protein selected from the group above; and (6) genotyping (M4) an individual comprising obtaining a nucleic acid sample, determining the nucleotide present in at least one polymorphic position, and comparing at least one position with a known data set. The genes, (M1, M2, M3 and M4) and compositions are useful for detecting, diagnosing, treating, preventing various disorders such as angioedema and diseases which involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's disease, trachomas, and cardiovascular diseases like angina pectoris, hypertension, heart failure, myocardial infarction, ventricular hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary artery disease, arteriosclerosis and/or atherosclerosis, and hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic obstructive pulmonary disease (COPD) and enterocolitis (many other diseases and disorders are listed in the specification). The polymucleotides are also useful for chromosome identification. Antibodies against the proteins may be utilised for immunophenotyping of cell lines and biological samples. The present sequence is a genotyping PCR primer for the gene encoding one of the proteins listed above, using the method of automated genetic bit analysis, GBA

Query Match	1.0%	Score 18,	DB 1,	Length 22,
Best Local Similarity	94.7%	Pred. NO. 1.2e-02,		
Matches 18:	Conservative	0;	Mismatches 1;	Indels 0;
			Gaps 0;	
SQ Sequence 22 BP; 5 A; 7 C; 4 G; 5 T; 0 U; 1 Other;				

```

QY      1681 AGTCGACCACTTTTCC 1699
          |||||
Db      1 AGTCGACCACTTTTCC 19

```

RESULT 173
ABT40254/c
ID ABT40254 standard; DNA; 21 BP.

AC ABT40254;

DT 12-JUN-2003 (first entry)

Human Chem23 PCR primer SEQ ID No 44.

KM Cytostatic; antiinflammatory; immunosuppressive; osteopathic; virucide;
KM antiparasitic; dermatological; antibacterial; antihelminthic; ChemR23;
KM antiparasitic; dermatological; antibacterial; antihelminthic; ChemR23;

gynaecological; G-Protein-Agonist; G-Protein-Antagonist; gene therapy; orphan G-protein coupled receptor; casareus-induced gene 2; rtg2; modulator; cancer; tumour metastasis; inflammatory disease; inherited; autoimmune disease; AIDS; osteoporosis; bone healing; bone tissue graft; graft rejection; psoriasis; eczema; inflammatory infection; bacterial; trophic diseases; skin; viral; parasitic infection; female infertility; ovarian; uterine tumour; PCR; primer; ss.

OS	Homo sapiens.
XX	
PN	WO2003006996-A2.

PD 23-JAN-2003

09-JUL-2002; 2002WO-EP007647.

09-JUL-2001; 2001US-0303858P.

PR 13-JUL-2001; 2001US-00905253.

PA (EURO-) EUROSCREEN SA.

PI	Wiltamer V, Communi D, Vandenbergaeerde A, Detheux M, Parmentier M,
XX	WPI; 2003-221782/21.
DR	

PT Identifying an agent that modulates ChemR23 polypeptide using TIG2 gene
PT useful for the preparation of a medicament for the treatment of
PT disorders, such as cancer, inflammatory and autoimmune diseases,
PT osteoporosis and psoriasis.

PS Example 10; Page 60; 99pp; English.

CC The invention relates to a novel method for identifying an agent that
CC modulates the function of an orphan G-protein coupled receptor, ChemR23.
CC The identification comprises contacting a ChemR23 polypeptide with a
CC tazarotene-induced gene 2 (TIG2) polypeptide in the presence and absence
CC of a candidate modulator to permit the binding of the TIG2 polypeptide to
CC the ChemR23 polypeptide, and measuring the binding of the ChemR23 to the
CC TIG2 polypeptide, where a decrease in the presence of the candidate
CC modulator, identifies the modulator as an agent that modulates the
CC function of ChemR23. The agent or composition is useful for the
CC preparation of a medicament for the treatment of a ChemR23- or TIG2-
CC related disease or disorder, such as cancer, tumour metastasis,
CC inflammatory disease, autoimmune disease, inherited or acquired immune
CC deficiencies, osteoporosis, bone healing, bone tissue grafts, graft
CC rejection, psoriasis, eczema, inflammatory infection, trophic diseases of
CC skin, viral, bacterial and parasitic infections, female infertility and
CC ovarian and uterine tumours. The truncated or full-length TIG2
CC polypeptide is useful for the production of a composition of an isolated
CC ChemR23 or TIG2 polypeptide, and/or for the production of a kit for
CC screening agents that modulate the signalling of ChemR23, and/or ligand
CC for ChemR23. This sequence represents a PCR primer used in the
CC exemplification of the invention

Sequence 21 BP; 9 A; 5 C; 6 G; 1 T; 0 U; 0 Other;

Query Match	1.0%	Score 17.8	DB 1	Length 21
Best Local Similarity	90.5%	Pred. No. 1.2e+02		
Matches 19	Conservative 0	Mismatches 2	Indels 0	Gaps 0

QY	669	CATCTGGGTCCTGGCTCTCCT	685
Db	21	CATCTGGGTCCTGGCTTCTT	1

RESULT 174
ADW43814/C
ID ADW43814 standard; DNA; 21 BP.

AC ADW43814;

DT 24-MAR-2005 (first entry)
XX

DE Human chemerin RT-PCR primer SEQ ID NO 38.
 XX gene therapy; diagnosis; cell signaling; gene therapy;
 KW lymphoproliferative disease; dermatological disease; dermatological;
 KW hemostatic; inflammation; antinflammatory; hematological disease;
 KW immune disorder; neoplasm; cardiovascular-gen.; cns-gen.;
 KW neurological disease; hyperproliferative disorders; cytostatic;
 KW chemerin; reverse transcriptase PCR; RT-PCR; primer; ss.
 XX Homo sapiens.
 XX WO200500875-A2.
 XX 06-JAN-2005.
 XX 25-JUN-2004; 2004WO-EP006945.
 XX 25-JUN-2003; 2003US-00603566.
 XX (EURO-) EUROSCREEN SA.
 XX Wiltamer V, Communi D, Detheux M, Parmentier M, Loison C;
 XX Ooms FDR;
 XX WPI; 2005-058121/06.
 XX
 XX New Chemerin polypeptides, useful for diagnosing and treating a disease,
 PT e.g. neoplasms, hypergammaglobulinemia, paraproteinemia, purpura,
 PT sarcoidosis, Sezary Syndrome, Waldenstrom's Macroglobulinemia, Gaucher's
 PT disease, or histiocytosis.
 XX
 XX Example 6; SEQ ID NO 38; 183bp; English.
 PS
 XX The invention describes a polypeptide (I) of up to 50 amino acids where
 XX the polypeptide binds specifically to a chemerin polypeptide. Also
 CC described are: a nucleic acid sequence encoding (I); an expression vector
 CC comprising the coding sequence of the nucleic acid; a transgenic animal
 CC transfected with the expression vector; a (therapeutic) composition
 CC comprising (I) and an isolated Chemerin polypeptide or a nucleic acid
 CC sequence of (I); an antibody that selectively binds to (I); identifying
 CC an agent that modulates the interaction between a Chemerin polypeptide and
 CC a Chemerin polypeptide; detecting the presence, in a sample, of an
 CC agent that modulates the interaction between a Chemerin polypeptide and a
 CC Chemerin polypeptide; in a sample; identifying an agent that modulates
 CC the function of Chemerin polypeptide; detecting the presence, in a
 CC sample, of an agent that modulates the function of Chemerin polypeptide;
 CC diagnosing a disease or disorder characterized by dysregulation of
 CC chemerin (polypeptide) signaling; a kit, for screening agents that
 CC modulate the signaling activity of Chemerin polypeptide or for
 CC diagnosing a disease or disorder characterized by dysregulation of
 CC Chemerin polypeptide signaling, comprising an isolated Chemerin
 CC polypeptide, (I), an isolated polynucleotide encoding (I), a cell
 CC transfected with a polynucleotide encoding (I), and its packaging
 CC materials; a non-human mammal transgenic for a Chemerin polynucleotide
 CC encoding (I); identifying an antibody inhibiting Chemerin activation;
 CC and an in vitro method of inhibiting cell proliferation. The
 CC (therapeutic) composition or expression vector is useful for preparing a
 CC medicament for ex vivo gene therapy or for in vivo gene therapy or a
 CC medicament for inhibiting cell proliferation, where the medicament is
 CC used for treating a disease, e.g. neoplasms, hypergammaglobulinemia,
 CC lymphoproliferative diseases, disorders, and/or conditions,
 CC paraproteinemia, purpura, sarcoidosis, Sezary Syndrome, Waldenstrom's
 CC Macroglobulinemia, Gaucher's disease, histiocytosis, and any other
 CC hyperproliferative disease. The polypeptides and polynucleotides and
 CC methods are useful for diagnosing and treating the cited diseases. This
 CC sequence represents a reverse transcriptase PCR primer used in an
 CC analysis of human chemerin receptor (chemerin) expression by quantitative
 CC RT-PCR.
 XX
 XX Sequence 21 BP; 9 A; 5 C; 6 G; 1 T; 0 U; 0 Other;
 XX
 XX Query Match 1.0%; Score 17.8; DB 1; Length 21;
 XX Best Local Similarity 90.5%; Pred. No. 1.2e+02;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 669 CATCGGATCCTGCTCCT 689
 Db 21 CATCGGATCCTGCTTCTT 1
 RESULT 175
 AAQ47385
 ID AAQ47385 standard; cDNA to mRNA; 22 BP.
 XX
 AC AAQ47385;
 XX
 DT 25-MAR-2003 (revised)
 DT 26-JAN-1994 (first entry)
 XX
 DE Substance P receptor mRNA-specific probe.
 XX
 KW Probe; quantification; human; substance P; specific mRNA; detection;
 KW hybridisation; diagnosis; pathophysiology; disease state; hereditary;
 KW cancer; infectious; neurotransmitter; nerves; pain receptor pathway;
 KW analgesics; ss.
 XX
 OS Synthetic.
 XX
 FT Key Location/Qualifiers
 FT modified_base 1
 FT /tag= a
 FT /note= "5' amino group"
 FT
 XX
 XX W09315221-A1.
 XX
 PD 05-AUG-1993.
 XX
 XX 29-JAN-1993; 93WO-US000977.
 XX
 XX 29-JAN-1992; 92US-00827208.
 XX 24-MAR-1992; 92US-00857059.
 PR 12-NOV-1992; 92US-00974409.
 XX
 PA (HITB) HITACHI CHEM CO LTD.
 PA (HITB) HITACHI CHEM RES CENT INC.
 PI Akitaya T, Cooper A, Mitsuhashi M;
 XX
 DR WPI; 1993-258695/32.
 PT Quantitating messenger RNA in sample - using immobilised-polynucleotide
 PT having sequence complementary to sequence unique to the mRNA.
 XX
 XX Claim 12 and 40; Page 56; 177bp; English.
 XX
 XX This sequence is a probe which was used in the quantification of human
 CC substance P receptor mRNA from substance P receptor cDNA-transferred
 CC cells. This probe was used in the method of the invention, for the
 CC detection and quantification of mRNA in a sample without the need to
 CC purify the mRNA from cells. The claimed method comprises identifying a
 CC polynucleotide sequence unique to the mRNA, and immobilising an oligomer
 CC complementary to this sequence to an insoluble support. The sample is
 CC then incubated with the bound oligomer and be immobilised. Non-immobilised
 CC will hybridise to the bound oligomer and be immobilised. Non-immobilised
 CC components are washed from the support and bound RNA is labeled in such
 CC a way that the label is incorporated onto the support relative to the
 CC amount of mRNA on the support. The amount of bound label is then
 CC determined. This method can be used for the reliable, rapid, simultaneous
 CC quantification and recognition of patho- physiology of various diseases.
 CC diagnosing and recognition of patho- physiology of various diseases.
 CC states, eg. hereditary diseases, cancer, and infectious diseases.
 CC Substance P is a neurotransmitter. Because the nerves expressing
 CC substance P are involved in pain receptor pathways, the ability to
 CC measure the mRNA of substance P would be useful in the development of
 CC analgesics. See also AAQ47381-666. (Updated on 25-MAR-2003 to correct PN
 CC field.)

XX Sequence 22 BP; 8 A; 4 C; 6 G; 4 T; 0 U; 0 Other;
 SQ Query Match 1.0%; Score 17.8; DB 1; Length 22;
 Best Local Similarity 90.5%; Pred. No. 1.3e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 780 GATTATGAGAAAGTGTACCA 800
 Db 2 GACTTATGAGAAAGGTACCA 22
 RESULT 176
 ABSS9964/C
 ID ABSS9964 standard; DNA; 19 BP.
 AC ABSS9964;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Human DNA representing a single nucleotide polymorphism #114.
 XX
 KM Aminopeptidase P; XPNBP2; bradykinin receptor B1; ds; SNP; BDKRB1;
 KM tachykinin receptor B1; TACR1; CI esterase inhibitor; C1NH; kallikrein 1;
 KM KKL1; bradykinin receptor B2; BDKRB2; gene therapy;
 KM angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;
 KM polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
 KM cardiovascular disease; angina pectoris; hypertension; heart failure;
 KM myocardial infarction; ventricular hypertrophy; vascular disease;
 KM aneurysm; embolism; thrombosis; coronary artery disease; angiodaema;
 KM arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;
 KM autoimmune disease; inflammatory arthritis; cancer; wound;
 KM viral infection; bacterial infection; fungal infection; COPD;
 KM Chronic obstructive pulmonary disease; enterocolitis;
 KM single-nucleotide polymorphism.
 XX
 OS Homo sapiens.
 XX
 FN WO200261131-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 03-DEC-2001; 2001WO-US047235.
 XX
 PR 04-DEC-2000; 2000US-0251015P.
 PR 23-JAN-2001; 2001US-0263678P.
 PR 02-MAR-2001; 2001US-0273037P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 PA (TSUC/) TSUCHIHASHI Z.
 PA (HUI/L/) HUI L.
 XX
 PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone M;
 PI Swanson BM, Powell JR;
 XX
 DR WPI; 2002-619265/66.
 XX
 PT New isolated nucleic acid with at least one polymorphic position, useful
 PT for detecting, diagnosing and treating disorders such as angiodema,
 PT cancer, viral, bacterial or fungal infection, cardiovascular and
 PT autoimmune diseases.
 XX
 PS Disclosure; Page 663; 977pp; English.
 XX
 CC The invention relates to an isolated nucleic acid from a human gene
 CC encoding aminopeptidase P (XPNBP2), bradykinin receptor B1 (BDKRB1),
 CC tachykinin receptor B1 (TACR1), CI esterase inhibitor (C1NH), kallikrein
 CC 1 (KKL1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme
 CC 2 (ACE2), or protease inhibitor 4 (P14), comprising at least one
 CC polymorphic position. Also included are (1) a probe that hybridises to a
 CC polymorphic position as provided in the detailed summary of single
 CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
 CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising

CC obtaining the sample from one or more individuals and determining the
 CC nucleic acid sequence at one or more polymorphic positions in a gene
 CC encoding a protein selected from the group above; (3) constructing (M2)
 CC haplotypes using the genes comprising grouping at least two nucleic acids
 CC ; (4) identifying (M3) an individual at risk of developing a disorder
 CC upon administration of an ACE inhibitor and/or vasopressin inhibitor
 CC using the polymorphic data; (5) a library of nucleic acids, each of which
 CC comprises one or more polymorphic positions within a gene encoding a
 CC human protein selected from the group above; and (6) genotyping (M4) an
 CC individual comprising obtaining a nucleic acid sample, determining the
 CC nucleotide present in at least one polymorphic position, and comparing at
 CC least one position with a known data set. The genes, (M1, M2, M3 and M4)
 CC and compositions are useful for detecting, diagnosing, treating,
 CC preventing various disorders such as angiodaema and diseases which
 CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's
 CC disease, trachomas, and cardiovascular diseases like angina pectoris,
 CC hypertension, heart failure, myocardial infarction, ventricular
 CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
 CC artery disease, arteriosclerosis and/or atherosclerosis, and
 CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory
 CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic
 CC obstructive pulmonary disease (COPD) and enterocolitis (many other
 CC diseases and disorders are listed in the specification). The
 CC polymorphisms are also useful for chromosome identification. Antibodies
 CC against the proteins may be utilised for immunophenotyping of cell lines
 CC and biological samples. The present sequence represents or contains the
 CC region surrounding a single-nucleotide polymorphism in one of the genes
 CC encoding one of the proteins listed above
 XX
 SQ Sequence 19 BP; 3 A; 2 C; 10 G; 4 T; 0 U; 0 Other;
 Query Match 1.0%; Score 17.4; DB 1; Length 19;
 Best Local Similarity 94.7%; Pred. No. 1.1e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1335 CACACCTCGTCCCTGGAC 1353
 Db 19 CACACCTCATCCTGGAC 1
 RESULT 177
 ABSS9962/C
 ID ABSS9962 standard; DNA; 19 BP.
 XX
 AC ABSS9962;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Human DNA representing a single nucleotide polymorphism #112.
 XX
 KM Aminopeptidase P; XPNBP2; bradykinin receptor B1; ds; SNP; BDKRB1;
 KM tachykinin receptor B1; TACR1; CI esterase inhibitor; C1NH; kallikrein 1;
 KM KKL1; bradykinin receptor B2; BDKRB2; gene therapy;
 KM angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;
 KM polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
 KM cardiovascular disease; angina pectoris; hypertension; heart failure;
 KM myocardial infarction; ventricular hypertrophy; vascular disease;
 KM aneurysm; embolism; thrombosis; coronary artery disease; angiodaema;
 KM arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;
 KM autoimmune disease; inflammatory arthritis; cancer; wound;
 KM viral infection; bacterial infection; fungal infection; COPD;
 KM Chronic obstructive pulmonary disease; enterocolitis;
 KM single-nucleotide polymorphism.
 XX
 OS Homo sapiens.
 XX
 FN WO200261131-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 03-DEC-2001; 2001WO-US047235.
 PF 23-JAN-2001; 2001US-0263678P.
 PF 04-DEC-2000; 2000US-0251015P.
 XX

CC hypertrophy, vascular diseases; aneurysm, embolism, thrombosis, coronary
CC artery disease, arteriosclerosis and/or atherosclerosis, and
CC hyperaenatitivity reactions, sepsis, autoimmune diseases, inflammatory
CC arthritis, cancer, wounds, viral, bacterial or fungal infection. Chronic
CC obstructive pulmonary disease (COPD) and enterocolitis (many other
CC diseases and disorders are listed in the specification). The
CC polynucleotides are also useful for chromosome identification. Antibodies
CC against the proteins may be utilised for immunophenotyping of cell lines
CC and biological samples. The present sequence represents or contains the
CC region surrounding a single-nucleotide polymorphism in one of the genes
XX encoding one of the proteins listed above

SO Sequence 19 BP; 7 A; 6 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

663 CTGTCATCATGCGTCCG 681
19 CTGTCATCATGCGTCCG 1

RESULT 179
ABSS59958
ID ABSS59958 standard; DNA; 19 BP.
XX
AC ABSS59958;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human DNA representing a single nucleotide polymorphism #108.

XX Aminopeptidase P; XPNP2; bradykinin receptor B1; ds; SNP; BDKRB1;
KM tachykinin receptor B1; TACR1; Cl esterase inhibitor; C1NH; kallikrein 1;
KM K1; bradykinin receptor B2; BDKRB2; gene therapy;
KM angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;
KM polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
KM cardiovascular disease; angina pectoris; hypertension; heart failure;
KM myocardial infarction; ventricular hypertrophy; vascular disease;
KM aneurysm; embolism; thrombosis; coronary artery disease; angiodaema;
KM arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;
KM autoimmune disease; inflammatory arthritis; cancer; wound;
KM viral infection; bacterial infection; fungal infection; COPD;
KM chronic obstructive pulmonary disease; enterocolitis;
KM single-nucleotide polymorphism.

XX Homo sapiens.
XX
XX WO200261131-A2.
XX
XX 08-AUG-2002.
XX
XX 03-DEC-2001; 2001WO-US047235.
XX
XX 04-DEC-2000; 2000US-0251015P.
PR 23-JAN-2001; 2001US-0263678P.
PR 02-MAR-2001; 2001US-0273037P.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
PA (TSCU) TSUCHIHASHI Z.
PA (HUI/L) HUI L.
XX
XX Teuchihaishi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;
PI Swanson BN, Powell JR;
XX
XX WPI; 2002-619265/66.
XX
XX New isolated nucleic acid with at least one polymorphic position, useful
PT for detecting, diagnosing and treating disorders such as angiodema,
PT cancer, viral, bacterial or fungal infection, cardiovascular and
PT autoimmune diseases.

PS Disclosure; Page 662; 977bp; English.

XX The invention relates to an isolated nucleic acid from a human gene
CC encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDKRB1),
CC tachykinin receptor B1 (TACR1), Cl esterase inhibitor (C1NH), kallikrein
CC 1 (K1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme
CC 2 (ACE2) or protease inhibitor 4 (P14), comprising at least one
CC polymorphic position. Also included are (1) a probe that hybridises to a
CC polymorphic position as provided in the detailed summary of single
CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising
CC obtaining the sample from one or more individuals and determining the
CC nucleic acid sequence at one or more polymorphic positions in a gene
CC encoding a protein selected from the group above; (3) constructing (M2)
CC haplotypes using the genes comprising grouping at least two nucleic acids
CC (4) identifying (M3) an individual at risk of developing a disorder
CC upon administration of an ACE inhibitor and/or vasopressinase inhibitor
CC using the polymorphic data; (5) a library of nucleic acids, each of which
CC comprises one or more polymorphic positions within a gene encoding a
CC human protein selected from the group above; and (6) genotyping (M4) an
CC individual comprising obtaining a nucleic acid sample, determining the
CC nucleotide present in at least one polymorphic position, and comparing at
CC least one position with a known data set. The genes, (M1, M2, M3 and M4)
CC and compositions are useful for detecting, diagnosing, treating,
CC preventing various disorders such as angiodaema and diseases which
CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's
CC disease, trachomas, and cardiovascular diseases like angina pectoris,
CC hypertension, heart failure, myocardial infarction, ventricular
CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
CC artery disease, arteriosclerosis and/or atherosclerosis, and
CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory
CC arthritis, cancer, wounds, viral, bacterial or fungal infection, chronic
CC obstructive pulmonary disease (COPD) and enterocolitis (many other
CC diseases and disorders are listed in the specification). The
CC polynucleotides are also useful for chromosome identification. Antibodies
CC against the proteins may be utilised for immunophenotyping of cell lines
CC and biological samples. The present sequence represents or contains the
CC region surrounding a single-nucleotide polymorphism in one of the genes
XX encoding one of the proteins listed above

SO Sequence 19 BP; 3 A; 10 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

534 CAACTTCTTCCATGCC 552
1 CAACTTCTTCCATGCC 19

RESULT 180
ABSS59900/c
ID ABSS59900 standard; DNA; 19 BP.
XX
XX ABSS59900;
XX
XX 05-NOV-2002 (first entry)
XX
XX Human DNA representing a single nucleotide polymorphism #50.

XX Aminopeptidase P; XPNP2; bradykinin receptor B1; ds; SNP; BDKRB1;
KM tachykinin receptor B1; TACR1; Cl esterase inhibitor; C1NH; kallikrein 1;
KM K1; bradykinin receptor B2; BDKRB2; gene therapy;
KM angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;
KM polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
KM myocardial infarction; ventricular hypertrophy; vascular disease;
KM cardiovascular disease; angina pectoris; hypertension; heart failure;
KM aneurysm; embolism; thrombosis; coronary artery disease; angiodaema;
KM arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;
KM autoimmune disease; inflammatory arthritis; cancer; wound;
KM viral infection; bacterial infection; fungal infection; COPD;
KM chronic obstructive pulmonary disease; enterocolitis;

KM single-nucleotide polymorphism.
 XX Homo sapiens.
 OS
 PN W0200261131-A2.
 XX
 XX 08-AUG-2002.
 FD
 PF 03-DEC-2001; 2001WO-US047235.
 XX
 XX 04-DEC-2000; 2000US-0251015P.
 PR 23-JAN-2001; 2001US-0263678P.
 PR 02-MAR-2001; 2001US-0273037P.
 BR
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 PA (TSUC/) TSUCHIHASHI Z.
 PA (HUI/) HUI L.
 XX
 PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;
 PI Swanson BN, Powell JR;
 DR WPI; 2002-619265/66.
 XX
 XX New isolated nucleic acid with at least one polymorphic position, useful
 PT for detecting, diagnosing and treating disorders such as angioedema,
 PT cancer, viral, bacterial or fungal infection, cardiovascular and
 PT autoimmune diseases.
 PS Disclosure; Page 653; 977pp; English.
 XX
 XX The invention relates to an isolated nucleic acid from a human gene
 CC encoding aminopeptidase P (APNPP2), bradykinin receptor B1 (BDRB1),
 CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein
 CC 1 (KLK1), bradykinin receptor B2 (BDRB2), angiotensin converting enzyme
 CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one
 CC polymorphic position. Also included are (1) a probe that hybridises to a
 CC polymorphic position as provided in the detailed summary of single
 CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
 CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising
 CC obtaining the sample from one or more individuals and determining the
 CC nucleic acid sequence at one or more polymorphic positions in a gene
 CC encoding a protein selected from the group above; (3) constructing (M2)
 CC haplotypes using the genes comprising grouping at least two nucleic acids
 CC ; (4) identifying (M3) an individual at risk of developing a disorder
 CC upon administration of an ACE inhibitor and/or vasopressinase inhibitor
 CC using the polymorphic data; (5) a library of nucleic acids, each of which
 CC comprises one or more polymorphic positions within a gene encoding a
 CC human protein selected from the group above; and (6) genotyping (M4) an
 CC individual comprising obtaining a nucleic acid sample, determining the
 CC nucleotide present in at least one polymorphic position, and comparing at
 CC least one position with a known data set. The genes, (M1, M2, M3 and M4)
 CC and compositions are useful for detecting, diagnosing, treating,
 CC preventing various disorders such as angioedema and diseases which
 CC involve angiotensins like haemangiomas, tumours, sarcomas, Crohn's
 CC disease, trachomas, and cardiovascular diseases like angina pectoris,
 CC hypertension, heart failure, myocardial infarction, ventricular
 CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
 CC artery disease, arteriosclerosis and/or atherosclerosis, and
 CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory
 CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic
 CC obstructive pulmonary disease (COPD) and enterocolitis (many other
 CC diseases and disorders are listed in the specification). The
 CC polymorphisms are also useful for immunophenotyping of cell lines
 CC and biological samples. The present sequence represents or contains the
 CC region surrounding a single-nucleotide polymorphism in one of the genes
 CC encoding one of the proteins listed above
 XX
 XX Sequence 19 BP; 4 A; 3 C; 7 G; 5 T; 0 U; 0 Other;
 SQ
 Query Match 1.0%; Score 17.4; DB 1; Length 19;
 Best Local Similarity 94.7%; Pred. No. 1.1e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1529 CCTCAGCTGAGCTTGCA 1547
 DB 19 CCTCAGCTGAGCTTGCA 1
 RESULT 181
 AEE77697
 ID AEE77697 standard; DNA; 20 BP.
 XX
 XX AEE77697;
 AC
 XX
 DT 09-FEB-2006 (first entry)
 XX
 XX Human dopamine receptor D2 (DRD2) DNA oligonucleotide SEQ ID NO:1318.
 DE
 XX Diagnosis; therapeutic; neurological disease; psychiatric disorder;
 KM neuropsychologic disorder; dopamine receptor D2; DRD2; ss.
 KM
 XX Homo sapiens.
 OS
 XX W02005118843-A1.
 PN
 XX 15-DEC-2005.
 PD
 XX 01-JUN-2005; 2005WO-AU000775.
 PE
 XX 01-JUN-2004; 2004AU-00902919.
 PR
 XX (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
 PA
 PI Morris CP, Van Daal A, Swagell CD, Lawford BR, Young RM;
 PI WPI; 2006-047555/05.
 DR
 XX Identifying genetic profile associated with a neurological, psychiatric,
 PT or psychological condition, comprises screening individuals for a
 PT polymorphism in a genetic locus comprising the dopamine receptor D2
 PT (DRD2) gene.
 XX
 XX Claim 31; SEQ ID NO 1318; 634pp; English.
 PS
 XX The invention relates to a method of identifying a genetic profile
 CC associated with a neurological, psychiatric or psychological condition,
 CC phenotypic or state including a sub-threshold neurological, psychiatric or
 CC psychological condition, phenotype or state in an individual, comprising
 CC screening individuals for a polymorphism in a genetic locus comprising
 CC the dopamine receptor D2 (DRD2) gene. The invention also relates to a
 CC genetic mutation providing a genetic marker for a neurological,
 CC psychiatric, or psychological condition, state or phenotype in an
 CC individual, where the presence of a 957C polymorphism is indicative of a
 CC predisposition to developing a neurological, psychiatric or psychological
 CC condition, phenotype or state. The compositions and methods are useful
 CC for identifying a genetic profile associated with a neurological,
 CC psychiatric or psychological condition. The method enables clinicians to
 CC make a genetic-based diagnosis of a neurological, psychiatric or
 CC psychological condition and can thereby implement treatment or
 CC preventative or symptom-ameliorating protocols to reduce the adverse
 CC consequences of the condition. This sequence represents a human dopamine
 CC receptor D2 (DRD2) DNA oligonucleotide used in the scope of the
 CC invention.
 XX
 XX Sequence 20 BP; 2 A; 8 C; 4 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 1.0%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 984 CATCTGCTGCTGCTGCT 1000
 DB 4 CATCTGCTGCTGCTGCT 20

RESULT 182
AE77702
ID ABE77702 standard; DNA; 20 BP.
XX
AC ABE77702;
XX
DT 09-FEB-2006 (first entry)
XX
DE Human dopamine receptor D2 (DRD2) DNA oligonucleotide SEQ ID NO:1323.
XX
KW Diagnosis; therapeutic; neurological disease; psychiatric disorder;
KM neuropsychologic disorder; dopamine receptor D2; DRD2, ss.
XX
OS Homo sapiens.
PN MO2005118843-A1.
XX
PD 15-DEC-2005.
XX
PF 01-JUN-2005; 2005MO-AU000775.
XX
PR 01-JUN-2004; 2004AU-00902919.
XX
PA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
PI Morris CP, Van Daal A, Swagell CD, Lawford BR, Young RM;
XX
DR WPI; 2006-047555/05.
XX
PS Identifying genetic profile associated with a neurological, psychiatric,
PT or psychological condition, comprises screening individuals for a
PT polymorphism in a genetic locus comprising the dopamine receptor D2
PT (DRD2) gene.
XX
XX
PS Claim 31; SEQ ID NO 1323; 634bp; English.
XX
CC The invention relates to a method of identifying a genetic profile
CC associated with a neurological, psychiatric or psychological condition,
CC phenotype or state including a sub-threshold neurological, psychiatric or
CC psychological condition, phenotype or state in an individual, comprising
CC screening individuals for a polymorphism in a genetic locus comprising
CC the dopamine receptor D2 (DRD2) gene. The invention also relates to a
CC genetic mutation providing a genetic marker for a neurological,
CC psychiatric, or psychological condition, state or phenotype in an
CC individual, where the presence of a 957C polymorphism is indicative of a
CC predisposition to developing a neurological, psychiatric or psychological
CC condition, phenotype or state. The compositions and methods are useful
CC for identifying a genetic profile associated with a neurological,
CC psychiatric or psychological condition. The method enables clinicians to
CC make a genetic-based diagnosis of a neurological, psychiatric or
CC psychological condition and can thereby implement treatment or
CC preventative or symptom-ameliorating protocols to reduce the adverse
CC consequences of the condition. This sequence represents a human dopamine
CC receptor D2 (DRD2) DNA oligonucleotide used in the scope of the
CC invention.
XX
SQ Sequence 20 BP; 0 A; 8 C; 4 G; 8 T; 0 U; 0 Other;
Query Match 1.0%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 986 TCTGCTGCTGCCCTTC 1002
DB 1 TCTGCTGCTGCCCTTC 17
RESULT 183
AAQ36818/c
ID AAQ36818 standard; DNA; 21 BP.
XX
AC AAQ36818;
XX

DT 25-MAR-2003 (revised)
DT 22-JUN-1993 (first entry)
XX
DE Oligomer SM 82 used in construction of SSP polypeptides.
XX
KW Heptad; plants; custom tailored storage proteins; in vivo; expression;
KM ss.
XX
OS Synthetic.
PN MO9303160-A1.
XX
PD 18-FEB-1993.
XX
PF 07-AUG-1992; 92WO-US006412.
XX
PR 09-AUG-1991; 91US-00743006.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PI Falco SC, Keeler SJ, Rice JA;
XX
DR WPI; 1993-076517/09.
XX
PS Synthetic polypeptide(s) contg. specified heptad units - expressed in
PT vivo in plants to serve as custom-tailored storage proteins with
PT specified aminoacid content.
XX
XX
PS Disclosure; Page 109; 176pp; English.
XX
CC The sequence represents the DNA sequence encoding a synthetic heptad
CC polypeptide. The synthetic polypeptide can be expressed in vivo in plants
CC to serve as a synthetic seed storage protein which can be custom-tailored
CC for specific end-user requirements. The DNA encoding the heptad may be
CC used to transform plants to increase the content of partic. amino acids
CC such as lysine or methionine in seeds or leaves. See also AAQ36810-28.
CC AAQ37265-301. (updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 21 BP; 7 A; 2 C; 10 G; 2 T; 0 U; 0 Other;
Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1404 CTTGAGCTTCTCTCCA 1420
DB 19 CTTGAGCTTCTCTCCA 3
RESULT 184
AAQ36820/c
ID AAQ36820 standard; DNA; 21 BP.
XX
AC AAQ36820;
XX
DT 25-MAR-2003 (revised)
DT 22-JUN-1993 (first entry)
XX
DE Oligomer SM 86 used in construction of SSP polypeptides.
XX
KW Heptad; plants; custom tailored storage proteins; in vivo; expression;
KM ss.
XX
OS Synthetic.
PN MO9303160-A1.
XX
PD 18-FEB-1993.
XX
PF 07-AUG-1992; 92WO-US006412.
XX
PR 09-AUG-1991; 91US-00743006.
XX

PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX Falco SC, Keeler SJ, Rice JA;
 XX WPI; 1993-076517/09.
 XX Synthetic polypeptide(s) contg. specified heptad units - expressed in
 PT vivo in plants to serve as custom-tailored storage proteins with
 PT specified aminoacid content.
 XX Disclosure; Page 110; 176pp; English.
 XX The sequence represents the DNA sequence encoding a synthetic heptad
 CC polypeptide. The synthetic polypeptide can be expressed in vivo in plants
 CC to serve as a synthetic seed storage protein which can be custom-tailored
 CC for specific end-user requirements. The DNA encoding the heptad may be
 CC used to transform plants to increase the content of partic. amino acids
 CC such as lysine or methionine in seeds or leaves. See also AAQ36810-28,
 CC AAQ37265-301. (Updated on 25-MAR-2003 to correct PN field.)
 CC
 SQ Sequence 21 BP; 9 A; 1 C; 9 G; 2 T; 0 U; 0 Other;
 Query Match 1.0%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1404 CTTGAGCTTCTCTCCA 1420
 DB 19 CTTGAGCTTCTCTCCA 3
 RESULT 185
 AAQ36822/C
 ID AAQ36822 standard; DNA; 21 BP.
 XX AAQ36822;
 AC 25-MAR-2003 (revised)
 DT 22-JUN-1993 (first entry)
 XX Oligomer SM 88 used in construction of SSP polypeptides.
 DE Heptad; plants; custom tailored storage proteins; in vivo; expression;
 XX ss.
 KM Synthetic.
 XX WO9303160-A1.
 PN 18-FEB-1993.
 PD 07-AUG-1992; 92WO-US006412.
 PF 09-AUG-1991; 91US-00743006.
 PR (DUPO) DU PONT DE NEMOURS & CO E I.
 PA Falco SC, Keeler SJ, Rice JA;
 PI WPI; 1993-076517/09.
 XX Synthetic polypeptide(s) contg. specified heptad units - expressed in
 PT vivo in plants to serve as custom-tailored storage proteins with
 PT specified aminoacid content.
 XX Disclosure; Page 111; 176pp; English.
 XX The sequence represents the DNA sequence encoding a synthetic heptad
 CC polypeptide. The synthetic polypeptide can be expressed in vivo in plants
 CC to serve as a synthetic seed storage protein which can be custom-tailored
 CC for specific end-user requirements. The DNA encoding the heptad may be
 CC used to transform plants to increase the content of partic. amino acids
 CC such as lysine or methionine in seeds or leaves. See also AAQ36810-28,
 CC

CC AAQ37265-301. (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 21 BP; 7 A; 1 C; 10 G; 3 T; 0 U; 0 Other;
 SQ Query Match 1.0%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1404 CTTGAGCTTCTCTCCA 1420
 DB 19 CTTGAGCTTCTCTCCA 3
 RESULT 186
 AAQ94986/C
 ID AAQ94986 standard; DNA; 21 BP.
 XX AAQ94986;
 AC 16-JUL-1996 (first entry)
 DT SSP9 Oligonucleotide SM 88.
 DE Lysine; synthetic storage protein; SSP; vector; pSK6;
 KM dihydrodipicolinic acid synthase; corn; maize; Zea mays; soybean;
 KM Glycine max; transgenic plant; essential amino acid; ss.
 XX Synthetic.
 OS Key Location/Qualifiers
 XX Key 1. .21
 FH misc_feature /*tag= a
 FT /standard_name= "SM 88"
 FT CDS 2. .21
 FT /*tag= b
 FT
 XX WO9515392-A1.
 PN 08-JUN-1995.
 PD 21-NOV-1994; 94WO-US013190.
 PF 30-NOV-1993; 93US-00160117.
 PR 17-JUN-1994; 94US-00261661.
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 PA Falco SC, Keeler SJ, Rice JA;
 PI WPI; 1995-215272/28.
 DR P-PSDB; AAR78246.
 DR New chimeric gene providing increased lysine content in plant seeds -
 XX contains di:hydro:di:picolinic acid synthase gene coupled to chloroplast
 PT transport sequence and seed specific promoter; also new plants of
 PT improved nutritional value.
 XX Example 8; Page 78; 180pp; English.
 PS Oligonucleotide SM88 (AAQ94986) and complementary sequence SM89
 XX (AAQ94987) code for heptad peptide SSP9 (AAR78246). They were annealed
 CC and used in the construction a DNA fragment (see also AAQ94995) that was
 CC inserted into vector pSK6 (see also AAR78236). The DNA fragment codes for
 CC a synthetic storage protein (SSP) contg. multiple lysine-rich heptad
 CC repeats (see AAR78252). This can be expressed in the seeds of transformed
 CC plants, e.g. soybean and corn, to increase lysine content
 XX Sequence 21 BP; 7 A; 1 C; 10 G; 3 T; 0 U; 0 Other;
 SQ Query Match 1.0%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY      1404 CTTGAGCTTCTCTCCA 1420
      |||||
      19 CTTGAGCTTCTCTCCA 3
Db

RESULT 187
AAQ94984/C
XX      AAQ94984 standard; DNA; 21 BP.
AC
XX      AAQ94984;
XX
XX      16-JUN-1996 (first entry)
XX
XX      SSP8 Oligonucleotide SM 86.
XX
XX      Lysine; synthetic storage protein; SSP; vector; pSK6;
XX      dihydrodipicolinic acid synthase; corn; maize; Zea mays; soybean;
XX      Glycine max; transgenic plant; essential amino acid; ss.
XX
XX      Synthetic.
XX
XX      Key
XX      Location/Qualifiers
XX      misc_feature
XX      1..21
XX      /tag= a
XX      /standard_name= "SM 86"
XX      2..21
XX      /*tag= b
XX
XX      CDS
XX
XX      MO9515392-A1.
XX
XX      PD      08-JUN-1995.
XX
XX      PF      21-NOV-1994; 94MO-US013190.
XX
XX      PR      30-NOV-1993; 93US-00160117.
XX      17-JUN-1994; 94US-00261661.
XX
XX      PA      (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX      PI      Falco SC, Keeler SJ, Rice JA;
XX
XX      DR      WPI; 1995-215272/28.
XX      P-PSDB; AAR78245.
XX
XX      PT      New chimeric gene providing increased lysine content in plant seeds -
XX      contains di:hydro:di:picolinic acid synthase gene coupled to chloroplast
XX      transport sequence and seed specific promoter, also new plants of
XX      improved nutritional value.
XX
XX      PS      Example 8; Page 78; 180pp; English.
XX
XX      CC      Oligonucleotide SM86 (AAQ94984) and complementary sequence SM87
XX      (AAQ94985) code for heptad peptide SSP8 (AAR78245). They were annealed
XX      and used in the construction a DNA fragment (see also AAQ94994) that was
XX      inserted into vector pSK6 (see also AAR78236). The DNA fragment codes for
XX      a synthetic storage protein (SSP) contg. multiple lysine-rich heptad
XX      repeats (see AAR78251). This can be expressed in the seeds of transformed
XX      plants; e.g. soybean and corn, to increase lysine content
XX
XX      SQ      Sequence 21 BP; 9 A; 1 C; 9 G; 2 T; 0 U; 0 Other;
XX
XX      Query March      1.0%; Score 17; DB 1; Length 21;
XX      Best Local Similarity 100.0%; Pred. No. 1.6e+02;
XX      Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1404 CTTGAGCTTCTCTCCA 1420
      |||||
      19 CTTGAGCTTCTCTCCA 3
Db

RESULT 188
AAQ94976/C
XX      AAQ94976 standard; DNA; 21 BP.
XX
XX      19 CTTGAGCTTCTCTCCA 3
XX
```

```
XX
XX      AAQ94976;
AC
XX      16-JUN-1996 (first entry)
XX
XX      SSP7 Oligonucleotide SM 82.
XX
XX      Lysine; synthetic storage protein; SSP; vector; pSK6;
XX      dihydrodipicolinic acid synthase; corn; maize; Zea mays; soybean;
XX      Glycine max; transgenic plant; essential amino acid; ss.
XX
XX      Synthetic.
XX
XX      Key
XX      Location/Qualifiers
XX      misc_feature
XX      1..21
XX      /tag= a
XX      /standard_name= "SM 82"
XX      2..21
XX      /*tag= b
XX
XX      CDS
XX
XX      MO9515392-A1.
XX
XX      PD      08-JUN-1995.
XX
XX      PF      21-NOV-1994; 94MO-US013190.
XX
XX      PR      30-NOV-1993; 93US-00160117.
XX      17-JUN-1994; 94US-00261661.
XX
XX      PA      (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX      PI      Falco SC, Keeler SJ, Rice JA;
XX
XX      DR      WPI; 1995-215272/28.
XX      P-PSDB; AAR78237.
XX
XX      PT      New chimeric gene providing increased lysine content in plant seeds -
XX      contains di:hydro:di:picolinic acid synthase gene coupled to chloroplast
XX      transport sequence and seed specific promoter, also new plants of
XX      improved nutritional value.
XX
XX      PS      Example 8; Page 76; 180pp; English.
XX
XX      CC      Oligonucleotide SM82 (AAQ94976) and complementary sequence SM83
XX      (AAQ94977) code for heptad peptide SSP7 (AAR78237). They were annealed
XX      and used in the construction DNA fragments (see also AAQ94978-80,
XX      AAQ94992, AAQ95004 and AAQ95006) that were inserted into vector pSK6 (see
XX      also AAR78236). The DNA fragments code for synthetic storage proteins
XX      (SSPs) contg. multiple lysine-rich heptad repeats (see AAR78239-41,
XX      AAR78249, AAR78258 and AAR78260). These can be expressed in the seeds of
XX      transformed plants; e.g. soybean and corn, to improve lysine content
XX
XX      SQ      Sequence 21 BP; 7 A; 2 C; 10 G; 2 T; 0 U; 0 Other;
XX
XX      Query March      1.0%; Score 17; DB 1; Length 21;
XX      Best Local Similarity 100.0%; Pred. No. 1.6e+02;
XX      Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1404 CTTGAGCTTCTCTCCA 1420
      |||||
      19 CTTGAGCTTCTCTCCA 3
Db

RESULT 189
AAV99519/C
XX      AAV99519 standard; DNA; 21 BP.
XX
XX      AAV99519;
XX
XX      29-MAR-1999 (first entry)
XX
XX      Oligonucleotide SM86 encoding SSP8 heptad repeat.
XX
```


XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX Falco SC, Mcdevitt RE, Epelbaum SU;
XX WPI, 1999-045139/04.
XX
XX Nucleic acids and chimeric genes for increasing seed lysine content -
XX comprise sequence encoding all or part of lysine ketoglutarate reductase,
XX useful to improve nutritional quality of seeds from transformed plants.
XX
XX Example 21; Page 104; 231pp; English.
XX
XX This synthetic double-stranded oligonucleotide encodes a lysine-rich
XX heptad repeat peptide. It can be inserted into the unique *Eari* site in
XX the 'base gene' (see AAV99505) of vector PSK5 to provide repetitive
XX heptad coding sequences. Chimeric genes for lysine-rich synthetic seed
XX storage proteins suitable for expression in the seeds of plants have been
XX constructed (see AAV99513-18, AAV99527-32, AAV99539-41). The invention
XX provides methods for improving the nutritional quality of seeds from
XX transgenic plants by increasing lysine content
XX
XX Sequence 21 BP; 7 A; 1 C; 10 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 1.6e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1404 CTTGAGCTTCTCTCCCA 1420
XX 19 CTTGAGCTTCTCTCCCA 3
XX
XX
XX RESULT 192
XX ADA15939/C
XX ID ADA15939 standard; DNA; 21 BP.
XX
XX ADA15939;
XX
XX 06-NOV-2003 (first entry)
XX
XX Synthetic storage protein oligonucleotide SM88.
XX
XX see: lysC; transgenic; lysine accumulation;
XX dihydrodipicolinic acid synthase; DHPS; lysine inhibition;
XX lysine ketoglutarate reductase; LKR; chloroplast transit sequence; CTS;
XX aspartokinase III; AKIII; synthetic seed storage protein; SSP.
XX
XX Synthetic.
XX
XX US6459019-B1.
XX
XX 01-OCT-2002.
XX
XX 24-MAR-1997; 97US-00823771.
XX
XX 19-MAR-1992; 92US-00855414.
XX PR 06-JAN-1994; 94US-00178212.
XX PR 07-JUN-1995; 95US-00474633.
XX
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX
XX Falco SC, Keeler SJ, Rice JA;
XX WPI; 2003-028272/02.
XX P-PSDB; ADA15946.
XX
XX Transformed plants that accumulate lysine at higher levels in its seeds
XX than untransformed plants, has gene fragments encoding lysine-insensitive
XX dihydrodipicolinic acid synthase and lysine ketoglutarate reductase.
XX
XX Example 21; Col 79; 109pp; English.
XX

XX The invention relates to a plant comprising two foreign nucleotide
XX sequences which cause seeds obtained from the plant to accumulate lysine
XX at a level of at least 10% higher than seeds of a plant that do not
XX comprise the nucleotide, where the nucleotide comprises a fragment
XX encoding a dihydrodipicolinic acid synthase (DHPS) that is insensitive
XX to lysine inhibition, and a fragment encoding a plant lysine
XX ketoglutarate reductase (LKR) or its subfragment. The nucleotide fragment
XX is operably linked to a plant chloroplast transit sequence (CTS) and the
XX plant lysine ketoglutarate reductase subfragment is used in antisense
XX inhibition or cosuppression. Also included are progeny plants from the
XX above mentioned plant and seeds obtained from the above mentioned plant.
XX The seeds obtained from the above mentioned plant (e.g., rapeseed,
XX soybean or corn) comprising the foreign nucleic acid sequences accumulate
XX lysine at a higher level, preferably at a level of at least 10% higher
XX than seeds of a plant that do not comprise the foreign nucleic acid
XX sequences. Chimeric gene comprising DHPS from *C. glutamicum* and
XX aspartokinase III (from the *lysC* gene) of *E. coli* (mutated to be lysine-
XX insensitive) are also used to generate the above transgenic plants. Also
XX disclosed are synthetic seed storage proteins (SSP) used as an internal
XX source of lysine, built up from synthetic peptide monomers based around
XX an *Eari* site sequence (for generating multimeric proteins). The present
XX sequence is a strand of an oligonucleotide encoding an SSP monomer.
XX
XX Sequence 21 BP; 7 A; 1 C; 10 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 1.6e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1404 CTTGAGCTTCTCTCCCA 1420
XX 19 CTTGAGCTTCTCTCCCA 3
XX
XX
XX RESULT 193
XX ADA15937/C
XX ID ADA15937 standard; DNA; 21 BP.
XX
XX ADA15937;
XX
XX 06-NOV-2003 (first entry)
XX
XX Synthetic storage protein oligonucleotide SM86.
XX
XX see: lysC; transgenic; lysine accumulation;
XX dihydrodipicolinic acid synthase; DHPS; lysine inhibition;
XX lysine ketoglutarate reductase; LKR; chloroplast transit sequence; CTS;
XX aspartokinase III; AKIII; synthetic seed storage protein; SSP.
XX
XX Synthetic.
XX
XX US6459019-B1.
XX
XX 01-OCT-2002.
XX
XX 24-MAR-1997; 97US-00823771.
XX
XX 19-MAR-1992; 92US-00855414.
XX PR 06-JAN-1994; 94US-00178212.
XX PR 07-JUN-1995; 95US-00474633.
XX
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX
XX Falco SC, Keeler SJ, Rice JA;
XX WPI; 2003-028272/02.
XX P-PSDB; ADA15945.
XX
XX Transformed plants that accumulate lysine at higher levels in its seeds
XX than untransformed plants, has gene fragments encoding lysine-insensitive
XX dihydrodipicolinic acid synthase and lysine ketoglutarate reductase.
XX
XX Example 21; Col 79; 109pp; English.
XX

XX The invention relates to a plant comprising two foreign nucleotide
CC sequences which cause seeds obtained from the plant to accumulate lysine
CC at a level of at least 10% higher than seeds of a plant that do not
CC comprise the nucleotide, where the nucleotide comprises a fragment
CC encoding a dihydrodipicolinic acid synthase (DHDS) that is insensitive
CC to lysine inhibition, and a fragment encoding a plant lysine
CC ketoglutarate reductase (LKR) or its subfragment. The nucleotide fragment
CC is operably linked to a plant chloroplast transit sequence (CTS) and the
CC plant lysine ketoglutarate reductase subfragment is used in antisense
CC inhibition or cosuppression. Also included are progeny plants from the
CC above mentioned plant and seeds obtained from the above mentioned plant.
CC The seeds obtained from the above mentioned plant (e.g., rapeseed,
CC soybean or corn) comprising the foreign nucleic acid sequences accumulate
CC lysine at a higher level, preferably at a level of at least 10% higher
CC than seeds of a plant that do not comprise the foreign nucleic acid
CC sequences. Chimeric gene comprising DHDS from *C. glutamicum* and
CC aspartokinase III (from the *lysC* gene) of *E. coli* (mutated to be lysine-
CC insensitive) are also used to generate the above transgenic plants. Also
CC disclosed are synthetic seed storage proteins (SSP) used as an internal
CC source of lysine, built up from synthetic peptide monomers based around
CC an Earl site sequence (for generating multimeric proteins). The present
CC sequence is a strand of an oligonucleotide encoding an SSP monomer.
XX
SQ Sequence 21 BP; 9 A; 1 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1404 CTTGAGCTTCTCTCCA 1420
|||
Db 19 CTTGAGCTTCTCTCCA 3

RESULT 194
ADA15921/c
ID ADA15921 standard; DNA; 21 BP.

XX ADA15921;

XX 06-NOV-2003 (first entry)

XX Synthetic storage protein oligonucleotide SM82.

XX ss; *lysC*; transgenic; lysine accumulation;

KW dihydrodipicolinic acid synthase; DHDS; lysine inhibition;

KW lysine ketoglutarate reductase; LKR; chloroplast transit sequence; CTS;

KW aspartokinase III; AKIII; synthetic seed storage protein; SSP.

XX Synthetic.

XX US6459019-B1.

XX 01-OCT-2002.

XX 24-MAR-1997; 97US-00823771.

XX 19-MAR-1992; 92US-00855414.

XX 06-JAN-1994; 94US-00178212.

XX 07-JUN-1995; 95US-00474633.

XX (DUPO) DU PONT DE NEMOURS & CO E. I.

XX Falco SC, Keeler SJ, Rice JA;

XX WPI; 2003-028272/02.

XX P-PSDB; ADA15923.

XX Transformed plants that accumulate lysine at higher levels in its seeds

XX than untransformed plants, has gene fragments encoding lysine-insensitive

XX dihydrodipicolinic acid synthase and lysine ketoglutarate reductase.

PS Example 21; Col 78; 109pp; English.

XX The invention relates to a plant comprising two foreign nucleotide
CC sequences which cause seeds obtained from the plant to accumulate lysine
CC at a level of at least 10% higher than seeds of a plant that do not
CC comprise the nucleotide, where the nucleotide comprises a fragment
CC encoding a dihydrodipicolinic acid synthase (DHDS) that is insensitive
CC to lysine inhibition, and a fragment encoding a plant lysine
CC ketoglutarate reductase (LKR) or its subfragment. The nucleotide fragment
CC is operably linked to a plant chloroplast transit sequence (CTS) and the
CC plant lysine ketoglutarate reductase subfragment is used in antisense
CC inhibition or cosuppression. Also included are progeny plants from the
CC above mentioned plant and seeds obtained from the above mentioned plant.
CC The seeds obtained from the above mentioned plant (e.g., rapeseed,
CC soybean or corn) comprising the foreign nucleic acid sequences accumulate
CC lysine at a higher level, preferably at a level of at least 10% higher
CC than seeds of a plant that do not comprise the foreign nucleic acid
CC sequences. Chimeric gene comprising DHDS from *C. glutamicum* and
CC aspartokinase III (from the *lysC* gene) of *E. coli* (mutated to be lysine-
CC insensitive) are also used to generate the above transgenic plants. Also
CC disclosed are synthetic seed storage proteins (SSP) used as an internal
CC source of lysine, built up from synthetic peptide monomers based around
CC an Earl site sequence (for generating multimeric proteins). The present
CC sequence is a strand of an oligonucleotide encoding an SSP monomer.
XX
SQ Sequence 21 BP; 7 A; 2 C; 10 G; 2 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1404 CTTGAGCTTCTCTCCA 1420
|||
Db 19 CTTGAGCTTCTCTCCA 3

RESULT 195
ACH03695/c
ID ACH03695 standard; DNA; 21 BP.

XX ACH03695;

XX 25-SEP-2003 (first entry)

XX Ear I-based lysine-rich heptad repeat oligonucleotide SM88.

XX Aspartokinase; AKIII; dihydrodipicolinic acid synthase; DHDS;

KW seed lysine content; seed threonine content; seed storage protein; SSP;

KW chloroplast transit sequence; lysine-rich protein;

KW lysine ketoglutarate reductase; LKR; transgenic; ss.

XX Synthetic.

XX US2003056242-A1.

XX 20-MAR-2003.

XX 17-DEC-2001; 2001US-00023066.

XX 19-MAR-1992; 92US-00855414.

XX 18-MAR-1993; 93WO-US002480.

XX 06-JAN-1994; 94US-00178212.

XX 07-JUN-1995; 95US-00474633.

XX 24-MAR-1997; 97US-00823771.

XX (FALC/) FALCO S. C.

XX Falco SC;

XX WPI; 2003-521669/49.

XX P-PSDB; ABO44333.

XX New nucleic acid fragment encoding aspartokinase and dihydrodipicolinic

XX PT

PT acid synthase, useful for increasing threonine or lysine content of seeds
PT of plant.
XX
XX Example 21; Page 43; 116pp; English.
XX
CC The invention relates to an isolated nucleic acid fragment comprising a
CC first nucleic acid subfragment encoding aspartokinase (AK) that is
CC substantially insensitive to inhibition by lysine, and a second nucleic
CC acid subfragment encoding dihydrodipicolinic acid synthase (DHDS) that
CC is substantially insensitive to inhibition by lysine. Also included are
CC an isolated nucleic acid fragment comprising a nucleic acid subfragment
CC encoding lysine ketoglutarate reductase (LKR), a chimeric gene (where
CC the nucleic acid fragment is operably linked to a plant chloroplast
CC transit sequence and to a seed-specific regulatory sequence, a plant
CC comprising the nucleic acid/chimeric gene in its genome, a seed obtained
CC from the plant, increasing threonine or lysine content of the seeds of
CC plant, a plant capable of transmitting the chimeric gene to a progeny of
CC plant having the ability to produce levels of free threonine or lysine at
CC least two times greater than the free threonine levels of untransformed
CC plants, a transformed (soybean) plant comprising seeds that accumulate
CC lysine at a level at least ten percent to four-fold higher than the seeds
CC of an untransformed plant, a transformed rapeseed comprising seeds that
CC accumulate lysine to a level between ten percent and one hundred percent
CC higher than that of the seeds of an untransformed plant, a monocot plant
CC comprising in its genome the nucleic acid fragment having the monocot-
CC embryo specific promoter and a transformed corn plant comprising seeds
CC that accumulate lysine to a level between ten percent and one hundred
CC thirty percent higher than the seeds of the untransformed plant. Also
CC disclosed are synthetic lysine-rich seed storage proteins (SSP), built up
CC from monomer lysine-rich heptad repeats (encoded by Bari restriction
CC enzyme-based oligonucleotides) used as a pool of lysine in a transformed
CC plant. The nucleic acid fragments, genes and methods are useful for
CC increasing threonine or lysine content of the seeds of the plant. Seeds
CC containing increased threonine or lysine content eliminate the need to
CC supplement mixed grain feeds with lysine or threonine produced via
CC microbial fermentation. The present sequence is one strand of a DNA
CC encoding a lysine-rich heptad repeat for use as a monomer unit in a
CC synthetic seed storage protein
XX
SQ Sequence 21 BP; 7 A; 1 C; 10 G; 3 T; 0 U; 0 Other;
Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1404 CTTGAGCTTCTCTCCA 1420
Db 19 CTTGAGCTTCTCTCCA 3
RESULT 196
ACH03685/c
ID ACH03685 standard; DNA; 21 BP.
XX
XX ACH03685;
XX
DT 25-SEP-2003 (first entry)
XX
DE Bar I-based lysine-rich heptad repeat oligonucleotide SM82.
XX
XX Aspartokinase; AKII; dihydrodipicolinic acid synthase; DHDS;
KM seed lysine content; seed threonine content; seed storage protein; SSP;
KM chloroplast transit sequence; lysine-rich protein;
KM lysine ketoglutarate reductase; LKR; transgenic; ss.
XX
XX Synthetic.
XX
XX US2003056242-A1.
XX
XX 20-MAR-2003.
XX
XX 17-DEC-2001; 2001US-00023066.
XX

PR 19-MAR-1992; 92US-00855414.
PR 18-MAR-1993; 93MO-US002480.
PR 06-JUN-1994; 94US-00178212.
PR 07-JUN-1995; 95US-00474633.
PR 24-MAR-1997; 97US-00823771.
XX
XX (PALC/) PALCO S. C.
XX
XX Falco SC;
XX
XX WPI; 2003-521869/49.
DR P-PSDB; ABO44324.
XX
XX
PT New nucleic acid fragment encoding aspartokinase and dihydrodipicolinic
PT acid synthase, useful for increasing threonine or lysine content of seeds
PT of plant.
XX
XX Example 21; Page 60; 116pp; English.
XX
CC The invention relates to an isolated nucleic acid fragment comprising a
CC first nucleic acid subfragment encoding aspartokinase (AK) that is
CC substantially insensitive to inhibition by lysine, and a second nucleic
CC acid subfragment encoding dihydrodipicolinic acid synthase (DHDS) that
CC is substantially insensitive to inhibition by lysine. Also included are
CC an isolated nucleic acid fragment comprising a nucleic acid subfragment
CC encoding lysine ketoglutarate reductase (LKR), a chimeric gene (where
CC the nucleic acid fragment is operably linked to a plant chloroplast
CC transit sequence and to a seed-specific regulatory sequence, a plant
CC comprising the nucleic acid/chimeric gene in its genome, a seed obtained
CC from the plant, increasing threonine or lysine content of the seeds of
CC plant, a plant capable of transmitting the chimeric gene to a progeny of
CC plant having the ability to produce levels of free threonine or lysine at
CC least two times greater than the free threonine levels of untransformed
CC plants, a transformed (soybean) plant comprising seeds that accumulate
CC lysine at a level at least ten percent to four-fold higher than the seeds
CC of an untransformed plant, a transformed rapeseed comprising seeds that
CC accumulate lysine to a level between ten percent and one hundred percent
CC higher than that of the seeds of an untransformed plant, a monocot plant
CC comprising in its genome the nucleic acid fragment having the monocot-
CC embryo specific promoter and a transformed corn plant comprising seeds
CC that accumulate lysine to a level between ten percent and one hundred
CC thirty percent higher than the seeds of the untransformed plant. Also
CC disclosed are synthetic lysine-rich seed storage proteins (SSP), built up
CC from monomer lysine-rich heptad repeats (encoded by Bari restriction
CC enzyme-based oligonucleotides) used as a pool of lysine in a transformed
CC plant. The nucleic acid fragments, genes and methods are useful for
CC increasing threonine or lysine content of the seeds of the plant. Seeds
CC containing increased threonine or lysine content eliminate the need to
CC supplement mixed grain feeds with lysine or threonine produced via
CC microbial fermentation. The present sequence is one strand of a DNA
CC encoding a lysine-rich heptad repeat for use as a monomer unit in a
CC synthetic seed storage protein
XX
SQ Sequence 21 BP; 7 A; 2 C; 10 G; 2 T; 0 U; 0 Other;
Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1404 CTTGAGCTTCTCTCCA 1420
Db 19 CTTGAGCTTCTCTCCA 3
RESULT 197
ACH03693/c
ID ACH03693 standard; DNA; 21 BP.
XX
XX ACH03693;
XX
XX 25-SEP-2003 (first entry)
XX
XX Bar I-based lysine-rich heptad repeat oligonucleotide SM86.
DE

XX Aspartokinase; AKII; dihydrodipicolinic acid synthase; DHDPs;
KW seed lysine content; seed threonine content; seed storage protein; SSP;
KM chloroplast transit sequence; lysine-rich protein;
KM lysine ketoglutarate reductase; LKR; transgenic; ss.
XX Synthetic.
OS
PN US200305642-A1.
XX
PD 20-MAR-2003.
XX
PF 17-DEC-2001; 2001US-00023066.
XX
PR 19-MAR-1992; 92US-00855414.
PR 18-MAR-1993; 93WO-US002480.
PR 06-JAN-1994; 94US-00178212.
PR 07-JUN-1995; 95US-00474633.
PR 24-MAR-1997; 97US-00823771.
XX
PA (FALCO/) FALCO S C.
XX
PI Falco SC;
XX
DR WPI; 2003-521869/49.
DR P-PSDB; ABO44332.
XX
PT New nucleic acid fragment encoding aspartokinase and dihydrodipicolinic
PT acid synthase, useful for increasing threonine or lysine content of seeds
PT of plant.
XX
PS Example 21; Page 43; 116bp; English.
XX
XX The invention relates to an isolated nucleic acid fragment comprising a
CC first nucleic acid subfragment encoding aspartokinase (AK) that is
CC substantially insensitive to inhibition by lysine, and a second nucleic
CC acid subfragment encoding dihydrodipicolinic acid synthase (DHDPs) that
CC is substantially insensitive to inhibition by lysine. Also included are
CC an isolated nucleic acid fragment comprising a nucleic acid subfragment
CC encoding lysine ketoglutarate reductase (LKR), a chimeric gene (where
CC the nucleic acid fragment is operably linked to a plant chloroplast
CC transit sequence and to a seed-specific regulatory sequence, a plant
CC comprising the nucleic acid/chimeric gene in its genome, a seed obtained
CC from the plant, increasing threonine or lysine content of the seeds of
CC plant, a plant capable of transmitting the chimeric gene to a progeny of
CC plant having the ability to produce levels of free threonine or lysine at
CC least two times greater than the free threonine levels of untransformed
CC plants, a transformed (soybean) plant comprising seeds that accumulate
CC lysine at a level at least ten percent to four-fold higher than the seeds
CC of an untransformed plant, a transformed rapeseed comprising seeds that
CC accumulate lysine to a level between ten percent and one hundred percent
CC higher than that of the seeds of an untransformed plant, a monocot plant
CC comprising in its genome the nucleic acid fragment having the monoco-
CC embryo specific promoter and a transformed corn plant comprising seeds
CC that accumulate lysine to a level between ten percent and one hundred
CC thirty percent higher than the seeds of the untransformed plant. Also
CC disclosed are synthetic lysine-rich seed storage proteins (SSP), built up
CC from monomer lysine-rich heptad repeats (encoded by Bari restriction
CC enzyme-based oligonucleotides) used as a pool of lysine in a transformed
CC plant. The nucleic acid fragments, genes and methods are useful for
CC increasing threonine or lysine content of the seeds of the plant. Seeds
CC containing increased threonine or lysine content eliminate the need to
CC supplement mixed grain feeds with lysine or threonine produced via
CC microbial fermentation. The present sequence is one strand of a DNA
CC encoding a lysine-rich heptad repeat for use as a monomer unit in a
CC synthetic seed storage protein
XX
SO Sequence 21 BP; 9 A; 1 C; 9 G; 2 T; 0 U; 0 Other;
Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1404 CTTGAGCTTCTCTCCA 1420
Db 19 CTTGAGCTTCTCTCCA 3
RESULT 198
ID ADW71666 standard; DNA; 21 BP.
XX
AC ADW71666;
XX
DT 24-MAR-2005 (first entry)
XX
DE Oligonucleotide SM88 SEQ ID NO:43.
XX
KW ss; transgenic plant; amino acid production; seed; enzyme engineering.
XX
OS Synthetic.
XX
PN US2005005330-A1.
XX
PD 06-JAN-2005.
XX
PF 19-MAR-2004; 2004US-00804678.
XX
PR 06-JAN-1994; 94US-00178212.
PR 07-JUN-1995; 95US-00474633.
PR 27-MAR-1997; 97US-00824627.
PR 27-MAR-1998; 98US-00049304.
XX
PA (FALCO/) FALCO S C.
PA (MCDEVIT R E.
PA (EPEL/) EPELBAUM S U.
XX
PI Falco SC, Mcdevitt RE, Epelbaum SU;
XX
DR WPI; 2005-065280/07.
XX
PT New isolated lysine ketoglutarate reductase/saccharopine dehydrogenase
PT nucleic acid fragment, useful for increasing levels of lysine in the
PT seeds of transformed plants.
XX
PS Example 21; SEQ ID NO 43; 142bp; English.
XX
XX The invention relates to a novel isolated nucleic acid sequence which is
CC useful in antisense inhibition or sense suppression of endogenous lysine
CC ketoglutarate reductase/saccharopine dehydrogenase activity in a corn
CC plant or corn plant cell, where the isolated nucleic acid fragment
CC comprises all or a part of a nucleic acid sequence (ADW71743). The
CC isolated nucleic acid fragment is useful for increasing levels of lysine
CC in the seeds of transformed plants. The present sequence represents an
CC oligonucleotide used to create chimeric genes of the invention.
XX
SQ Sequence 21 BP; 7 A; 1 C; 10 G; 3 T; 0 U; 0 Other;
Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1404 CTTGAGCTTCTCTCCA 1420
Db 19 CTTGAGCTTCTCTCCA 3
RESULT 199
ID ADW71648 standard; DNA; 21 BP.
XX
AC ADW71648;
XX
DT 24-MAR-2005 (first entry)
XX
DE Oligonucleotide SM82 SEQ ID NO:25.

XX 86; transgenic plant; amino acid production; seed; enzyme engineering.
KM Synthetic.
XX US2005005330-A1.
XX
XX 06-JAN-2005.
PD
XX 19-MAR-2004; 2004US-00804678.
PF
XX 06-JAN-1994; 94US-00178212.
PR 07-JUN-1995; 95US-00474633.
PR 27-MAR-1997; 97US-00824627.
PR 27-MAR-1998; 98US-00049304.
XX
XX (FALC/) FALCO S C.
PA (MCDEV/) MCDEVITT R E.
PA (EBEL/) EBELBAUM S U.
XX
XX Falco SC, Mcdevitt RE, Ebelbaum SU;
PI
XX WPI; 2005-065280/07.
XX
XX New isolated lysine ketoglutarate reductase/saccharopine dehydrogenase
PT nucleic acid fragment, useful for increasing levels of lysine in the
PI seeds of transformed plants.
XX
XX Example 21; SEQ ID NO 25; 142pp; English.
XX
XX The invention relates to a novel isolated nucleic acid sequence which is
CC useful in antisense inhibition or sense suppression of endogenous lysine
CC ketoglutarate reductase/saccharopine dehydrogenase activity in a corn
CC plant or corn plant cell, where the isolated nucleic acid fragment
CC comprises all or a part of a nucleic acid sequence (ADW71743). The
CC isolated nucleic acid fragment is useful for increasing levels of lysine
CC in the seeds of transformed plants. The present sequence is used in the
CC invention to to insert repeats of the SSP7 heptad in to a base gene
CC construct of the invention.
XX
XX Sequence 21 BP; 7 A; 2 C; 10 G; 2 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. NO. 1.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1404 CTTGAGCTTCTCTCCA 1420
Db 19 CTTGAGCTTCTCTCCA 3
XX
XX RESULT 200
ADW71664/c
ID ADW71664 standard; DNA; 21 BP.
XX
XX ADM71664;
AC
XX 24-MAR-2005 (first entry)
DT
XX Oligonucleotide SM86 SEQ ID NO:41.
DE
XX 86; transgenic plant; amino acid production; seed; enzyme engineering.
KM
XX Synthetic.
OS
XX US2005005330-A1.
PN
XX 06-JAN-2005.
PD
XX 19-MAR-2004; 2004US-00804678.
PF
XX 06-JAN-1994; 94US-00178212.
PR 07-JUN-1995; 95US-00474633.
PR

PR 27-MAR-1997; 97US-00824627.
PR 27-MAR-1998; 98US-00049304.
XX
XX (FALC/) FALCO S C.
PA (MCDEV/) MCDEVITT R E.
PA (EBEL/) EBELBAUM S U.
XX
XX Falco SC, Mcdevitt RE, Ebelbaum SU;
PI
XX WPI; 2005-065280/07.
XX
XX New isolated lysine ketoglutarate reductase/saccharopine dehydrogenase
PT nucleic acid fragment, useful for increasing levels of lysine in the
PT seeds of transformed plants.
XX
XX Example 21; SEQ ID NO 41; 142pp; English.
XX
XX The invention relates to a novel isolated nucleic acid sequence which is
CC useful in antisense inhibition or sense suppression of endogenous lysine
CC ketoglutarate reductase/saccharopine dehydrogenase activity in a corn
CC plant or corn plant cell, where the isolated nucleic acid fragment
CC comprises all or a part of a nucleic acid sequence (ADW71743). The
CC isolated nucleic acid fragment is useful for increasing levels of lysine
CC in the seeds of transformed plants. The present sequence represents an
CC oligonucleotide used to create chimeric genes of the invention.
XX
XX Sequence 21 BP; 9 A; 1 C; 9 G; 2 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. NO. 1.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1404 CTTGAGCTTCTCTCCA 1420
Db 19 CTTGAGCTTCTCTCCA 3
XX
XX RESULT 201
ABT44412/c
ID ABT44412 standard; DNA; 20 BP.
XX
XX ABR44412;
AC
XX 06-NOV-2003 (first entry)
DT
XX Chimeric antisense oligonucleotide ISIS 192387 to inhibit human ESRB.
DE
XX Oestrogen receptor beta; ERSB; steroid hormone; female sexual maturation;
KM bone maintenance; cardiovascular system; ER beta; oestrogen receptor 2;
KM ERS2; Alzheimer's; uterine leiomyomata; cytostatic; kidney neoplasm; 86;
KM cellular proliferation; cancer; human; antisense; chimeric.
XX
XX Chimeric - Homo sapiens.
OS
XX WO2003050133-A1.
PN
XX 19-JUN-2003.
PD
XX 06-DEC-2002; 2002WO-US039200.
PF
XX 07-DEC-2001; 2001US-00005058.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX Dobie KW, Roach MP, Koller E;
PI
XX WPI; 2003-577284/54.
DR
XX
XX New antisense oligonucleotides for modulating estrogen receptor beta gene
PT expression, particularly useful for treating cancer, specifically
PT leiomyoma, pancreatic cancer, prostate cancer, breast cancer, bone cancer
PT or lymphoma.
XX

PS Claim 3; Page 81; 160pp; English.

XX This invention relates to a novel antisense compounds that modulate the
 CC expression of oestrogen receptor beta (ERSB). Oestrogen is a steroid
 CC hormone that exerts a wide range of effects throughout the human body
 CC being primarily involved in female sexual maturation. Additionally,
 CC however, oestrogen targets male reproductive tissues, is known to be
 CC important in bone maintenance and plays a protective role in the
 CC cardiovascular system. This hormone receptor, ERB (also known as ER
 CC beta, oestrogen receptor 2 and ERS2) has been mapped to chromosome 14q22-
 CC q24, a region known to be associated with early onset of Alzheimer's
 CC disease, uterine leiomyomata and neoplasms of the kidney. Furthermore,
 CC ERB has been localised to metastatic cells indicating an involvement in
 CC cellular proliferation. Accordingly, the selective inhibition of ERB by
 CC the cytoskeletal antisense oligonucleotides of this invention could provide
 CC a therapeutic target for the treatment of cancer, as well as other ERB-
 CC related disorders. This oligonucleotide sequence is the chimeric human
 CC antisense oligo used to inhibit expression of human ERB, the aim of the
 CC invention. Note that it has two terminal five nucleotide 2'-methoxyethyl
 CC (2'-MOE) wings separated by a ten deoxynucleotide gap. The
 CC oligonucleotide backbone is phosphorothioate throughout

CC SQ Sequence 20 BP; 4 A; 4 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 1.0%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.5e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 434 CCTTCGCGAGGCGCTTCATG 453
 DB 20 CCTTCACCGAGCGCTTCATG 1

RESULT 202
 ADB90814/C
 ID ADB90814 standard; DNA; 20 BP.

AC ADB90814;
 XX 04-DEC-2003 (first entry)

DE Human selenophosphate synthetase sense PCR primer.

XX ss; PCR; human; selenophosphate synthetase; abnormal physiology;
 KM abnormal development; selenium poisoning; abnormal iron tolerance;
 KM abnormal oxygen tolerance; autoimmune disorder; primer.

OS Homo sapiens.
 XX
 XX US6586217-B1.
 PN 01-JUL-2003.
 PD 18-DEC-1998; 98US-00215418.
 PF 17-MAR-1995; 95US-00406359.
 PR (SCHE) SCHERING CORP.
 XX
 XX (SCHE) SCHERING CORP.
 PA
 XX Guimaraes MJ, Bazan JF, Zlotnik A;
 PI WPI; 2003-677803/64.
 DR

XX New isolated or recombinant polynucleotide encoding a selenophosphate
 PT synthetase protein, useful for diagnosing and treating abnormal
 PT physiology or development, selenium poisoning and autoimmune disorders.
 XX
 XX Example; Col 32; 30pp; English.

XX The invention relates to an isolated or recombinant polynucleotide
 CC encoding a mature polypeptide with selenophosphate synthetase activity.
 CC The methods and compositions of the present invention are disclosed as
 CC being useful for diagnosing and treating conditions associated with the

CC selenophosphate synthetase (SPS) protein, such as abnormal physiology or
 CC development, selenium poisoning, abnormal iron or oxygen tolerance and
 CC autoimmune disorders. They can also be used as probes for detecting an
 CC levels of protein message in samples from patients suspected of having an
 CC abnormal conditions, such as cancer or developmental problem, and as
 CC diagnostic kits which test for the qualitative or quantitative presence
 CC of other markers. The enzymes may be used to screen for chemical
 CC modulators of SPS. Antibodies to SPS may be useful as SPS antagonists.
 CC The present sequence represents the human selenophosphate synthetase
 CC sense PCR primer.

CC SQ Sequence 20 BP; 5 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 1.0%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.5e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1270 CTGAGAGCCACCATCTCCAC 1289
 DB 20 CTGAGAGCCACCATCTTAC 1

RESULT 203
 AEE77695
 ID AEE77695 standard; DNA; 20 BP.

AC AEE77695;
 XX 09-FEB-2006 (first entry)

DE Human dopamine receptor D2 (DRD2) DNA oligonucleotide SEQ ID NO:1316.

XX Diagnosis; therapeutic; neurological disease; psychiatric disorder;
 KM neuropsychologic disorder; dopamine receptor D2; DRD2; ss.

OS Homo sapiens.
 XX
 XX WO2005118843-A1.
 PN 15-DEC-2005.
 PD 01-JUN-2005; 2005MO-AU000775.
 PF 01-JUN-2004; 2004AU-00902919.
 PR (UQU-) UNIV QUEENSLAND TECHNOLOGY.
 XX
 XX Morris CP, Van Daal A, Swagell CD, Lawford BR, Young RM;
 PI WPI; 2006-047555/05.
 DR

XX Identifying genetic profile associated with a neurological, psychiatric,
 PT or psychological condition, comprises screening individuals for a
 PT polymorphism in a genetic locus comprising the dopamine receptor D2
 PT (DRD2) gene.

PS Claim 31; SEQ ID NO 1316; 634pp; English.

XX The invention relates to a method of identifying a genetic profile
 CC associated with a neurological, psychiatric or psychological condition,
 CC phenotype or state including a sub-threshold neurological, psychiatric or
 CC psychological condition, phenotype or state in an individual, comprising
 CC screening individuals for a polymorphism in a genetic locus comprising
 CC the dopamine receptor D2 (DRD2) gene. The invention also relates to a
 CC genetic mutation providing a genetic marker for a neurological,
 CC psychiatric, or psychological condition, state or phenotype in an
 CC individual, where the presence of a 957C polymorphism is indicative of a
 CC predisposition to developing a neurological, psychiatric or psychological
 CC condition, phenotype or state. The compositions and methods are useful
 CC for identifying a genetic profile associated with a neurological,
 CC psychiatric or psychological condition. The method enables clinicians to
 CC make a genetic-based diagnosis of a neurological, psychiatric or
 CC psychological condition and can thereby implement treatment or

CC preventative or symptom-ameliorating protocols to reduce the adverse
CC consequences of the condition. This sequence represents a human dopamine
CC receptor D2 (DRD2) DNA oligonucleotide used in the scope of the
CC invention.
XX
SQ Sequence 20 BP; 2 A; 7 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 979 TTGCGCATCTGCTGCTGCGC 998
Db 1 TTGATCATCTCTGCTGCTGCC 20
RESULT 204
AEE77704
ID AEE77704 standard; DNA; 20 BP.
XX
AC AEE77704;
XX
DT 09-FEB-2006 (first entry)
XX
DE Human dopamine receptor D2 (DRD2) DNA oligonucleotide SEQ ID NO:1325.
XX
KM Diagnosis; therapeutic; neurological disease; psychiatric disorder;
KM neuropsychological disorder; dopamine receptor D2; DRD2; ss.
XX
OS Homo sapiens.
XX
PN WO2005118843-A1.
XX
PD 15-DEC-2005.
PF 01-JUN-2005; 2005WO-AU000775.
XX
PR 01-JUN-2004; 2004AU-00902919.
PA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
PI Morris CP, Van Daal A, Swagell CD, Lawford BR, Young RM;
XX WPI; 2006-047555/05.
DR
XX
XX Identifying genetic profile associated with a neurological, psychiatric,
PT or psychological condition, comprises screening individuals for a
PT polymorphism in a genetic locus comprising the dopamine receptor D2
PT (DRD2) gene.
XX
XX Claim 31; SEQ ID NO 1325; 634pp; English.
PS
XX The invention relates to a method of identifying a genetic profile
CC associated with a neurological, psychiatric or psychological condition,
CC phenotype or state including a sub-threshold neurological, psychiatric or
CC psychological condition, phenotype or state in an individual, comprising
CC screening individuals for a polymorphism in a genetic locus comprising
CC the dopamine receptor D2 (DRD2) gene. The invention also relates to a
CC genetic mutation providing a genetic marker for a neurological,
CC psychiatric, or psychological condition, state or phenotype in an
CC individual, where the presence of a 957C polymorphism is indicative of a
CC predisposition to developing a neurological, psychiatric or psychological
CC condition, phenotype or state. The compositions and methods are useful
CC for identifying a genetic profile associated with a neurological,
CC psychiatric or psychological condition. The method enables clinicians to
CC make a genetic-based diagnosis of a neurological, psychiatric or
CC psychological condition and can thereby implement treatment or
CC preventative or symptom-ameliorating protocols to reduce the adverse
CC consequences of the condition. This sequence represents a human dopamine
CC receptor D2 (DRD2) DNA oligonucleotide used in the scope of the
CC invention.
XX
SQ Sequence 20 BP; 1 A; 7 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 988 TGCTGGCTGCGCCTTCACAT 1007
Db 1 TGCTGGCTGCGCCTTCTCAT 20
RESULT 205
AEE77703
ID AEE77703 standard; DNA; 20 BP.
XX
AC AEE77703;
XX
DT 09-FEB-2006 (first entry)
XX
DE Human dopamine receptor D2 (DRD2) DNA oligonucleotide SEQ ID NO:1324.
XX
KM Diagnosis; therapeutic; neurological disease; psychiatric disorder;
KM neuropsychological disorder; dopamine receptor D2; DRD2; ss.
XX
OS Homo sapiens.
XX
PN WO2005118843-A1.
XX
PD 15-DEC-2005.
PF 01-JUN-2005; 2005WO-AU000775.
XX
PR 01-JUN-2004; 2004AU-00902919.
PA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
PI Morris CP, Van Daal A, Swagell CD, Lawford BR, Young RM;
XX WPI; 2006-047555/05.
DR
XX
XX Identifying genetic profile associated with a neurological, psychiatric,
PT or psychological condition, comprises screening individuals for a
PT polymorphism in a genetic locus comprising the dopamine receptor D2
PT (DRD2) gene.
XX
XX Claim 31; SEQ ID NO 1324; 634pp; English.
PS
XX The invention relates to a method of identifying a genetic profile
CC associated with a neurological, psychiatric or psychological condition,
CC phenotype or state including a sub-threshold neurological, psychiatric or
CC psychological condition, phenotype or state in an individual, comprising
CC screening individuals for a polymorphism in a genetic locus comprising
CC the dopamine receptor D2 (DRD2) gene. The invention also relates to a
CC genetic mutation providing a genetic marker for a neurological,
CC psychiatric, or psychological condition, state or phenotype in an
CC individual, where the presence of a 957C polymorphism is indicative of a
CC predisposition to developing a neurological, psychiatric or psychological
CC condition, phenotype or state. The compositions and methods are useful
CC for identifying a genetic profile associated with a neurological,
CC psychiatric or psychological condition. The method enables clinicians to
CC make a genetic-based diagnosis of a neurological, psychiatric or
CC psychological condition and can thereby implement treatment or
CC preventative or symptom-ameliorating protocols to reduce the adverse
CC consequences of the condition. This sequence represents a human dopamine
CC receptor D2 (DRD2) DNA oligonucleotide used in the scope of the
CC invention.
XX
SQ Sequence 20 BP; 1 A; 8 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 987 CTGCTGGCTGCGCCTTCACA 1006

Db 1 CTGCTGCTGCTGCTTCTTCA 20

RESULT 206
AEE77696 standard; DNA; 20 BP.

AC AEE77696;

DT 09-FEB-2006 (first entry)

DE Human dopamine receptor D2 (DRD2) DNA oligonucleotide SEQ ID NO:1317.

KW Diagnosis; therapeutic; neurological disease; psychiatric disorder;
neuropsychological disorder; dopamine receptor D2; DRD2; ss.

OS Homo sapiens.

PN MO2005118843-A1.

PD 15-DEC-2005.

PF 01-JUN-2005; 2005MO-AU000775.

PR 01-JUN-2004; 2004AU-00902919.

PA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.

PI Morris CP, Van Daal A, Swagell CD, Lawford BR, Young RM;

XX WPI; 2006-047555/05.

XX Identifying genetic profile associated with a neurological, psychiatric,
PT or psychological condition, comprises screening individuals for a
PT polymorphism in a genetic locus comprising the dopamine receptor D2
PT (DRD2) gene.

PS Claim 31; SEQ ID NO 1317; 634bp; English.

XX The invention relates to a method of identifying a genetic profile
XX associated with a neurological, psychiatric or psychological condition,
XX phenotype or state including a sub-threshold neurological, psychiatric or
XX psychological condition, phenotype or state in an individual, comprising
XX screening individuals for a polymorphism in a genetic locus comprising
XX the dopamine receptor D2 (DRD2) gene. The invention also relates to a
XX genetic mutation providing a genetic marker for a neurological,
XX psychiatric, or psychological condition, state or phenotype in an
XX individual, where the presence of a 957C polymorphism is indicative of a
XX predisposition to developing a neurological, psychiatric or psychological
XX condition, phenotype or state. The compositions and methods are useful
XX for identifying a genetic profile associated with a neurological,
XX psychiatric or psychological condition. The method enables clinicians to
XX make a genetic-based diagnosis of a neurological, psychiatric or
XX psychological condition and can thereby implement treatment or
XX preventative or symptom-ameliorating protocols to reduce the adverse
XX consequences of the condition. This sequence represents a human dopamine
XX receptor D2 (DRD2) DNA oligonucleotide used in the scope of the
XX invention.

SQ Sequence 20 BP; 2 A; 8 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 1.0%; Score 16.8; DB 1; Length 20;

Best Local Similarity 90.0%; Pred. No. 1.5e+02; Mismatches 2; Indels 0; Gaps 0;

QY 980 TCGGCATCTGCTGCTGCC 999

Db 1 TCATCATCTGCTGCTGCC 20

RESULT 207
AEE77705

ID AEE77705 standard; DNA; 20 BP.

AC AEE77705;

DT 09-FEB-2006 (first entry)

DE Human dopamine receptor D2 (DRD2) DNA oligonucleotide SEQ ID NO:1326.

KW Diagnosis; therapeutic; neurological disease; psychiatric disorder;
neuropsychological disorder; dopamine receptor D2; DRD2; ss.

OS Homo sapiens.

PN MO2005118843-A1.

PD 15-DEC-2005.

PF 01-JUN-2005; 2005MO-AU000775.

PR 01-JUN-2004; 2004AU-00902919.

PA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.

PI Morris CP, Van Daal A, Swagell CD, Lawford BR, Young RM;

XX WPI; 2006-047555/05.

XX Identifying genetic profile associated with a neurological, psychiatric,
PT or psychological condition, comprises screening individuals for a
PT polymorphism in a genetic locus comprising the dopamine receptor D2
PT (DRD2) gene.

PS Claim 31; SEQ ID NO 1326; 634bp; English.

XX The invention relates to a method of identifying a genetic profile
XX associated with a neurological, psychiatric or psychological condition,
XX phenotype or state including a sub-threshold neurological, psychiatric or
XX psychological condition, phenotype or state in an individual, comprising
XX screening individuals for a polymorphism in a genetic locus comprising
XX the dopamine receptor D2 (DRD2) gene. The invention also relates to a
XX genetic mutation providing a genetic marker for a neurological,
XX psychiatric, or psychological condition, state or phenotype in an
XX individual, where the presence of a 957C polymorphism is indicative of a
XX predisposition to developing a neurological, psychiatric or psychological
XX condition, phenotype or state. The compositions and methods are useful
XX for identifying a genetic profile associated with a neurological,
XX psychiatric or psychological condition. The method enables clinicians to
XX make a genetic-based diagnosis of a neurological, psychiatric or
XX psychological condition and can thereby implement treatment or
XX preventative or symptom-ameliorating protocols to reduce the adverse
XX consequences of the condition. This sequence represents a human dopamine
XX receptor D2 (DRD2) DNA oligonucleotide used in the scope of the
XX invention.

SQ Sequence 20 BP; 1 A; 8 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 1.0%; Score 16.8; DB 1; Length 20;

Best Local Similarity 90.0%; Pred. No. 1.5e+02; Mismatches 2; Indels 0; Gaps 0;

QY 989 GCTGCTGCCCTTCACATC 1008

Db 1 GCTGCTGCCCTTCATC 20

RESULT 208
AAZ50619/c

ID AAZ50619 standard; DNA; 21 BP.

AC AAZ50619;

DT 20-JUN-2000 (first entry)

PT	17-MAY-1991;	91US-00701935.	
PR	17-MAY-1991;	91US-00701937.	
XX			
XX	(MERI) MERCK & CO INC.		
PA			
PI	Strader CD, Fong TM;		
XX			
DR	WPI, 1992-384034/47.		
XX			
PT	New human neurokinin-1 receptor short form protein - useful for		
PT	identifying and determining substance P antagonists in arthritic		
PT	patients.		
XX			
XX	Example 1; Page 8; 36pp; English.		
XX			
CC	Human mRNA was prepared from 3 glioblastoma cell lines T98G, CCF-SSTG1		
CC	and U87MG. First strand cDNA was synthesised and used as template with		
CC	rat primers rspr284, rspr284h and rspr7a2 (AAQ30774-6) in first round PCR		
CC	amplification. Secondary PCR was performed on the amplified product using		
CC	the same 3 primers prior to a third round of amplification, this time		
CC	using the primers rspr284, rspr284h, rspr7a1 (AAQ30777) and rspr7a1h		
CC	(AAQ30778). The tertiary PCR product was sequenced and was found to have		
CC	90% identity at the nucleotide level with the central core region of the		
CC	rat NK1R from amino acid 91 to 280. Primer rspr284 is a sense primer		
CC	based on the rat NK1R sequence 238-255 (numbering as in J.Biol.Chem. 264:		
CC	17649-17652, 1989). (Updated on 25-MAR-2003 to correct PN field.)		
XX			
SQ	Sequence 18 BP; 4 A; 4 C; 4 G; 6 T; 0 U; 0 Other;		
Query Match	0.9%;	Score 16.4;	DB 1; Length 18;
Best Local Similarity	94.4%;	Pred. No. 1.3e+02;	
Matches 17; Conservative	0;	Mismatches 1;	Indels 0; Gaps 0
QY	448	TCCATGGCTGCATTCAT 465	
DB	1	TGCATGGCTGCATTCAT 18	
RESULT 210			
AAW73459/c			
ID	AAW73459 standard; RNA; 18 BP.		
AC			
XX	AAW73459;		
DT			
XX	28-JUL-1999 (first entry)		
DE			
XX	Mouse flk-1 VEGF receptor hairpin ribozyme substrate #6.		
KW	Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;		
KW	KDR; hammetthead ribozyme; hairpin ribozyme; cleavage;		
KW	tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;		
KW	fmf-like tyrosine kinase 1; kinase insert domain containing receptor;		
XX	fetal liver kinase 1; ss.		
XX			
MS	sp.		
XX			
PN	MO9715662-A2.		
PD			
XX	01-MAY-1997.		
XX			
PF	25-OCT-1996;	96WO-US017480.	
XX			
PR	26-OCT-1995;	95US-0005974P.	
PR	11-JAN-1996;	96US-00584040.	
XX			
PA	(RIBO-) RIBOZYME PHARM INC.		
PA	(CHIR) CHIRON CORP.		
PI	Pavco P, Mcswigen J, Stinchcomb D, Escobedo J;		
XX			
DR	WPI; 1997-259017/23.		
XX			
PT	Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA		

PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
PS Claim 4; Page 150; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAY57275 to AAY5752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
SQ Sequence 18 BP; 2 A; 6 C; 8 G; 0 T; 2 U; 0 Other;
Query Match 0.9%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 624 CCAGCCCGGCTGTCAGC 641
18 CCAGCCGCGGCTGTCAGC 1
DB
RESULT 211
ADJ47994/C
ID ADJ47994 standard; DNA; 19 BP.
XX
XX ADJ47994;
AC
XX
XX 06-MAY-2004 (first entry)
DT
XX
DE Human OGR-1 probe1, seq id 4.
XX
XX Cardiovascular; cytostatic; antiinflammatory; gastrointestinal; CNS;
XX central nervous system; gene therapy; antagonist; antisense therapy;
XX haematological disease; cancer; cardiovascular disease;
XX inflammatory disease; gastrointestinal disease;
XX ovarian cancer G-protein coupled receptor 1; OGR-1; probe; ss.
XX
XX Homo sapiens.
OS
XX
XX WO2004015422-A2.
PN
XX
XX 19-FEB-2004.
PD
XX
XX 23-JUL-2003; 2003WO-EP008048.
PF
XX
XX 05-AUG-2002; 2002EP-00016980.
PR
XX
XX (PARB) BAYER HEALTHCARE AG.
PA
XX
XX Golz S, Brueggemeier U, Summer H;
PI
XX
XX WPI; 2004-191805/18.
DR
XX
XX Screening for therapeutic agents, useful in treating e.g., cancer,
PT cardiovascular disorders or central nervous system disorder, comprises
PT contacting a test compound with ovarian cancer G-protein coupled receptor
PT 1 and determining activity.
PT
XX
XX Example 2; SEQ ID NO 4; 118pp; English.
PS
XX
XX The invention relates to the screening of therapeutic agents useful in
CC the treatment of haematological diseases, cancer, cardiovascular
CC diseases, inflammatory diseases, gastrointestinal diseases and disorders
CC of the peripheral and central nervous system in a mammal. The method
CC comprises contacting a test compound with an ovarian cancer G-protein
CC coupled receptor 1 (OGR-1) polypeptide or polynucleotide. The method is
CC useful in screening for therapeutic agents, and also for the treatment of

CC diseases mentioned above. The regulators of an OGR-1 are useful for
CC regulating OGR-1 activity or for preparing a pharmaceutical composition
CC for the treatment of the stated diseases in a mammal. The current
CC sequence represents a probe used in the expression profiling of human OGR
CC -1 receptor encoding DNA.
XX
XX
SQ Sequence 19 BP; 7 A; 3 C; 8 G; 1 T; 0 U; 0 Other;
Query Match 0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 985 ATCTGCTCGGCTGCCCTTC 1002
19 ATCTGCTCGGCTGCCCTTC 2
DB
RESULT 212
ACCT0594/C
ID ACCT0594 standard; DNA; 20 BP.
XX
XX ACCT0594;
AC
XX
XX 13-AUG-2003 (first entry)
DT
XX
XX Sphingosine-1-phosphate lyase antisense oligonucleotide, SEQ ID 87.
DE
XX
XX Cytostatic; antimicrobial; antiinflammatory; tumour; infection;
XX sphingosine-1-phosphate lyase; developmental disorder; apoptosis;
XX inflammation; antisense; phosphorothioate; ss.
XX
XX Synthetic.
OS
XX
XX
XX Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "This oligonucleotide has a phosphorothioate
FT backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'
FT and 3' ends, which are 5 nucleotides in length. Also all
FT cytidine residues are 5-methylcytidines"
XX
XX
XX WO2003028637-A2.
PN
XX
XX 10-APR-2003.
PD
XX
XX 26-SEP-2002; 2002WO-US030575.
PF
XX
XX 28-SEP-2001; 2001US-00967669.
PR
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX
XX Bennett FC, Freier SM;
PI
XX
XX WPI; 2003-381581/36.
DR
XX
XX New antisense oligonucleotides for modulating sphingosine-1-phosphate
PT lyase gene expression, useful for preventing or treating a developmental
PT disorder or aberrant apoptosis, e.g. infection, inflammation or tumor
PT formation.
PT
XX
XX Claim 3; Page 74; 118pp; English.
PS
XX
XX The present invention relates to novel antisense oligonucleotides
CC (ACCT0520-ACCT0597) which are targeted to a sphingosine-1-phosphate lyase
CC DNA sequence, and specifically hybridizes with the nucleic acid and
CC inhibits the expression of sphingosine-1-phosphate lyase. The antisense
CC oligonucleotides are useful for treating an animal having a disease or
CC condition associated with sphingosine-1-phosphate lyase, particularly a
CC developmental disorder, or a disease or condition arising from aberrant
CC apoptosis, e.g. infection, inflammation or tumour formation
XX
XX
SQ Sequence 20 BP; 7 A; 7 C; 4 G; 2 T; 0 U; 0 Other;

Best Local Similarity 94.4%; Pred. No. 1.7e+02;

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RESULT 215
 ABLK03471
 ID ABLK03471 standard; RNA; 17 BP.
 XX
 AC ABLK03471;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human CD20 zinzyme #22.
 XX
 KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNAzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 KW
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 XX
 PN WO200159103-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US004273.
 XX
 PR 11-FEB-2000; 2000US-0181797P.
 PR 28-FEB-2000; 2000US-0185516P.
 PR 06-MAR-2000; 2000US-0187128P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSM/) MCSWIGGEN J.
 PA (CHOW/) CHOWMIRA B M.
 XX
 PI Blatt L, Mcswiggen J, Chowmira BM;
 XX
 DR WPI; 2001-607195/69.
 XX
 PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX
 PS Claim 30; Page 154; 2000P; English.
 XX
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNAzyme) an inozyme (an endolytic nucleic acid cleaving a an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a condition associated with the level
 CC of the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the

cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is a zinzyme molecule of the invention
 XX
 SQ Sequence 17 BP; 2 A; 4 C; 5 G; 0 T; 6 U; 0 Other;
 XX
 QY 801 CACCTGNGTACTGTG 816
 DB 2 CAUCUGUGACUGUG 17
 XX
 Query Match 0.9%; Score 16; DB 1; Length 17;
 Best Local Similarity 62.5%; Pred. No. 1.3e+02;
 Matches 10; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 XX
 RESULT 216
 ABL53529
 ID ABL53529 standard; DNA; 20 BP.
 XX
 AC ABL53529;
 XX
 DT 10-JUN-2002 (first entry)
 XX
 DE Mouse SAM1b sense oligonucleotide.
 XX
 KW SAM1b; meiosis activating sterol; MAS; receptor; mouse; oocyte;
 KW signal transduction; fertility; antisense; ss.
 XX
 OS Mus musculus.
 XX
 FH Key location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /note= "phosphorothioate linkage"
 XX
 PN WO200216433-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 24-AUG-2001; 2001WO-DK00558.
 XX
 PR 25-AUG-2000; 2000DK-00001259.
 PR 20-AUG-2001; 2001WO-DK00550.
 XX
 PA (NOVO) NOVO NORDISK AS.
 PA (SCHD) SCHERING AG.
 XX
 PI Wahl P, Vissing H, Grondahl C;
 XX
 DR WPI; 2002-257907/30.
 XX
 PT Receptors and signaling proteins of Meiotic Acting Sterols and nucleic
 PT acids, useful in modulating in gamete maturation process induced by beta
 PT -hydroxy-4,4-dimethylcholesterol-8,14,24-triene.
 XX
 PS Example 1; Page 19; 60P; English.
 XX
 CC The present sequence is that of a phosphorothioate sense oligonucleotide
 CC that corresponds to the Kozak sequence of SAM1b mRNA. It was
 CC microinjected into mouse oocytes where, unlike the corresponding
 CC antisense sequence (see ABL53527), it did not selective inhibition of
 CC SAM1b mRNA. SAM1b is a receptor of meiosis activating sterols (MAS) and
 CC is involved in the gamete maturation process induced by beta-hydroxy-4,4
 CC -dimethylcholesterol-8,14,24-triene (PP-MAS), specifically inducing, upon
 CC ligand activation, germinal vesicle breakdown in oocytes. The invention
 CC provides SAM1a polynucleotides (including RNA antisense sequences),

CC	compounds for use in men and women
XX	
SQ	Sequence 20 BP; 5 A; 6 C; 7 G; 2 T; 0 U; 0 Other;
	Query Match 0.9%; Score 16; DB 1; Length 20;
	Best Local Similarity 100.0%; Pred. No. 1.9e+02;
	Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	680 TTGGCTCTCTGCTGGC 695
Db	16 TTGGCTCTCTGCTGGC 1
RESULT 218	
ACF79553	ACF79553 standard; DNA; 20 BP.
XX	ACF79553;
AC	ACF79553;
XX	18-DEC-2003 (first entry)
XX	Oligonucleotide sense to SAM1b mRNA Kozak sequence.
DE	Mouse; SAM1b, meiotic acting sterol; signal transduction;
KW	antifertility; contraceptive; ss.
XX	
OS	Mus sp.
XX	
FH	Key Location/Qualifiers
FT	modified_site 1..20
FT	/*tag= a
FT	/mod Base= OTHER
XX	/note= "OTHER= phosphorothioate oligonucleotides"
PN	MO2003070766-A2.
PD	28-AUG-2003.
XX	
PF	31-JAN-2003; 2003MO-DK000058.
XX	
PR	22-FEB-2002; 2002DK-00000277.
XX	
PA	(NOVO) NOVO NORDISK AS.
PI	Grondahl C, Wahl P, Norby PL, Stenmicke VM;
XX	
DR	WPI; 2003-671806/63.
XX	
PT	New polynucleotide encoding a transducer of meiotic acting sterol-
PT	signaling or its regulatory domain, useful for isolating tissue specific
PT	variants of the transducer which may be used as anti-fertility or
PT	contraception drugs.
XX	
XX	Example 1; Page 18; 55pp; English.
XX	
XX	The present sequence is that of a sense oligonucleotide that corresponds
CC	to the Kozak sequence of mouse SAM1b mRNA (see ACF79541). It was used as
CC	a control in experiments with the corresponding antisense oligonucleotide
CC	(see ACF79551). Selective inhibition of the mRNA showed that SAM1b is
CC	crucially involved in meiotic acting sterol (MAS) signalling, since a
CC	functional knockout of de novo protein synthesis partly disrupted MAS
CC	signals in oocytes. SAM1b is a transducer of MAS signalling and is
CC	involved in the gamete maturation process induced by 3beta-hydroxy-4,4-
CC	diethyl cholesterol-8,14,24-triene (FF-MAS), specifically inducing germinal
CC	vesicle breakdown in mouse oocyte cultures in vitro. SAM1b can be used to
CC	screen for agonists or antagonists of FF-MAS activity for use as
CC	antifertility or contraceptive drugs
XX	
SQ	Sequence 20 BP; 2 A; 7 C; 6 G; 5 T; 0 U; 0 Other;
Query Match	0.9%; Score 16; DB 1; Length 20;
Best Local Similarity	100.0%; Pred. No. 1.9e+02;
Matches 16; Conservative	0; Mismatches 0; Indels 0; Gaps 0;

AC ADH49397;
XX
XX 25-MAR-2004 (first entry)
DE MAS-signalling transducer related SAM1 cDNA primer, SEQ ID 12.
XX
XX transducer of meiosis activating sterols; MAS; signalling;
XX antifertility; MAS-signalling transducer;
KM 4,4-dimethyl-5-alpha-cholesta-8,14,24-triene-3-beta-ol; FP-MAS; tissue;
KM organ specific; meiosis; infertility; contraception; ss; primer; SAM1.
XX
XX Unidentified.
XX
XX US2003219791-A1.
XX
XX 27-NOV-2003.
XX
XX 20-FEB-2003; 2003US-00370860.
XX
XX 20-FEB-2003; 2003US-00370860.
XX
XX (STEN/) STENNICKE V W.
XX (NOR/) NORBY P L.
XX (GRON/) GRONDAHL C.
XX (WAHL/) WAHL P.
XX
XX Stennicke VM, Norby PL, Grondahl C, Wahl P;
XX
XX WPI; 2004-060179/06.
XX
XX Novel transducer of meiosis activating sterols designated SAM1a and SAM1b
XX useful for screening for agonist or antagonist of meiosis activating
XX PT sterols used to treat infertility or to provide a way of contraception.
XX
XX Example 2; SEQ ID NO 12; 31pp; English.
XX
XX The invention relates to a novel isolated transducer of meiosis
XX activating sterols (MAS)-signalling, its peptide fragment or a salt. The
XX isolated MAS-signalling transducer has antifertility activity. The MAS-
XX signalling transducer is useful for detecting the presence of a compound
XX or its salt which has affinity for the MAS-signalling transducer. The MAS
XX -signalling transducer is useful for detecting the presence of an
XX antagonist or agonist of the MAS-signalling transducer. The MAS-
XX signalling transducer is useful for detecting the presence of an
XX antagonist or agonist of the MAS-signalling transducer. The MAS-
XX signalling transducer is useful for detecting the presence of an agonist
XX or antagonist of the MAS-signalling transducer. The MAS-signalling
XX transducer is useful for screening for agonist or antagonist activity of
XX 4,4-dimethyl-5-alpha-cholesta-8,14,24-triene-3-beta-ol (FP-MAS) or MAS. An
XX expression vector containing the nucleic acid which encodes the MAS-
XX signalling transducer is useful for isolation of tissue and/or organ
XX specific variants of the MAS-signalling transducer. The agonist or
XX antagonist of the MAS-signalling transducer identified using the
XX transducer provides a way to control meiosis in order to treat
XX infertility or to achieve a novel principle of contraception. This
XX polynucleotide sequence represents a primer used in the exemplification
XX of the invention.
XX
XX Sequence 20 BP; 2 A; 7 C; 6 G; 5 T; 0 U; 0 Other;
SQ
Query Match 0.9%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 680 TGGCTCTCCTGCTGCG 695
Db 5 TGGCTCTCCTGCTGCG 20
RESULT 222
AAV01172/c
ID AAV01172 standard; DNA; 19 BP.
XX
AC AAV01172;
XX

DT 23-MAR-1998 (first entry)
XX
XX Adrenergic receptor beta 2 PCR primer for universal mammalian STS's.
DE
XX PCR primer; polymerase chain reaction; amplification; UM-STS;
XX universal mammalian sequence tagged site; genomic map; clone; ss.
XX
XX Synthetic.
XX
XX WO9731012-A1.
XX
XX 28-AUG-1997.
XX
XX 18-FEB-1997; 97WO-US002403.
XX
XX 22-FEB-1996; 96US-0012061P.
XX
XX (UNMI) UNIV MICHIGAN.
XX (UNMS) UNIV MICHIGAN STATE.
XX
XX Brewer GJ, Venta PJ, Yuzbasiyan-Gurkan V;
XX
XX WPI; 1997-435083/40.
XX
XX New oligonucleotide primers amplifying gene regions conserved among
XX PT mammals - useful for developing genomic maps, isolating clones and making
XX cross-species comparisons.
XX
XX Claim 1; Page 10; 26pp; English.
XX
XX The present sequence represents a specifically claimed oligonucleotide
XX PCR primer. The oligonucleotide can be used for polymerase chain reaction
XX (PCR) amplification of DNA, specifically regions of specific genes that
XX are conserved among mammalian species, i.e. pairs of oligonucleotides
XX from the present specification represent universal mammalian sequence-
XX tagged site (UM-STS) primers. The primers are used to develop genomic
XX maps, to isolate clones from libraries, to make cross-species comparisons
XX and to develop additional genetic markers. UM-STS allow genomic
XX comparisons to be made between more species
XX
XX Sequence 19 BP; 6 A; 4 C; 8 G; 1 T; 0 U; 0 Other;
SQ
Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.8e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 979 TTCGCATCTGCTGCTGCG 997
Db 19 TTCGCATCTGCTGCTGCG 1
RESULT 223
ADO26346/c
ID ADO26346 standard; DNA; 19 BP.
XX
XX ADO26346;
XX
XX 18-NOV-2004 (first entry)
DT
XX
XX Haemofiltrate-chondro-osteomodulin protein PCR primer #6.
DE
XX
XX osteopathic; antirheumatic; antidiabetic; antiarthritic; immunomodulator;
KM nephrotropic; dermatological; antipruritic; antiseborrheic; virucide;
KM antiinflammatory; cytostatic; CDM; haemofiltrate-chondro-osteomodulin;
XX ss; primer; PCR.
XX
XX Unidentified.
XX
XX OS
XX WO2004039978-A2.
XX
XX 13-MAY-2004.
XX
XX 24-OCT-2003; 2003WO-EP011799.
XX

XX 31-OCT-2002; 2002DE-01051205.
 PR (IPFP-) IPF PHARM GMBH.
 PA Meder W, Wendland M, John H, Richter R, Meyer M, Forssmann W;
 PI WPI; 2004-376193/35.
 DR
 XX New polypeptide hemofiltrate-chondro-osteomodulin, useful for treatment
 PT and diagnosis of e.g. parathyroid disease and diabetes, also as part of a
 PT receptor-ligand system for drug screening.
 XX
 XX Claim 13; Page 17; 24pp; German.
 PS
 XX The present invention relates to the polypeptide haemofiltrate (HP) -
 CC chondro-osteomodulin (COM) and its natural or pharmacologically tolerable
 CC derivatives, especially amidated, acetylated, phosphorylated or
 CC glycosylated derivatives, or with N-terminal pyroglutamate. COM and its
 CC derivatives are useful for treatment of parathyroid disease (especially
 CC hypoparathyroidism), degenerative bone disease (especially osteoporosis),
 CC bone fractures, cartilage and connective tissue diseases, rheumatism and
 CC arthritis, fatty degeneration and diabetes type II, immune system
 CC disorders, disorders that can be treated by modifying migration of stem
 CC cells, kidney diseases associated with disrupted electrolyte excretion
 CC (especially renal insufficiency), also phosphate/calcium excretion, and
 CC skin diseases, e.g. psoriasis, eczema and acne, also viral, bacterial and
 CC parasitic infections, female infertility, ovarian and uterine tumours,
 CC autoimmune diseases and immune defects. They are also useful for
 CC diagnosis. The present sequence is a PCR primer used to isolate the
 CC protein of the invention.
 XX
 SQ Sequence 19 BP; 9 A; 5 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 1.8e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

671 TCTGGGTCCTGGCTCTCT 689
 19 TCTGGGTCCTGGCTTTCT 1

RESULT 224
 ADO26348/c
 ID ADO26348 standard; DNA; 19 BP.
 XX
 AC ADO26348;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Haemofiltrate-chondro-osteomodulin protein PCR primer #8.
 XX
 KW osteopathic; antirheumatic; antidiabetic; antiarthritic; immunomodulator;
 KW nephrotropic; dermatological; antipsoriatic; antiseborrheic; virucide;
 KW antiinflammatory; cytostatic; COM; haemofiltrate-chondro-osteomodulin;
 KW ss; primer; PCR.
 XX
 OS Unidentified.
 OS
 PN WO2004039978-A2.
 PD 13-MAY-2004.
 XX
 PF 24-OCT-2003; 2003WO-EP011799.
 XX
 PR 31-OCT-2002; 2002DE-01051205.
 PA (IPFP-) IPF PHARM GMBH.
 PI Meder W, Wendland M, John H, Richter R, Meyer M, Forssmann W;
 DR WPI; 2004-376193/35.

XX New polypeptide hemofiltrate-chondro-osteomodulin, useful for treatment
 PT and diagnosis of e.g. parathyroid disease and diabetes, also as part of a
 PT receptor-ligand system for drug screening.
 XX
 XX Claim 13; Page 17; 24pp; German.
 PS
 XX The present invention relates to the polypeptide haemofiltrate (HP) -
 CC chondro-osteomodulin (COM) and its natural or pharmacologically tolerable
 CC derivatives, especially amidated, acetylated, phosphorylated or
 CC glycosylated derivatives, or with N-terminal pyroglutamate. COM and its
 CC derivatives are useful for treatment of parathyroid disease (especially
 CC hypoparathyroidism), degenerative bone disease (especially osteoporosis),
 CC bone fractures, cartilage and connective tissue diseases, rheumatism and
 CC arthritis, fatty degeneration and diabetes type II, immune system
 CC disorders, disorders that can be treated by modifying migration of stem
 CC cells, kidney diseases associated with disrupted electrolyte excretion
 CC (especially renal insufficiency), also phosphate/calcium excretion, and
 CC skin diseases, e.g. psoriasis, eczema and acne, also viral, bacterial and
 CC parasitic infections, female infertility, ovarian and uterine tumours,
 CC autoimmune diseases and immune defects. They are also useful for
 CC diagnosis. The present sequence is a PCR primer used to isolate the
 CC protein of the invention.
 XX
 SQ Sequence 19 BP; 9 A; 5 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 1.8e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

671 TCTGGGTCCTGGCTCTCT 689
 19 TCTGGGTCCTGGCTTTCT 1

RESULT 225
 AEC90914
 ID AEC90914 standard; RNA; 19 BP.
 XX
 AC AEC90914;
 XX
 DT 17-NOV-2005 (first entry)
 XX
 DE STAT-3 siRNA antisense strand, SEQ ID 512.
 XX
 KW Signal-transducer and activator of transcription-3; RNA interference;
 KW gene silencing; cytostatic; antipsoriatic; dermatological;
 KW antiinflammatory; gastrointestinal-Gen.; cancer; inflammation; psoriasis;
 KW eczema; dermatitis; Crohn's disease; inflammatory bowel disease; siRNA;
 KW short interfering RNA; ss.
 XX
 OS Synthetic.
 OS
 PN US2005196781-A1.
 PD 08-SEP-2005.
 XX
 PF 15-DEC-2004; 2004US-00014373.
 XX
 PR 18-MAY-2001; 2001US-0292217P.
 PR 20-JUL-2001; 2001US-0306883P.
 PR 13-AUG-2001; 2001US-0311865P.
 PR 20-FEB-2002; 2002US-038580P.
 PR 06-MAR-2002; 2002US-0362016P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 17-MAY-2002; 2002US-0015111P.
 PR 17-MAY-2002; 2002WO-US015876.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 22-JUL-2002; 2002US-0020139P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 PR 15-JAN-2003; 2003US-0440129P.

PR 20-FEB-2003; 2003WO-US005028.
PR 20-FEB-2003; 2003WO-US005346.
PR 30-APR-2003; 2003US-00427160.
PR 23-MAY-2003; 2003US-00444853.
PR 23-OCT-2003; 2003US-00693059.
PR 24-NOV-2003; 2003US-00720448.
PR 03-DEC-2003; 2003US-00727780.
PR 14-JAN-2004; 2004US-00757803.
PR 10-FEB-2004; 2004US-0543480P.
PR 13-FEB-2004; 2004US-00780447.
PR 16-APR-2004; 2004US-00826966.
PR 30-APR-2004; 2004WO-US013456.
PR 24-MAY-2004; 2004WO-US016390.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
PI Robin H, Mcswigen J;
XX WPI; 2005-604649/62.
DR
XX
XX Novel chemically synthesized double stranded short interfering nucleic
PT acid molecule that directs cleavage of STAT3 RNA through RNA
PT interference, useful for treating cancer and inflammatory diseases e.g.
PT psoriasis in subject or organism.
XX
PS Example 3; SEQ ID NO 512; 266pp; English.
XX
XX The invention relates to a novel chemically synthesized double stranded
CC short interfering nucleic acid molecule that directs cleavage of a signal
CC transducer and activator of transcription 3 (STAT3) RNA by RNA
CC interference. The invention further includes a composition comprising the
CC short interfering nucleic acid in a carrier or diluent. The short
CC interfering nucleic acid has cytosolic, antiposrotatic, dermatological,
CC antiinflammatory, and gastrointestinal-Gen. activities. The short
CC interfering nucleic acid or its composition is useful for treating,
CC preventing, inhibiting, or reducing cancer, proliferative, and/or
CC inflammatory diseases, disorders, or conditions in a subject or organism,
CC such as psoriasis, eczema, dermatitis, Crohn's disease, and inflammatory
CC bowel disease, and for any other disease, trait, or condition that is
CC related to or will respond to the levels of STAT3 in a cell or tissue,
CC alone or in combination with other treatments or therapies. This oligo
CC sequence represents a STAT-3 siRNA strand of the invention.
XX
SQ Sequence 19 BP; 4 A; 5 C; 10 G; 0 T; 0 U; 0 Other;
Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 AGCCACCGCGGCGGCGG 26
DB 1 AGCCACCGCGGCGGCGG 19
RESULT 226
AEC90637/C
ID AEC90637 standard; RNA; 19 BP.
XX
AC AEC90637;
XX
DT 17-NOV-2005 (first entry)
XX
DE STAT-3 siRNA target/sense strand, SEQ ID 235.
XX
KM Signal-transducer and activator of transcription-3; RNA interference;
KM gene silencing; cytosolic; antiposrotatic; dermatological;
KM antiinflammatory; gastrointestinal-Gen.; cancer; inflammation; psoriasis;
KM eczema; dermatitis; Crohn's disease; inflammatory bowel disease; siRNA;
KM short interfering RNA; ss.
XX
XX Synthetic.
OS
XX
PN US2005196781-A1.

XX
PD 08-SEP-2005.
XX
XX 15-DEC-2004; 2004US-00014373.
XX
XX 18-MAY-2001; 2001US-0292217P.
PR 20-JUL-2001; 2001US-0306883P.
PR 13-AUG-2001; 2001US-0311865P.
PR 20-FEB-2002; 2002US-0358580P.
PR 06-MAR-2002; 2002US-0362016P.
PR 11-MAR-2002; 2002US-0363124P.
PR 17-MAY-2002; 2002US-00151116.
PR 17-MAY-2002; 2002WO-US015876.
PR 06-JUN-2002; 2002US-0386782P.
PR 22-JUL-2002; 2002US-00201394.
PR 29-AUG-2002; 2002US-0406780P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
PR 20-FEB-2003; 2003WO-US005028.
PR 20-FEB-2003; 2003WO-US005346.
PR 30-APR-2003; 2003US-00427160.
PR 23-MAY-2003; 2003US-00444853.
PR 23-OCT-2003; 2003US-00693059.
PR 24-NOV-2003; 2003US-00720448.
PR 03-DEC-2003; 2003US-00727780.
PR 14-JAN-2004; 2004US-00757803.
PR 10-FEB-2004; 2004US-0543480P.
PR 13-FEB-2004; 2004US-00780447.
PR 16-APR-2004; 2004US-00826966.
PR 30-APR-2004; 2004WO-US013456.
PR 24-MAY-2004; 2004WO-US016390.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
PI Robin H, Mcswigen J;
XX WPI; 2005-604649/62.
DR
XX
XX Novel chemically synthesized double stranded short interfering nucleic
PT acid molecule that directs cleavage of STAT3 RNA through RNA
PT interference, useful for treating cancer and inflammatory diseases e.g.
PT psoriasis in subject or organism.
XX
XX
PS Example 3; SEQ ID NO 235; 266pp; English.
XX
XX The invention relates to a novel chemically synthesized double stranded
CC short interfering nucleic acid molecule that directs cleavage of a signal
CC transducer and activator of transcription 3 (STAT3) RNA by RNA
CC interference. The invention further includes a composition comprising the
CC short interfering nucleic acid in a carrier or diluent. The short
CC interfering nucleic acid has cytosolic, antiposrotatic, dermatological,
CC antiinflammatory, and gastrointestinal-Gen. activities. The short
CC interfering nucleic acid or its composition is useful for treating,
CC preventing, inhibiting, or reducing cancer, proliferative, and/or
CC inflammatory diseases, disorders, or conditions in a subject or organism,
CC such as psoriasis, eczema, dermatitis, Crohn's disease, and inflammatory
CC bowel disease, and for any other disease, trait, or condition that is
CC related to or will respond to the levels of STAT3 in a cell or tissue,
CC alone or in combination with other treatments or therapies. This oligo
CC sequence represents a STAT-3 siRNA strand of the invention.
XX
SQ Sequence 19 BP; 0 A; 10 C; 5 G; 0 T; 4 U; 0 Other;
Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 AGCCACCGCGGCGGCGG 26
DB 19 AGCCACCGCGGCGGCGG 1

```
RESULT 227
AEC73577/c
ID AEC73577 standard; RNA; 19 BP.
XX
XX AEC73577;
AC
XX 17-NOV-2005 (first entry)
DT
XX
XX RNAi sense strand, targeting CD83, SEQ ID NO:256.
DE
XX
XX hypersensitivity; anti-allergic; immunosuppressive; sepsis; antibacterial;
KM shock; vasotrophic; burns; vulnerability; drug screening; diagnosis;
KM allergic rhinitis; anti-inflammatory; asthma; antiasthmatic;
KM RNA interference; gene silencing; siRNA; short interfering RNA; ss; CD83.
XX
XX Mus musculus.
OS
XX WO2005085443-A2.
XX
XX 15-SEP-2005.
XX
XX 01-MAR-2005; 2005WO-US006445.
XX
XX 01-MAR-2004; 2004US-0549070P.
XX
XX (MASI ) MASSACHUSETTS INST TECHNOLOGY.
PA
XX Chen J, Eisen HN, Ge Q;
PI
XX WPI; 2005-630722/64.
XX
XX New RNAi agent targeted to a target transcript encoding a protein
PT involved in the development, pathogenesis, or symptoms of an IGE-mediated
PT disease or condition, useful for treating or preventing, e.g. allergic
PT rhinitis or asthma.
XX
XX Claim 10; SEQ ID NO 256; 133pp; English.
XX
XX The present invention relates to an RNAi agent targeted to a transcript
XX that encodes a protein involved in the development, pathogenesis, or
XX symptoms of an IGE-mediated disease or condition. Also claimed are a
XX composition comprising an RNAi agent; a method of treating or preventing
XX a disease characterized by inappropriate or excessive mast cell activity
XX or Th2 helper cell responses, or an IGE-mediated disease or condition
XX (e.g. hypersensitivity), or sepsis, shock or a burn-related injury; an
XX analog of the siRNA or shRNA; inhibiting expression of a target
XX transcript; and identifying an RNAi agent as comprising a sequence
XX suitable for treatment of a condition characterized by IGE-mediated
XX hypersensitivity or inappropriate or excessive mast cell activity or Th2
XX helper cell activity. The transcript encodes a protein selected from
XX FcεR1α, chain, FcεR1β, chain, c-Kit, Lyn, Syk, ICOS,
XX CD40, CD80, CD86, RelB, 4-1BB ligand, TLR1, TLR2, TLR3,
XX TLR4, TLR5, TLR6, TLR7, TLR8, TLR9, SLAMF, common gamma chain, and
XX COX-2. The RNAi agent is an RNAi vector, siRNA or shRNA. The composition
XX and methods are useful for diagnosing, preventing or treating IGE-
XX mediated diseases, such as allergic rhinitis, asthma, hypersensitivity,
XX sepsis, shock or a burn-related injury. These may also be used in
XX screening for agents that may treat or prevent such disease conditions.
XX The present sequence is a RNAi sense strand, targeting CD83.
XX
XX Sequence 19 BP; 5 A; 7 C; 1 G; 0 T; 6 U; 0 Other;
SQ
Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

RESULT 228
AEB41027/c

```
ID AEB41027 standard; cDNA; 19 BP.
XX
XX AEB41027;
AC
XX 09-FEB-2006 (first entry)
DT
XX
XX Human hairless homolog cDNA 19-mer fragment SEQ ID NO 163.
DE
XX
XX ss; hirsutism; depilatory; hairless homolog.
XX
XX Homo sapiens.
OS
XX WO2005105157-A2.
XX
XX 10-NOV-2005.
XX
XX 22-APR-2005; 2005WO-US013770.
XX
XX 23-APR-2004; 2004US-0565127P.
XX
XX (UYCO ) UNIV COLUMBIA NEW YORK.
PA
XX Christiano AM;
PI
XX WPI; 2005-769492/78.
XX
XX Removing human hair comprises applying to a human in an area comprising
PT hair follicles a double stranded nucleic acid molecule comprising a
PT sequence of at least a portion of human hairless protein mRNA.
XX
XX Disclosure; SEQ ID NO 163; 216pp; English.
XX
XX The invention relates to a method of human hair removal which comprises
XX applying to a human in an area comprising hair follicles a double
XX stranded nucleic acid molecule comprising a sequence of at least a
XX portion of human hairless protein mRNA or its complement. In the method
XX of human hair removal, inhibition of hair growth in the area persists at
XX least one month. The method comprises synchronizing hair growth cycles
XX for hair follicles in the area. The method alternatively comprises at
XX contacting hair follicles in the region with a composition comprising a
XX least one double stranded nucleic acid molecule able to inhibit hairless
XX mRNA translation. The mammal is a human, mouse, rat, or bovine. The
XX method, nucleic acid molecules and compositions useful for removing
XX undesirable hair e.g. hirsutism. The present sequence represents a human
XX hairless homolog cDNA 19-mer fragment.
XX
XX Sequence 19 BP; 3 A; 6 C; 8 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

1234 CTCGAGACCCGAGCGACGTG 1252
19 CTCGAGACCCCGGCGCTGG 1

Db

RESULT 229
AEB41028
ID AEB41028 standard; cDNA; 19 BP.
XX
XX AEB41028;
AC
XX 09-FEB-2006 (first entry)
DT
XX
XX Human hairless homolog cDNA 19-mer fragment SEQ ID NO 164.
DE
XX
XX ss; hirsutism; depilatory; hairless homolog.
XX
XX Homo sapiens.
OS
XX WO2005105157-A2.
XX
XX

PD 10-NOV-2005.
XX 22-APR-2005; 2005SWO-US013770.
PF 23-APR-2004; 2004US-0565127P.
XX (UYCO) UNIV COLUMBIA NEW YORK.
PA Christiano AM;
PI WPI; 2005-769492/78.
XX Removing human hair comprises applying to a human in an area comprising
PT hair follicles a double stranded nucleic acid molecule comprising a
PT sequence of at least a portion of human hairless protein mRNA.
XX
XX Disclosure; SEQ ID NO 164; 216bp; English.
XX The invention relates to a method of human hair removal which comprises
CC applying to a human in an area comprising hair follicles a double
CC stranded nucleic acid molecule comprising a sequence of at least a
CC portion of human hairless protein mRNA or its complement. In the method
CC of human hair removal, inhibition of hair growth in the area persists at
CC least one month. The method comprises synchronizing hair growth cycles
CC for hair follicles in the area. The method alternatively comprises
CC contacting hair follicles in the region with a composition comprising at
CC least one double stranded nucleic acid molecule able to inhibit hairless
CC mRNA translation. The mammal is a human, mouse, rat, or bovine. The
CC method, nucleic acid molecules and compositions useful for removing
CC undesirable hair e.g. hirsutism. The present sequence represents a human
CC hairless homolog cDNA 19-mer fragment.
XX
SQ Sequence 19 BP; 2 A; 8 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1234 CTCGAGACCCGAGGCACTG 1252
Db 1 CTCGAGACCCGAGGCGCTGTG 19
RESULT 230
AEF75464/C
ID AEF75464 standard; RNA; 19 BP.
XX AEF75464;
AC
XX 06-APR-2006 (first entry)
DT
XX Human NOGO-A transcript target sequence/siRNA sense strand, SEQ:14.
DE
XX RNA interference; gene silencing; short interfering RNA; siRNA;
KM nervous system injury; spinal cord injury; neuroprotective; vulnery;
KM cerebrovascular ischemia; cerebroprotective; multiple sclerosis;
KM muscular dystrophy; muscular-gen.; neuropathy; motor neurone disease;
KM CNS-gen.; ataxia; Parkinsons disease; antiparkinsonian;
KM Huntingtons chorea; anticonvulsant; nootropic; dementia;
KM Creutzfeldt Jakob disease; Alzheimers disease; NOGO-A; KIAA0886;
KM reticulon 4; RTN4; ss.
XX
XX Homo sapiens.
OS
XX
XX US2005261212-A1.
PN
XX 24-NOV-2005.
PD
XX 26-JUL-2002; 2002US-00206693.
PF
XX 11-FEB-2000; 2000US-0181797P.
PR 09-FEB-2001; 2001US-00780533.
PR 05-APR-2001; 2001US-00827395.
PR

PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 03-APR-2002; 2002WO-US010512.
PR 06-JUN-2002; 2002US-0386782P.
XX (MCSW/) MCSWIGEN J A.
XX
XX Mcswigen JA;
PI WPI; 2006-190836/20.
DR
XX New chemically modified double stranded short interfering nucleic acid
PT (siRNA) molecule that directs cleavage of a NOGO receptor (NOGOR) RNA via
PT RNA interference (RNAi), useful for modulating gene expression.
XX
XX Disclosure; SEQ ID NO 14; 171bp; English.
XX
XX The invention relates to chemically synthesized short interfering nucleic
CC acids (siRNAs) which downregulate expression of a NOGO receptor gene by
CC RNA interference. The siRNAs may or may not comprise ribonucleotides, can
CC contain deoxyribonucleotides, can be chemically modified and may be,
CC double or single stranded. They further comprise sense and antisense
CC regions, or alternatively are assembled from a sense oligonucleotide and
CC an antisense oligonucleotide. Specifically, the siRNAs include short
CC interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short
CC hairpin RNA (shRNA). The invention also relates to pharmaceutical
CC compositions comprising a siRNA targeted to a NOGO receptor mRNA. It
CC further discloses siRNAs targeted to a NOGO receptor gene, siRNAs targeted
CC to a NOGO gene itself, and expression vectors and host cells comprising
CC a siRNA of the invention. In particular, the invention discloses siRNAs
CC (AEF75903-AEF76100 and AEF76101-AEF76112) targeted to the human NOGO
CC receptor gene of GenBank accession number BC011787, and siRNAs (AEF75451-
CC AEF75902) targeted to the human NOGO-A (KIAA0886) gene of DDBJ accession
CC number AB020693. The siRNAs are used to modulate expression of NOGO
CC receptor or NOGO genes in cells, tissue explants or organisms (e.g., by
CC ex vivo gene therapy), or in grafts and transplants for the treatment of
CC a variety of neurodegenerative conditions such as central nervous system
CC (CNS) injury (e.g., spinal cord injury or stroke), multiple sclerosis
CC (MS), muscular dystrophy, chemotherapy-induced neuropathy, amyotrophic
CC lateral sclerosis (ALS), ataxia, Parkinson's disease, Huntington's
CC disease, dementia, Creutzfeldt-Jakob disease and especially Alzheimer's
CC disease. The siRNAs may also be used in drug screening, diagnosis,
CC therapeutic target identification and validation, genetic engineering,
CC pharmacogenomics, studying gene function, and gene mapping (e.g., of
CC single nucleotide polymorphisms). The present sequence represents the
CC sense strand of a human NOGO-A-targeted double-stranded siRNA, which is
CC identical to the NOGO-A transcript target sequence.
XX
SQ Sequence 19 BP; 9 A; 0 C; 10 G; 0 T; 0 U; 0 Other;
Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1001 TCCGACATCTCTCCCTCT 1019
Db 19 TCCCTCTCTCTCTCTCTCT 1
RESULT 231
AEF75690
ID AEF75690 standard; RNA; 19 BP.
XX AEF75690;
AC
XX 06-APR-2006 (first entry)
DT
XX Human NOGO-A siRNA antisense strand, SEQ:240.
DE
XX RNA interference; gene silencing; short interfering RNA; siRNA;
KM nervous system injury; spinal cord injury; neuroprotective; vulnery;
KM cerebrovascular ischemia; cerebroprotective; multiple sclerosis;
KM muscular dystrophy; muscular-gen.; neuropathy; motor neurone disease;
KM

KW CNS-gen.; ataxia; Parkinsons disease; antiparkinsonian;
KW Huntingtons chorea; anticonvulsant; noctropic; dementia;
KW Creutzfeldt Jakob disease; Alzheimers disease; NCOG-A; KIAA0886;
KW reticulon 4; RTN4; ss.
XX Homo sapiens.
XX US2005261212-A1.
PN US2005261212-A1.
XX 24-NOV-2005.
PD 26-JUN-2002; 2002US-00206693.
XX 11-FEB-2000; 2000US-0181797P.
PR 09-FEB-2001; 2001US-00780533.
PR 05-APR-2001; 2001US-00827395.
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 03-APR-2002; 2002MO-US010512.
PR 06-JUN-2002; 2002US-0386782P.
PR (MCSW/) MCSWIGGEN J A.
PA Mcswigen JA;
PI WPI; 2006-190836/20.
XX New chemically modified double stranded short interfering nucleic acid
PT (siRNA) molecule that directs cleavage of a NCOG receptor (NCOGR) RNA via
PT RNA interference (RNAi), useful for modulating gene expression.
XX Disclosure; SEQ ID NO 240; 171bp; English.
XX The invention relates to chemically synthesized short interfering nucleic
CC acid (siRNAs) which downregulate expression of a NCOG receptor gene by
CC RNA interference. The siRNAs may or may not comprise ribonucleotides, can
CC contain deoxyribonucleotides, can be chemically modified and may be
CC double or single stranded. They further comprise sense and antisense
CC regions, or alternatively are assembled from a sense oligonucleotide and
CC an antisense oligonucleotide. Specifically, the siRNAs include short
CC interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short
CC hairpin RNA (shRNA). The invention also relates to pharmaceutical
CC compositions comprising an siRNA targeted to a NCOG receptor mRNA. It
CC further discloses siRNAs targeted to a NCOG receptor gene, siRNAs targeted
CC to a NCOG gene itself, and expression vectors and host cells comprising
CC an siRNA of the invention. In particular, the invention discloses siRNAs
CC (AEF75903-AEF76100 and AEF76101-AEF76112) targeted to the human NCOG
CC receptor gene of Genbank accession number BC011787, and siRNAs (AEF75451-
CC AEF75902) targeted to the human NCOG-A (KIAA0886) gene of DDBJ accession
CC number AB020693. The siRNAs are used to modulate expression of NCOG
CC receptor or NCOG genes in cells, tissue explants or organisms (e.g., by
CC ex vivo gene therapy), or in grafts and transplants for the treatment of
CC a variety of neurodegenerative conditions such as central nervous system
CC (CNS) injury (e.g., spinal cord injury or stroke), multiple sclerosis
CC (MS), muscular dystrophy, chemotherapy-induced neuropathy, amyotrophic
CC lateral sclerosis (ALS), ataxia, Parkinson's disease, Huntingtons
CC disease, dementia, Creutzfeldt-Jakob disease and especially Alzheimers
CC disease. The siRNAs may also be used in drug screening, diagnosis,
CC therapeutic target identification and validation, genetic engineering,
CC pharmacogenetics, studying gene function, and gene mapping (e.g., of
CC single nucleotide polymorphisms). The present sequence represents the
CC antisense strand of a human NCOG-A-targeted double-stranded siRNA.
XX
SQ Sequence 19 BP; 0 A; 10 C; 0 G; 0 T; 9 U; 0 Other;
Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 47.4%; Pred. No. 1.8e+02;
Matches 9; Conservative 8; Mismatches 2; Indels 0; Gaps 0;
OY 1001 TCACATCTTCTCTCTCT 1019
DB 1 UCUUCUCUCUCUCUCUCU 19

RESULT 232
AAK72794/C
ID AAK72794 strand; RNA; 17 BP.
XX AAK72794;
AC AAK72794;
XX 28-JUL-1999 (first entry)
DT Mouse ftk-1 VEGF receptor hammerhead ribozyme substrate #227.
XX
DE Vascular endothelial growth factor receptor; VEGF receptor; ftk-1; ftk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Mus sp.
XX MO9715662-A2.
PN 01-MAY-1997.
PD 25-OCT-1996; 96MO-US017480.
PE 26-OCT-1995; 95US-0005974P.
PR 11-JAN-1996; 96US-00584040.
PR (RIBO-) RIBOZYME PHARM INC.
PA (CHIR) CHIRON CORP.
PI Payco P, Mcswigen J, Stinchcomb D, Escobedo J;
XX WPI; 1997-259017/23.
DR Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
XX stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
PT Claim 4; Page 129; 218bp; English.
XX
PS The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAK7275 to AAK75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
SQ Sequence 17 BP; 1 A; 4 C; 5 G; 0 T; 7 U; 0 Other;
Query Match 0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 716 CAACCAAGAGACCATG 732
DB 17 CAACCAAGAGACCATG 1
RESULT 233
ABK01841
ID ABK01841 strand; RNA; 17 BP.
XX ABK01841;
AC ABK01841;
XX 12-MAR-2002 (first entry)
DT Human NCOG zinzyme #163.
XX

KM Human; ss; antisense therapy; cyrostatic; antiinflammatory; haemostatic;
KM cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
KM muscular; CD20; neurite growth inhibitor gene; NOGO; hammetthead ribozyme;
KM DNazyme; inozyme; G-cleaver; amberyne; zinzyme; lymphoma; leukaemia;
KM B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KM human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KM MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
KM inflammatory arthropathy; central nervous system injury;
KM cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KM chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KM Parkinson's disease; ataxia; Huntington's disease;
KM Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX
OS Homo sapiens.
OS Synthetic.
PN MO200159103-A2.
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US004273.
XX
PR 11-FEB-2000; 2000US-0181797P.
PR 28-FEB-2000; 2000US-0185516P.
PR 06-MAR-2000; 2000US-0187128P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGEN J.
PA (CHOW/) CHOWRIRA B M.
XX
PI Blatt L, Mcswigen J, Chowrira BM;
XX WPI; 2001-607195/69.
XX
PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
PT constructs, which down regulate expression of a CD20 gene or neurite
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
PT central nervous system injury.
XX
PS Claim 88; Page 98; 200Pp; English.
XX
CC The invention relates to a nucleic acid molecule which down regulates
CC expression of a CD20 gene and a nucleic acid molecule which down
CC regulates expression of a neurite growth inhibitor gene (NOGO). The
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
CC DNazyme) an inozyme (an endolytic nucleic acid cleaving a an RNA molecule
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
CC an amberyne (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
CC with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA
CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
CC the cell and treat a patient having a condition associated with the level
CC of CD20. The treatment may further comprise the use of one or more
CC therapies. In particular, the CD20 targeting nucleic acid may be used to
CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-
CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
CC cell and treat a patient having a condition associated with the level of
CC NOGO. The treatment may further comprise the use of one or more
CC therapies. In particular, the NOGO-targetting nucleic acid may be used to
CC treat central nervous system (CNS) injury and cerebrovascular accident
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NOGO expression. The present
CC sequence is a zinzyme molecule of the invention

XX
SQ Sequence 17 BP; 1 A; 11 C; 4 G; 0 T; 1 U; 0 Other;
Query Match 0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.6e+02;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 619 CCCCTCCAGCCCGGCT 635
DB 1 CCCCGCAGCCCGGCT 17
RESULT 234
ADU94309
ID ADU94309 standard; DNA; 17 BP.
XX
AC ADU94309;
XX
DT 10-FEB-2005 (first entry)
XX
DE Human TERT NCH ribozyme substrate sequence #991.
XX
KM Enzymatic nucleic acid molecule; gene expression; down regulation;
KM protein-cytosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;
KM MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
KM beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
KM c-erbB; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
KM hepatitis B virus; HBV; hammetthead; HH; halpin; NCH; inozyme; G-cleaver;
KM amberyne; zinzyme; DNazyme; cancer; breast cancer; Alzheimer's disease;
KM diabetes; obesity; cardiac disease; heart disease; age-related disease;
KM hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
KM ds.
XX
XX Homo sapiens.
OS
XX
PN WO200116312-A2.
XX
PD 08-MAR-2001.
XX
PF 30-AUG-2000; 2000WO-US023998.
XX
PR 31-AUG-1999; 99US-0151713P.
PR 27-SEP-1999; 99US-00406643.
PR 27-SEP-1999; 99US-0156236P.
PR 08-NOV-1999; 99US-0156467P.
PR 06-DEC-1999; 99US-00436430.
PR 29-DEC-1999; 99US-0049100P.
PR 29-DEC-1999; 99US-00474432.
PR 30-DEC-1999; 99US-0173612P.
PR 04-FEB-2000; 2000US-00498824.
PR 20-MAR-2000; 2000US-00531025.
PR 14-APR-2000; 2000US-0197769P.
PR 23-MAY-2000; 2000US-00578223.
PR 09-AUG-2000; 2000US-00636385.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PI Mcswigen J, Ueman N, Blatt L, Beigelman L, Burgin A;
PI Kapelsky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sprout BS;
XX WPI; 2001-244406/25.
XX
PT Enzymatic nucleic acid molecules able to cleave separate RNA molecules
PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
PT obesity and heart disease.
XX
PS Example 1; Page 297; 717Pp; English.
XX
CC The present invention relates to the use of enzymatic nucleic acid
CC molecules (e.g. ribozymes) to modulate gene expression. The invention
CC also methods for their use to down regulate or inhibit the expression of

CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine
CC aminopeptidase (MeLAP-2), human telomerase (hTERT), protein kinase C
CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
CC nucleic acid molecules used to inhibit the expression of the said genes
CC include hammerhead (HH), hairpin, NCH (inosyme), G-cleaver, amberzyme,
CC zincyme, and/or DNzyme motifs. The methods of the invention are useful
CC for treating cancer, in particular breast cancer, Alzheimer's disease,
CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related
CC diseases, hepatitis B infections, and hepatitis and hepatocellular
CC carcinoma. The enzymatic nucleic acid molecules can also be used as
CC diagnostic tools to examine genetic drift and mutations within diseased
CC cells and to detect the presence of specific RNA in a cell. The present
CC sequence represents a substrate/target sequence for a ribozyme used in
CC the examples of the present invention. Note: Some SEQ ID Nos are repeated
CC more than once in the specification, but these have different sequences
CC associated with them.

CC
XX
SQ Sequence 17 BP; 2 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 17;

Best Local Similarity 94.1%; Pred. No. 1.6e+02; Mismatches 1; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1686 GGACGAGCTTCTCTCA 1702

1 GGCGCAGCTTCTCTCA 17

RESULT 235
AADS0872/c

ID AADS0872 standard; DNA; 18 BP.

XX
AC AADS0872;

XX
DT 04-APR-2003 (first entry)

XX
DB Human OGR1 gene specific reverse RT-PCR primer.

XX
KW Human; G-protein coupled receptor; GPCR; breast; ovary; lung; prostate;
KW colorectal; cancer; GPCR24; GPR4; GPR65; OGR1; gene therapy; cyostatic;

XX
KW reverse transcription; RT; PCR; primer; ss.

XX
OS Homo sapiens.

XX
PN WO200290925-A2.

XX
PD 14-NOV-2002.

XX
PF 03-MAY-2002; 2002WO-US014164.

XX
PR 07-MAY-2001; 2001US-00850948.

XX
PA (TULA-) TULARIK INC.

XX
PI Yang J, An S;

XX
DR WPI; 2003-103529/09.

XX
PT Detecting breast, ovarian, prostate, colorectal or lung cancer in
PT mammals, comprises detecting an overexpression of G-protein coupled

PT receptors (GPCRs), such as GPCR24, GPR4, GPR65 and ORGRI relative to a
PT control.

XX
PS Example 1; Page 62; 83pp; English.

XX
CC The invention relates to a method for detecting breast, ovarian, lung,
CC prostate or colorectal cancer in mammals, which involves detecting an

CC overexpression of G-protein coupled receptors (GPCRs), such as GPCR24,
CC GPR4, GPR65 and OGR1 relative to a control. The methods, GPCR polypeptide

CC and inhibitors are useful for treating cancer, e.g. breast, ovarian,
CC prostate, colorectal or lung cancer. The detection of the polypeptides is

CC useful for monitoring the efficacy of cancer treatment and number or
CC location of cancer cells in a patient to monitor the progression of
CC cancer over time. The invention is also used in gene therapy. The present
CC sequence is a reverse transcription (RT)-PCR primer specific for human
CC OGR1 gene. This sequence is used to illustrate the method of the
CC invention

CC
XX
SQ Sequence 18 BP; 7 A; 3 C; 8 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 18;

Best Local Similarity 94.1%; Pred. No. 1.8e+02; Mismatches 1; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

986 TTTGCTGCTGCTGCTTC 1002

18 TTGCTGCTGCTGCTTC 2

RESULT 236
ADRI5253

ID ADRI5253 standard; DNA; 18 BP.

XX
AC ADRI5253;

XX
DT 21-OCT-2004 (first entry)

XX
DB Human HGRBM9 PCR primer #1.

XX
KW se; human; G-protein coupled receptor; GPCR; HGRBM9; analgesic;
KW antiaddictive; antibacterial; anticonvulsant; antidepressant;
KW antiinflammatory; antimanic; antiparkinsonian; antiserotonergic;

XX
KW cardiatic; cyostatic; haemostatic; hypotonic; neuroleptic;
KW neuroprotective; nootropic; tranquiliser; vasotropic; vulnary;

XX
KW neurodegenerative disease; behavioural disorder; memory disorder;
KW serotonin; anxiety; neurotransmitter; addiction; Alzheimer's disease;

XX
KW cognitive disorders; Parkinson's disease; Huntington's disease;
KW Tourette's syndrome; meningitis; encephalitis; demyelinating disease;

XX
KW ischaemia; haemorrhage; schizophrenia; mania; dementia; paranoia; autism;
KW balance; perception; lung cancer; NPKB expression; primer; PCR.

XX
OS Homo sapiens.

XX
PN US2004147732-A1.

XX
PD 29-JUL-2004.

XX
PF 07-OCT-2003; 2003US-00680402.

XX
PR 27-SEP-2000; 2000US-0235709P.

XX
PR 16-JAN-2001; 2001US-0261775P.

XX
PR 02-AUG-2001; 2001US-0309625P.

XX
PR 26-SEP-2001; 2001US-00964923.

XX
PA (FERDE/) FEDER J N.

XX
PA (MINT/) MINTIER G.

XX
PA (RAMA/) RAMANATHAN C S.

XX
PA (HAWK/) HAWKEN D R.

XX
PA (CACA/) CACACE A M.

XX
PA (BENN/) BENNETT K L.

XX
PI Feder JN, Mintier G, Ramanathan CS, Hawken DR, Cacace AM;

XX
PI Bennett KL;

XX
DR WPI; 2004-561410/54.

XX
PT New human G-protein coupled receptor, HGRBM9, expressed highly in brain
PT and testes, useful in the treatment and diagnosis of conditions such as
PT neurodegenerative diseases, schizophrenia, lung cancer, and inflammation.

XX
PS Example 11; SEQ ID NO 70; 69pp; English.

XX
CC This invention describes a novel human G-protein coupled receptor (GPCR),
CC HGRBM9 which is included in the American Type Culture Collection

CC Deposit No. PTA-2675. The protein of the invention has analgesic,
CC antiaddictive, antibacterial, anticonvulsant, antidepressant,
CC antiinflammatory, antianemic, antiparkinsonian, antiserotonergic,
CC cardiant, cyostatic, haemostatic, hypnotic, neuroleptic,
CC neuroprotective, nootropic, tranquiliser, vasotropic and vulnery (II),
CC activity. The nucleic acid molecule (I), the encoded polypeptide (II),
CC and the associated reagents and methods are useful for diagnosing,
CC preventing or treating conditions selected from neurodegenerative disease
CC states, behavioural disorders, inflammatory conditions, aberrant
CC behaviour, memory disorders, aberrant cognitive functioning, dorsal raphe
CC disorders, serotonin expression, serotonin uptake, anxiety, fear,
CC depression, sleep disorders, pain, locus coeruleus disorders, disorders
CC associated with a failure to maintain an attentive or alert state,
CC nucleus accumbens disorders, disorders associated with the expression
CC and/or release of neurotransmitters such as dopamine, opioid peptides,
CC serotonin, GABA, and glutamate, addiction, hypothalamus disorders,
CC disorders affecting ability of the brain to maintain homeostasis,
CC neuroendocrine functions, hippocampus disorders, long term potentiation
CC disorders, substantia nigra disorders, disorders affecting dopaminergic
CC function, Alzheimer's, cognitive disorders, Parkinson's Disease,
CC Huntington's Disease, Tourette's Syndrome, meningitis, encephalitis,
CC demyelinating diseases, peripheral neuropathies, neoplasia, trauma,
CC congenital malformations, spinal cord injuries, ischaemia and infarction,
CC aneurysms, haemorrhages, schizophrenia, mania, dementia, paranoia,
CC obsessive compulsive disorder, depression, panic disorder, learning
CC disabilities, AIDS, psychoses, autism and altered behaviours, including
CC disorders in feeding, sleep patterns, balance, perception, lung cancer,
CC proliferative lung disorder, disorders associated with aberrant E-
CC selectin expression or activity; disorders associated with aberrant NFkB
CC expression or activity; disorders associated with aberrant IKKb/Ikba
CC expression or activity; an inflammatory disorder; an inflammatory
CC disorder associated with aberrant NFkB regulation or regulation of the
CC NFkB pathway; and proliferative disorders associated with aberrant NFkB
CC regulation or regulation of the NFkB pathway. This sequence represents a
CC PCR primer used to amplify the human HGPRTMY9 gene for
CC immunohistochemistry hybridisation expression profiling.
CC
XX

SO Sequence 18 BP; 1 A; 6 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 18;

Best Local Similarity 94.1%; Pred. No. 1.8e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 309 CCTTGGCAGCTGCT 325

Db 2 CCTTGGCAGCTTCT 18

RESULT 237

AEF82508

ID AEF82508 standard; DNA, 18 BP.

AC AEF82508;

DT 20-APR-2006 (first entry)

DE Common marmoset 18S ribosome RNA gene RT-PCR primer SEQ ID NO:10.

KM 18S ribosomal RNA; 18S RNA; RNA detection; DNA detection; expression;
KM 8S; RT-PCR; primer; reverse transcriptase PCR.

OS Callithrix jacchus.

PN JP2006042804-A.

PD 16-FEB-2006.

PF 04-MAR-2005; 2005JP-00060329.

PR 09-JUL-2004; 2004JP-00202891.

XX (SUMO) SUMITOMO CHEM CO LTD.

XX

PI Yamada T, Oeda K;
XX
XX WPI; 2006-150097/16.

PT Novel 18S ribosome RNA gene derived from common marmoset, or its partial
PT fragment, useful as internal standard for measuring difference in
PT expression level of gene of interest in two or more types of test
PT samples.

XX
XX
PS Disclosure; SEQ ID NO 10; 21bp; Japanese.

XX The invention relates to a novel 18S ribosome RNA gene (I) derived from a
CC common marmoset, or its partial fragment (AEF82499). Also claimed is a
CC composition for detecting DNA or RNA, comprising the 18S RNA gene. The
CC 18S RNA gene is useful as an internal standard or a reference of the
CC expression level of a gene in the test sample during the measurement of
CC the difference in the expression level of a gene of interest in two or
CC more types of test sample, based on the difference in the transcription
CC product amount of the gene, where the test sample is derived from a
CC common marmoset. The transcription product amount of the gene of interest
CC is measured using a DNA array or by quantitative reverse transcriptase-
CC PCR. The present sequence represents an RT-PCR primer (see also AEF82507)
CC directed at the 18S RNA gene.
XX

SO Sequence 18 BP; 4 A; 2 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 18;

Best Local Similarity 94.1%; Pred. No. 1.8e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1245 GGGCAGCTGTACCAAG 1261

Db 1 GGGCAGCTGTACCAAG 17

RESULT 238

ADF37473/C

ID ADF37473 standard; RNA, 19 BP.

AC ADF37473;

DT 12-FEB-2004 (first entry)

DE Human VEGFR3 short interfering nucleic acid (siNA) SEQ ID NO:1762.

XX double-stranded short interfering nucleic acid;

KM short interfering nucleic acid; siNA; downregulation;

KM vascular endothelial growth factor receptor; VEGFR; antiangiogenic;

KM cyostatic; antidiabetic; ophthalmological; antiarthritic; antipsoriatic;

KM nephrotropic; gynaecological; angiogenesis-associated condition; cancer;

KM diabetic retinopathy; macular degeneration; neovascular glaucoma;

KM arthritis; psoriasis; endometriosis; angiodioma;

KM polycystic kidney disease; ss.

XX
OS Synthetic.

OS Homo sapiens.

PN WO2003070910-A2.

PD 28-AUG-2003.

PF 20-FEB-2003; 2003WO-US005022.

PR 20-FEB-2002; 2002US-0358580P.

PR 11-MAR-2002; 2002US-0363124P.

PR 29-MAY-2002; 2002WO-US017674.

PR 06-JUN-2002; 2002US-0386782P.

PR 03-JUL-2002; 2002US-0393796P.

PR 29-JUL-2002; 2002US-0399348P.

PR 29-AUG-2002; 2002US-0406784P.

PR 05-SEP-2002; 2002US-0408378P.

PR 09-SEP-2002; 2002US-0409293P.

PR 04-NOV-2002; 2002US-00287949.

PR 27-NOV-2002; 2002US-00306747.
PR 15-JAN-2003; 2003US-0440129P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PI Mcswigen J, Beigelman L, Pavco P;
XX WPI; 2003-679876/64.
XX
XX New double-stranded interfering nucleic acid, useful e.g. for treatment
PT and diagnosis of cancer, downregulates the vascular endothelial growth
PT factor receptor gene.
XX
XX Example 3; SEQ ID NO 1762; 207pp; English.
XX
XX The present invention describes a double-stranded short interfering
CC nucleic acid (siNA) that downregulates expression of the vascular
CC endothelial growth factor receptor (VEGFR) gene. Also described: (1) a
CC siNA that downregulates the VEGF gene; (2) kits for in vitro or in vivo
CC delivery of siNA; (3) conjugates and/or complexes of siNA; (4) vectors
CC that express siNA; and (5) single-stranded siNA with similar properties.
CC The siNAs have antiangiogenic, cytostatic, antidiabetic,
CC ophthalmological, antiarthritic, antipsoriatic, nephrotropic and
CC gynaecological activities. The siNA are useful for modulating
CC (downregulating) the expression of VEGFR genes. The siNA are potentially
CC useful for treating a wide range of angiogenesis-associated conditions,
CC particularly cancers, diabetic retinopathy, macular degeneration,
CC neovascular glaucoma, arthritis, psoriasis, endometriosis, angiofibroma,
CC and polycystic kidney disease. The siNA may also be useful for diagnosis,
CC drug screening, target identification and validation, genetic
CC engineering, studying gene function, and also for gene mapping (e.g. of
CC single-nucleotide polymorphisms). The present sequence is used in the
CC exemplification of the present invention.
XX
XX Sequence 19 BP; 0 A; 8 C; 7 G; 0 T; 4 U; 0 Other;
SQ
Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 139 AGGCGCCAGCCACAGCA 155
DB 18 AGGCGCCAGCCACCGCA 2
RESULT 239
ADP37226
ID ADP37226 standard; RNA; 19 BP.
XX
XX ADP37226;
DT 12-FEB-2004 (first entry)
XX
DE Human VEGFR3 short interfering nucleic acid (siNA) SEQ ID NO:1515.
XX
XX double-stranded short interfering nucleic acid;
KM short interfering nucleic acid; siNA; downregulation;
KM vascular endothelial growth factor receptor; VEGFR; antiangiogenic;
KM cytosstatic; antidiabetic; ophthalmological; antiarthritic; antipsoriatic;
KM nephrotropic; gynaecological; angiogenesis-associated condition; cancer;
KM diabetic retinopathy; macular degeneration; neovascular glaucoma;
KM arthritis; psoriasis; endometriosis; angiofibroma;
KM polycystic kidney disease; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO2003070910-A2.
XX
XX 28-AUG-2003.
XX
XX 20-FEB-2003; 2003WO-US005022.
XX

PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 29-MAY-2002; 2002WO-US017674.
PR 06-JUN-2002; 2002US-0386782P.
PR 03-JUL-2002; 2002US-0393796P.
PR 29-JUL-2002; 2002US-0399348P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 04-NOV-2002; 2002US-00287949.
PR 27-NOV-2002; 2002US-00306747.
PR 15-JAN-2003; 2003US-0440129P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PI Mcswigen J, Beigelman L, Pavco P;
XX WPI; 2003-679876/64.
XX
XX New double-stranded interfering nucleic acid, useful e.g. for treatment
PT and diagnosis of cancer, downregulates the vascular endothelial growth
PT factor receptor gene.
XX
XX Example 3; SEQ ID NO 1515; 207pp; English.
XX
XX The present invention describes a double-stranded short interfering
CC nucleic acid (siNA) that downregulates expression of the vascular
CC endothelial growth factor receptor (VEGFR) gene. Also described: (1) a
CC siNA that downregulates the VEGF gene; (2) kits for in vitro or in vivo
CC delivery of siNA; (3) conjugates and/or complexes of siNA; (4) vectors
CC that express siNA; and (5) single-stranded siNA with similar properties.
CC The siNAs have antiangiogenic, cytostatic, antidiabetic,
CC ophthalmological, antiarthritic, antipsoriatic, nephrotropic and
CC gynaecological activities. The siNA are useful for modulating
CC (downregulating) the expression of VEGFR genes. The siNA are potentially
CC useful for treating a wide range of angiogenesis-associated conditions,
CC particularly cancers, diabetic retinopathy, macular degeneration,
CC neovascular glaucoma, arthritis, psoriasis, endometriosis, angiofibroma,
CC and polycystic kidney disease. The siNA may also be useful for diagnosis,
CC drug screening, target identification and validation, genetic
CC engineering, studying gene function, and also for gene mapping (e.g. of
CC single-nucleotide polymorphisms). The present sequence is used in the
CC exemplification of the present invention.
XX
XX Sequence 19 BP; 4 A; 7 C; 8 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 139 AGGCGCCAGCCACAGCA 155
DB 2 AGGCGCCAGCCACCGCA 18
RESULT 240
ADP37226
ID ADP37226 standard; RNA; 19 BP.
XX
XX ADP37226;
DT 26-FEB-2004 (first entry)
XX
DE Human TERT siNA lower strand, SEQ ID 449.
XX
XX Cytostatic; vasotropic; protozoacide; immunosuppressive; dermatological;
KM neuroprotective; anti-HIV; ophthalmological; antifolcer; antirheumatic;
KM antiarthritic; antiinflammatory; gene therapy; telomerase; human; terc;
KM RNA interference; short interfering nucleic acid; siNA;
KM short interfering siRNA; siRNA; double-stranded RNA; micro-RNA; miRNA;
KM short hairpin RNA; shRNA; expression modulation; gene therapy;
KM drug screening; diagnosis; therapeutic target identification;
KM pharmacogenomics; gene function analysis; gene mapping; TERC; TERT; ss.
XX


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XX OS Homo sapiens.
XX PN WO2003070742-A1.
XX PD 28-AUG-2003.
XX PF 11-FEB-2003; 2003WO-US004088.
XX PR 20-FEB-2002; 2002US-0358580P.
XX PR 11-MAR-2002; 2002US-0363124P.
XX PR 06-JUN-2002; 2002US-0366782P.
XX PR 17-JUL-2002; 2002US-0396600P.
XX PR 29-AUG-2002; 2002US-0406784P.
XX PR 05-SEP-2002; 2002US-0408378P.
XX PR 09-SEP-2002; 2002US-0409293P.
XX PR 15-JAN-2003; 2003US-0440129P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Mcawiggen J, Beigelman L;
XX DR WPI; 2003-689777/65.
XX PT New short interfering nucleic acid downregulates expression of the
XX telomerase gene useful e.g. for treatment and diagnosis of cancer.
XX PS Example 3; SEQ ID NO 449; 145bp; English.
XX CC The invention relates to short interfering nucleic acids (siNA) which
XX CC downregulate expression of the one or more telomerase genes by RNA
XX CC interference. The siNAs may or may not comprise ribonucleotides and may
XX CC be double or single stranded. They further comprise sense and antisense
XX CC regions, or alternatively are assembled from a sense oligonucleotide and
XX CC an antisense oligonucleotide. Specifically, the siNAs include short
XX CC interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short
XX CC hairpin RNA (shRNA). The siNAs can be unmodified or chemically modified,
XX CC can contain deoxyribonucleotides, and can be chemically synthesised,
XX CC expressed from a vector or enzymatically synthesised. The invention also
XX CC relates to kits for the in vitro or in vivo delivery of siNA; conjugates
XX CC and/or complexes of siNA; and vectors that express siNA. The siNAs are
XX CC used to modulate expression of the telomerase genes in cells, tissue
XX CC explants or organisms (e.g., by ex vivo gene therapy), or in grafts and
XX CC transplants for the treatment of a variety of conditions. They may be
XX CC used for treating cancer, restenosis, infectious diseases (specifically
XX CC protozoal), transplant rejection, or autoimmune or age-related diseases,
XX CC e.g. multiple sclerosis, lupus erythematosus, AIDS, macular degeneration,
XX CC skin ulcers and rheumatoid arthritis. The siNAs are also useful for drug
XX CC screening, diagnosis, therapeutic target identification and validation,
XX CC genetic engineering, pharmacogenomics, studying gene function, and gene
XX CC mapping (e.g., of single nucleotide polymorphisms). The present sequence
XX CC represents the lower strand of a human TERT-targeted double-stranded
XX CC siNA.
XX SQ Sequence 19 BP; 4 A; 7 C; 2 G; 0 T; 6 U; 0 Other;
OY Query Match 0.9%; Score 15.4; DB 1; Length 19;
Db Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 463 AATACAGTGGTGAACCTT 479
Db 17 AAGACAGTGGTGAACCTT 1
RESULT 241
ADP93468 ID ADF93468 standard; RNA; 19 BP.
XX ADF93468;
XX AC ADF93468;
XX DT 26-FEB-2004 (first entry)
XX
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DE Human TERT transcript target sequence/siNA upper strand, SEQ ID 185.
XX CC Cytostatic; vasotropic; protozoacide; immunosuppressive; dermatological;
XX CC neuroprotective; anti-HIV; ophthalmological; antiviral; antineoplastic;
XX CC antiarthritic; antiinflammatory; gene therapy; telomerase; human; terc;
XX CC RNA interference; short interfering nucleic acid; siNA;
XX CC short interfering RNA; shRNA; double-stranded RNA; micro-RNA; miRNA;
XX CC short hairpin RNA; shRNA; expression modulation; gene therapy;
XX CC drug screening; diagnosis; therapeutic target identification;
XX CC pharmacogenomics; gene function analysis; gene mapping; TERC; TERT; ss.
XX OS Homo sapiens.
XX PN WO2003070742-A1.
XX PD 28-AUG-2003.
XX PF 11-FEB-2003; 2003WO-US004088.
XX PR 20-FEB-2002; 2002US-0358580P.
XX PR 11-MAR-2002; 2002US-0363124P.
XX PR 06-JUN-2002; 2002US-0366782P.
XX PR 17-JUL-2002; 2002US-0396600P.
XX PR 29-AUG-2002; 2002US-0406784P.
XX PR 05-SEP-2002; 2002US-0408378P.
XX PR 09-SEP-2002; 2002US-0409293P.
XX PR 15-JAN-2003; 2003US-0440129P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Mcawiggen J, Beigelman L;
XX DR WPI; 2003-689777/65.
XX PT New short interfering nucleic acid downregulates expression of the
XX telomerase gene useful e.g. for treatment and diagnosis of cancer.
XX PS Example 3; SEQ ID NO 185; 145bp; English.
XX CC The invention relates to short interfering nucleic acids (siNA) which
XX CC downregulate expression of the one or more telomerase genes by RNA
XX CC interference. The siNAs may or may not comprise ribonucleotides and may
XX CC be double or single stranded. They further comprise sense and antisense
XX CC regions, or alternatively are assembled from a sense oligonucleotide and
XX CC an antisense oligonucleotide. Specifically, the siNAs include short
XX CC interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short
XX CC hairpin RNA (shRNA). The siNAs can be unmodified or chemically modified,
XX CC can contain deoxyribonucleotides, and can be chemically synthesised,
XX CC expressed from a vector or enzymatically synthesised. The invention also
XX CC relates to kits for the in vitro or in vivo delivery of siNA; conjugates
XX CC and/or complexes of siNA; and vectors that express siNA. The siNAs are
XX CC used to modulate expression of the telomerase genes in cells, tissue
XX CC explants or organisms (e.g., by ex vivo gene therapy), or in grafts and
XX CC transplants for the treatment of a variety of conditions. They may be
XX CC used for treating cancer, restenosis, infectious diseases (specifically
XX CC protozoal), transplant rejection, or autoimmune or age-related diseases,
XX CC e.g. multiple sclerosis, lupus erythematosus, AIDS, macular degeneration,
XX CC skin ulcers and rheumatoid arthritis. The siNAs are also useful for drug
XX CC screening, diagnosis, therapeutic target identification and validation,
XX CC genetic engineering, pharmacogenomics, studying gene function, and gene
XX CC mapping (e.g., of single nucleotide polymorphisms). The present sequence
XX CC represents the upper strand of a human TERT-targeted double-stranded
XX CC siNA, which is identical to the c-fos transcript target sequence.
XX SQ Sequence 19 BP; 6 A; 2 C; 7 G; 0 T; 4 U; 0 Other;
OY Query Match 0.9%; Score 15.4; DB 1; Length 19;
Db Best Local Similarity 70.6%; Pred. No. 2.1e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
OY 463 AATACAGTGGTGAACCTT 479
Db 3 AAGACAGTGGTGAACCTT 19
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RESULT 242
ADK97381/C
ID ADK97381 standard; DNA; 19 BP.
XX
XX ADK97381;
XX
XX 06-MAY-2004 (first entry)
DT
XX
XX Primer of the invention #3101.
DE
XX
XX human; single nucleotide polymorphism; SNP; ss; primer.
XX
XX Synthetic.
OS
XX
XX JP2003259875-A.
PN
XX
XX 16-SEP-2003.
PD
XX
XX 08-MAR-2002; 2002JP-00064373.
PF
XX
XX 08-MAR-2002; 2002JP-00064373.
PR
XX
XX (KAGA-) KAGAKU GIUTTSU SHINKO JIGYODAN.
PA
XX
XX WPI; 2004-093977/10.
DR
XX
XX Novel polynucleotide useful for PCR amplification along with two DNA
PT fragment from another set of sequences, or for detecting single
PT nucleotide polymorphism in human gene.
XX
XX Claim 2; SEQ ID NO 6410; 2627bp; Japanese.
XX
XX
XX The present invention relates to a polynucleotide isolated from a human
CC gene and is useful for detecting a single nucleotide polymorphism in a
CC human gene or for diagnosing of disease. The invention enables the
CC detection of a single nucleotide polymorphism in a human gene. The
CC present sequence represents a primer of the invention.
XX
XX
XX Sequence 19 BP; 0 A; 8 C; 3 G; 8 T; 0 U; 0 Other;
SQ
Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0.
QY 1309 GAGGAGCCGAGGAGCG 1325
DB 19 GAGGAGCCGAGGAGCG 3
RESULT 243
AD062492
ID AD062492 standard; RNA; 19 BP.
XX
XX AD062492;
XX
XX 09-SEP-2004 (first entry)
DT
XX
XX Anti-TERT siRNA SEQ ID NO:2195.
DE
XX
XX ss; siRNA; gene silencing; Bcl-2; optimised; short interfering RNA;
KM RNA interference.
XX
XX Synthetic.
OS
XX
XX WO2004045543-A2.
PN
XX
XX 03-JUN-2004.
PD
XX
XX 14-NOV-2003; 2003WO-US036787.
PF
XX
XX 14-NOV-2002; 2002US-0426137P.
PR

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10-SEP-2003; 2003JUS-0502050P.
XX (DHAR-) DHARMACON INC.
XX Anastasia K, Angela R, Devin L, William M, Stephen S;
XX WPI; 2004-420527/39.
XX
XX Selecting siRNA by selecting an siRNA molecule of 19-25 nucleoside bases
XX by selecting a target gene and measuring the functionality of the
XX nucleotide sequences that are complementary to a stretch of nucleotides
XX of the target sequence.
XX
XX Example 12; SEQ ID NO 2195; 199pp; English.
XX
XX The invention relates to a novel method for selecting siRNA (short
XX interfering RNA) comprising selecting an siRNA molecule of 19-25
XX nucleoside bases by selecting a target gene and measuring the
XX functionality of sequences of 19-25 nucleotides in length that are
XX substantially complementary to a stretch of nucleotides of the target
XX sequence, where the functionality is dependent upon non-target specific
XX criteria. Also claimed are methods for gene-silencing, developing an
XX siRNA algorithm for selecting siRNA, selecting an siRNA with improved
XX functionality, selecting hyperfunctional siRNA, an siRNA molecule
XX effective at silencing Bcl-2, and a kit for gene silencing comprising the
XX siRNA. The siRNA molecule comprises a sequence substantially similar to a
XX sequence consisting of GGGAGAGAGUGAGAGACAU; GAAGACUCCUCUCAGUU;
XX GUACGACACCGGAGUA; AGAUAUGAUGAUGAGACAU; UGAAGACUCCUCUCAGUU;
XX CAUCCGCGCUGUGUA; UGCGGCCUCUGUCAGUU; GAGAUAGUAGUAGACAU;
XX GGAGAUAGUAGUAGACAU; and GAAGACUCCUCUCAGUU. The siRNA molecule
XX comprises a sense strand and an anti-sense strand. The siRNA molecule
XX comprises a hairpin. The siRNA molecule comprises between 18 and 30 base
XX pairs. The kit comprises at least two siRNA, comprising a first optimised
XX siRNA and a second optimised siRNA. The method is useful in selecting
XX siRNA for generating a gene silencing reagent. The present sequence is
XX used in the exemplification of the invention.
XX
XX Sequence 19 BP; 6 A; 2 C; 7 G; 0 T; 4 U; 0 Other;
XX
XX Query Match 0.9%; Score 15.4; DB 1; Length 19;
XX Best Local Similarity 70.6%; Pred. No. 2.1e+02;
XX Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0
XX
XX 463 AATACAGTCGTGACTT 479
XX |||||:|||||:|
XX 3 AAGACGUGUGAUAU 19
XX
XX RESULT 244
XX ADR05766/c
XX ID ADR05766 standard; DNA; 19 BP.
XX
XX ADR05766;
XX
XX 21-OCT-2004 (first entry)
XX
XX Ribosome binding site-related oligonucleotide, SEQ ID 3.
XX
XX Transposase; mariner mobile genetic element; transposon; Mos-1 element;
XX ribosome binding site; ss.
XX
XX Synthetic.
XX
XX FR2850395-A1.
XX
XX 30-JUL-2004.
XX
XX 28-JAN-2003; 2003FR-00000905.
XX
XX 28-JAN-2003; 2003FR-00000905.
XX
XX (CNRS ) CNRS CENT NAT RECH SCI.
XX (UYTO-) UNIV TOURS RABELAIS FRANCOIS.
XX

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XX PI Bigot Y, Auge GC, Hamelin MH, Brillet B;
XX DR WPI; 2004-546139/53.
XX PT New hyperactive mutant of the mariner transposase, useful for targeted
XX insertion of DNA, particularly for gene therapy, has at least one
XX phosphorylatable amino residue replaced by non-phosphorylatable residue.
XX PS Disclosure; SEQ ID NO 3; 62pp; French.
XX CC The present invention relates to a hyperactive transposase mutant (A)
XX from a mariner mobile genetic element (BGM). It has at least one mutation
XX at a phosphorylatable residue (pr), in at least one phosphorylation site,
XX that renders the site non-phosphorylatable. The BGM is from *Drosophila*
XX *mauriliiana* and represents the transposon from the Mos-1 element
XX (ADR05764). Unlike the wild-type transposase, (A), when expressed in
XX eukaryotes, is not subjected to phosphorylation (post-translation
XX modification), a process that reduces affinity for DNA and limits
XX conformational activity, resulting in a low capacity for catalysis of
XX transposition. The non-phosphorylatable mutants are at least 25,
XX preferably 100, times more active. (A) is useful for in vitro
XX transposition of transposable DNA of interest into a target DNA,
XX particularly for use in gene therapy where the transposable DNA is
XX introduced into a host cell genome. The present sequence was used for
XX cloning a ribosome binding site for vector construction.
XX SQ Sequence 19 BP; 5 A; 4 C; 8 G; 2 T; 0 U; 0 Other;
Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 891 GATCCCCGGGACTCTCT 907
Db 19 GATCCCCGGGACTCTCT 3
RESULT 245
ADY88479
XX ID ADY88479 standard; RNA; 19 BP.
XX AC ADY88479;
XX DT 16-JUN-2005 (first entry)
XX DE VEGFR siRNA SEQ ID NO 1515.
XX KM ss; siRNA; short interfering RNA; RNA interference; gene silencing;
XX KW VEGFR; pharmaceutical; cancer; neoplasm; Cytostatic.
XX OS Synthetic.
XX PN WO2005028649-A1.
XX PD 31-MAR-2005.
XX PF 16-SEP-2004; 2004WO-US030488.
XX XX
XX 16-SEP-2003; 2003US-00664767.
XX PR 16-SEP-2003; 2003US-00665255.
XX PR 23-SEP-2003; 2003US-00670011.
XX PR 23-OCT-2003; 2003US-00693059.
XX PR 24-NOV-2003; 2003US-00720448.
XX PR 03-DEC-2003; 2003US-00727780.
XX PR 14-JAN-2004; 2004US-00757803.
XX PR 26-JAN-2004; 2004US-00764957.
XX PR 10-FEB-2004; 2004US-0543480P.
XX PR 13-FEB-2004; 2004US-00780447.
XX PR 16-APR-2004; 2004US-00826966.
XX PR 23-APR-2004; 2004US-00831620.
XX PR 30-APR-2004; 2004US-00013456.
XX PR 11-MAY-2004; 2004US-00844076.

XX PA (SIRN-) SIRNA THERAPEUTICS INC.
XX XX Jadhav V, Kossen K, Zinnen S, Vaish N, Mswiggen J;
XX PI WPI; 2005-254128/26.
XX DR
XX XX
XX PT New multifunctional siRNA molecule that directs cleavage of the first and
XX second VEGF or VEGFR target sequences via RNA interference, useful in
XX preparing a composition for treating cell proliferative disorders e.g.
XX cancers.
XX PS Disclosure; SEQ ID NO 1515; 396pp; English.
XX CC The invention relates to a multifunctional siRNA molecule comprising a
XX structure having formula MF-III and which directs cleavage of the first
XX and second VEGF or VEGFR target sequences via RNA interference. The
XX multifunctional siRNA molecule is useful in preparing a pharmaceutical
XX composition for treating cell proliferative disorders, e.g. cancer. The
XX present sequence represents a VEGFR siRNA.
XX SQ Sequence 19 BP; 4 A; 7 C; 8 G; 0 T; 0 U; 0 Other;
Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 139 AGGCGCCAGCCACAGGA 155
Db 2 AGGCGCCAGCCACCGGA 18
RESULT 246
ADY88726/C
XX ID ADY88726 standard; RNA; 19 BP.
XX AC ADY88726;
XX DT 16-JUN-2005 (first entry)
XX DE VEGFR siRNA SEQ ID NO 1762.
XX KM ss; siRNA; short interfering RNA; RNA interference; gene silencing;
XX KW VEGFR; pharmaceutical; cancer; neoplasm; Cytostatic.
XX OS Synthetic.
XX PN WO2005028649-A1.
XX PD 31-MAR-2005.
XX PF 16-SEP-2004; 2004WO-US030488.
XX XX
XX 16-SEP-2003; 2003US-00664767.
XX PR 16-SEP-2003; 2003US-00665255.
XX PR 23-SEP-2003; 2003US-00670011.
XX PR 23-OCT-2003; 2003US-00693059.
XX PR 24-NOV-2003; 2003US-00720448.
XX PR 03-DEC-2003; 2003US-00727780.
XX PR 14-JAN-2004; 2004US-00757803.
XX PR 26-JAN-2004; 2004US-00764957.
XX PR 10-FEB-2004; 2004US-0543480P.
XX PR 13-FEB-2004; 2004US-00780447.
XX PR 16-APR-2004; 2004US-00826966.
XX PR 23-APR-2004; 2004US-00831620.
XX PR 30-APR-2004; 2004US-00013456.
XX PR 11-MAY-2004; 2004US-00844076.
XX PA (SIRN-) SIRNA THERAPEUTICS INC.
XX XX Jadhav V, Kossen K, Zinnen S, Vaish N, Mswiggen J;
XX PI WPI; 2005-254128/26.
XX DR

XX New multifunctional siRNA molecule that directs cleavage of the first and
PT second VEGF or VEGFR target sequences via RNA interference, useful in
PT preparing a composition for treating cell proliferative disorders e.g.
PT cancers.
XX
XX Disclosure; SEQ ID NO 1762; 396pp; English.
PS
XX
XX The invention relates to a multifunctional siRNA molecule comprising a
CC structure having Formula MF-II and which directs cleavage of the first
CC and second VEGF or VEGFR target sequences via RNA interference. The
CC multifunctional siRNA molecule is useful in preparing a pharmaceutical
CC composition for treating cell proliferative disorders, e.g. cancer. The
CC present sequence represents a VEGFR siRNA.
CC
XX
SQ Sequence 19 BP; 0 A; 8 C; 7 G; 0 T; 4 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 139 AGGCGCCAGCCACGAGA 155
DB 18 AGGCGCCAGCCACCGGA 2

RESULT 247
AEA06712/c
ID AEA06712 standard; DNA; 19 BP.
XX
AC AEA06712;
XX
DT 28-JUL-2005 (first entry)
XX
DE G protein-coupled receptor 154 siRNA target SEQ ID NO 149.
XX
XX respiratory-gen.; antiasthmatic; antiinflammatory; RNA interference;
KM gene expression; diagnosis; respiratory disease; inflammation;
KM G protein-coupled receptor 154; GPR154; ss.
XX
OS Homo sapiens.
XX
XX WO2005045038-A2.
PN
PD 19-MAY-2005.
XX
PF 20-AUG-2004; 2004WO-US027231.
XX
PR 23-OCT-2003; 2003US-00693059.
PR 24-NOV-2003; 2003US-00720448.
PR 03-DEC-2003; 2003US-00727780.
PR 14-JAN-2004; 2004US-00757803.
PR 10-FEB-2004; 2004US-0543480P.
PR 13-FEB-2004; 2004US-00780447.
PR 16-APR-2004; 2004US-00826966.
PR 30-APR-2004; 2004WO-US013456.
PR 11-MAY-2004; 2004US-0570086P.
PR 24-MAY-2004; 2004WO-US016390.
XX
XX (SIRN-) SIRNA THERAPEUTICS INC.
PA
XX
XX Richards I, Polisky B, Mcswigen J;
PI
XX WPI; 2005-366846/37.
DR
XX
XX Novel chemically synthesized double stranded short interfering nucleic
PT acid molecule useful for cleaving G protein-coupled receptor for asthma
PT susceptibility RNA or treating respiratory or inflammatory disorders.
XX
XX Example 3; SEQ ID NO 149; 210pp; English.
XX
XX The invention describes a chemically synthesized double stranded short
CC interfering nucleic acid (siRNA) molecule (I) that directs cleavage of a G

CC protein-coupled receptor for asthma susceptibility (GPR) RNA through RNA
CC interference (RNAi), where each strand of (I) has 18-23 nucleotides and
CC one strand of (I) comprises nucleotide sequence having sufficient
CC complementarity to the GPR RNA to direct cleavage of the GPR RNA by RNA
CC interference. Also described is a composition comprising (I) and a siRNA
CC carrier or diluent; validating GPR; a kit comprising (I); and an siRNA
CC construct. (I) exhibits improved stability, bioavailability and
CC activation of cellular responses, thus mediating RNA interference. This
CC sequence represents the target polynucleotide of a G protein-coupled
CC receptor 154 (GPR154) specific siRNA used to control GPR gene
CC expression.
XX
SQ Sequence 19 BP; 5 A; 0 C; 9 G; 0 T; 5 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1110 CAACCCCTCATCTACT 1126
DB 17 CAACCCCTCATCTACT 1

RESULT 248
AEA06625
ID AEA06625 standard; DNA; 19 BP.
XX
AC AEA06625;
XX
DT 28-JUL-2005 (first entry)
XX
DE G protein-coupled receptor 154 siRNA target SEQ ID NO 62.
XX
XX respiratory-gen.; antiasthmatic; antiinflammatory; RNA interference;
KM gene expression; diagnosis; respiratory disease; inflammation;
KM G protein-coupled receptor 154; GPR154; ss.
XX
OS Homo sapiens.
XX
XX WO2005045038-A2.
PN
PD 19-MAY-2005.
XX
PF 20-AUG-2004; 2004WO-US027231.
XX
PR 23-OCT-2003; 2003US-00693059.
PR 24-NOV-2003; 2003US-00720448.
PR 03-DEC-2003; 2003US-00727780.
PR 14-JAN-2004; 2004US-00757803.
PR 10-FEB-2004; 2004US-0543480P.
PR 13-FEB-2004; 2004US-00780447.
PR 16-APR-2004; 2004US-00826966.
PR 30-APR-2004; 2004WO-US013456.
PR 11-MAY-2004; 2004US-0570086P.
PR 24-MAY-2004; 2004WO-US016390.
XX
XX (SIRN-) SIRNA THERAPEUTICS INC.
PA
XX
XX Richards I, Polisky B, Mcswigen J;
PI
XX WPI; 2005-366846/37.
DR
XX
XX Novel chemically synthesized double stranded short interfering nucleic
PT acid molecule useful for cleaving G protein-coupled receptor for asthma
PT susceptibility RNA or treating respiratory or inflammatory disorders.
XX
XX Example 3; SEQ ID NO 62; 210pp; English.
XX
XX The invention describes a chemically synthesized double stranded short
CC interfering nucleic acid (siRNA) molecule (I) that directs cleavage of a G
CC protein-coupled receptor for asthma susceptibility (GPR) RNA through RNA
CC interference (RNAi), where each strand of (I) has 18-23 nucleotides and
CC one strand of (I) comprises nucleotide sequence having sufficient

CC complementarity to the GPR RNA to direct cleavage of the GPR RNA by RNA
CC interference. Also described is a composition comprising (1) and a
CC carrier or diluent; validating GPR; a kit comprising (1); and an siRNA
CC construct. (1) exhibits improved stability, bioavailability and
CC activation of cellular responses, thus mediating RNA interference. This
CC sequence represents the target polynucleotide of a G protein-coupled
CC receptor 154 (GPR154) specific siRNA used to control GPR gene
CC expression.
XX
SQ Sequence 19 BP; 5 A; 9 C; 0 G; 0 T; 5 U; 0 Other;
Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 2.1e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1110 CAACCCGATCATCTACT 1126
DB 3 CAACCCGCAUCUACU 19
||||| :|||:
RESULT 249
AEA21650/c
ID AEA21650 standard; RNA; 19 BP.
XX
AC AEA21650;
XX
DT 11-AUG-2005 (first entry)
XX
DE Short interfering RNA (siRNA) molecule #76.
XX
KM RNA interference; gene silencing; short interfering RNA; siRNA; ss.
XX
OS Synthetic.
XX
PN WO2005049830-A1.
XX
PD 02-JUN-2005.
XX
PF 19-NOV-2004; 2004WO-JP017648.
XX
PR 20-NOV-2003; 2003JP-00390763.
PR 01-MAR-2004; 2004JP-00055924.
XX
PA (SUZU/) SUZUKI T.
XX
PI Suzuki T, Katoh T;
XX
WPI; 2005-396112/40.
XX
PT Designing siRNA for suppressing expression of target gene having sequence
PT complementary for target mRNA sequence in target gene, and having bases
PT constituting double-stranded portion for inhibiting expression of target
PT gene.
XX
PS Example 1; Fig 5B; 39pp; Japanese.
XX
CC The invention relates to a method for designing an siRNA molecule having
CC a sequence complementary to a target mRNA sequence in a target gene and
CC having 19 bases constituting a double-stranded portion for inhibiting
CC expression of the target gene. The invention also relates to a method of
CC searching a base sequence and use of the base sequence as siRNA, and a
CC method of estimating siRNA activity. The method is useful for designing
CC siRNA for suppressing the expression of a target gene. This sequence
CC represents an siRNA molecule used in the method of the invention.
XX
SQ Sequence 19 BP; 2 A; 6 C; 7 G; 0 T; 4 U; 0 Other;
Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1089 GGCCATGAGTCCACCA 1105
||||| |||||

DB 18 GGCCATGAGTCCACCA 2
RESULT 250
AEA21651/c
ID AEA21651 standard; RNA; 19 BP.
XX
AC AEA21651;
XX
DT 11-AUG-2005 (first entry)
XX
DE Short interfering RNA (siRNA) molecule #77.
XX
KM RNA interference; gene silencing; short interfering RNA; siRNA; ss.
XX
OS Synthetic.
XX
PN WO2005049830-A1.
XX
PD 02-JUN-2005.
XX
PF 19-NOV-2004; 2004WO-JP017648.
XX
PR 20-NOV-2003; 2003JP-00390763.
PR 01-MAR-2004; 2004JP-00055924.
XX
PA (SUZU/) SUZUKI T.
XX
PI Suzuki T, Katoh T;
XX
WPI; 2005-396112/40.
XX
PT Designing siRNA for suppressing expression of target gene having sequence
PT complementary for target mRNA sequence in target gene, and having bases
PT constituting double-stranded portion for inhibiting expression of target
PT gene.
XX
PS Example 1; Fig 5B; 39pp; Japanese.
XX
CC The invention relates to a method for designing an siRNA molecule having
CC a sequence complementary to a target mRNA sequence in a target gene and
CC having 19 bases constituting a double-stranded portion for inhibiting
CC expression of the target gene. The invention also relates to a method of
CC searching a base sequence and use of the base sequence as siRNA, and a
CC method of estimating siRNA activity. The method is useful for designing
CC siRNA for suppressing the expression of a target gene. This sequence
CC represents an siRNA molecule used in the method of the invention.
XX
SQ Sequence 19 BP; 3 A; 6 C; 6 G; 0 T; 4 U; 0 Other;
Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1089 GGCCATGAGTCCACCA 1105
||||| |||||
DB 17 GGCCATGAGTCCACCA 1
RESULT 251
AEA21649/c
ID AEA21649 standard; RNA; 19 BP.
XX
AC AEA21649;
XX
DT 11-AUG-2005 (first entry)
XX
DE Short interfering RNA (siRNA) molecule #75.
XX
KM RNA interference; gene silencing; short interfering RNA; siRNA; ss.
XX
OS Synthetic.
XX

PN WO2005049830-A1.
 XX 02-JUN-2005.
 PD 19-NOV-2004; 2004WO-JP017648.
 XX 20-NOV-2003; 2003JP-00390763.
 XX 01-MAR-2004; 2004JP-00055924.
 PR 20-NOV-2003; 2003JP-00390763.
 PR 01-MAR-2004; 2004JP-00055924.
 XX (SUZUKI) SUZUKI T.
 PA Suzuki T, Katoh T;
 PI WPI; 2005-396112/40.
 DR WPI; 2005-396112/40.
 XX Designing siRNA for suppressing expression of target gene having sequence
 PT complementary for target mRNA sequence in target gene, and having bases
 PT constituting double-stranded portion for inhibiting expression of target
 PT gene.
 PS Example 1; Fig 5B; 39pp; Japanese.
 XX The invention relates to a method for designing an siRNA molecule having
 CC a sequence complementary to a target mRNA sequence in a target gene and
 CC having 19 bases constituting a double-stranded portion for inhibiting
 CC expression of the target gene. The invention also relates to a method of
 CC searching a base sequence and use of the base sequence as siRNA, and a
 CC method of estimating siRNA activity. The method is useful for designing
 CC siRNA for suppressing the expression of a target gene. This sequence
 CC represents an siRNA molecule used in the method of the invention.
 XX
 SQ Sequence 19 BP; 2 A; 5 C; 8 G; 0 T; 4 U; 0 Other;
 QY Query Match 0.9%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 2.1e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 1089 GGCCATGAGCTCCACCA 1105
 19 GGCCATGAGCTCCACCA 3
 RESULT 252
 AEB15725
 ID AEB15725 standard; RNA; 19 BP.
 AC AEB15725;
 DT 22-SEP-2005 (first entry)
 XX Human telomerase-targeted siRNA strand SeqID216.
 DE RNA interference; gene silencing; short interfering RNA; siRNA;
 KW cytosolic; immunosuppressive; vasotropic; antimicrobial; cancer;
 KW restenosis; transplant rejection; autoimmune disease; hyperproliferation;
 KW aging; drug screening; diagnostic; genetic engineering; gene mapping; ss;
 KW telomerase.
 KM Homo sapiens.
 OS US2005153916-A1.
 PN 14-JUN-2005.
 PD 20-AUG-2004; 2004US-00923330.
 XX 18-MAY-2001; 2001US-0292217P.
 PR 20-JUN-2001; 2001US-0306883P.
 PR 13-AUG-2001; 2001US-0311865P.
 PR 20-FEB-2002; 2002US-0358580P.
 PR 06-MAR-2002; 2002US-0362016P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 20-MAY-2002; 2002WO-US015876.

PR 06-JUN-2002; 2002US-0386782P.
 PR 17-JUN-2002; 2002US-0396600P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409239P.
 PR 15-JAN-2003; 2003US-0440129P.
 PR 11-FEB-2003; 2003WO-US004088.
 PR 20-FEB-2003; 2003WO-US005028.
 PR 20-FEB-2003; 2003WO-US005346.
 PR 30-APR-2003; 2003US-00427160.
 PR 23-MAY-2003; 2003US-00444853.
 PR 23-OCT-2003; 2003US-00693059.
 PR 24-NOV-2003; 2003US-00720448.
 PR 03-DEC-2003; 2003US-00727780.
 PR 14-JAN-2004; 2004US-00757803.
 PR 10-FEB-2004; 2004US-0543480P.
 PR 13-FEB-2004; 2004US-00780447.
 PR 16-APR-2004; 2004US-00826966.
 PR 30-APR-2004; 2004WO-US013456.
 PR 24-MAY-2004; 2004WO-US016390.
 XX (SIRN) SIRNA THERAPEUTICS INC.
 PA Mcswigen J, Beigelman L;
 PI WPI; 2005-496858/50.
 DR Novel chemically synthesized double-stranded short interfering nucleic
 XX acid molecule directing cleavage of telomerase RNA by RNA interference,
 PT useful for treating cancer and restenosis.
 PT Claim 33; SEQ ID NO 216; 304pp; English.
 XX The invention relates to chemically synthesized short interfering nucleic
 CC acids (siRNAs) which downregulate expression of telomerase genes by RNA
 CC interference. The siRNAs may or may not comprise ribonucleotides, can
 CC contain deoxyribonucleotides, can be chemically modified and may be
 CC double or single stranded. They further comprise sense and antisense
 CC regions, or alternatively are assembled from a sense oligonucleotide and
 CC an antisense oligonucleotide. Specifically, the siRNAs include short
 CC interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short
 CC hairpin RNA (shRNA). The invention also relates to pharmaceutical
 CC compositions comprising an siRNA targeted to the human telomerase mRNA
 CC which may have a cytosolic, immunosuppressive, vasotropic or
 CC antimicrobial activity. The invention further discloses expression
 CC vectors and host cells comprising an siRNA of the invention. The siRNAs are
 CC used to modulate expression of the telomerase gene in cells, tissue
 CC explants or organisms (for example by ex vivo gene therapy), or in grafts
 CC and transplants for the treatment of a variety of conditions. They may be
 CC used in the treatment of cancer, restenosis, infectious, and age-related
 CC rejection, and/or autoimmune, proliferative, and age-related
 CC diseases, disorders or conditions. The siRNAs may also be used in drug
 CC screening, diagnosis, therapeutic target identification and validation,
 CC genetic engineering, pharmacogenomics, studying gene function, and gene
 CC mapping (for example of single nucleotide polymorphisms). The present
 CC sequence represents the sense strand of a human telomerase-targeted
 CC double-stranded siRNA, which is identical to the telomerase transcript
 CC target sequence.
 XX
 SQ Sequence 19 BP; 6 A; 2 C; 7 G; 0 T; 4 U; 0 Other;
 QY Query Match 0.9%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 70.6%; Pred. No. 2.1e+02;
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 Db 463 AATACAGTGTGAATT 479
 3 AAGACAGUGUGAACUU 19
 RESULT 253
 AEB15948/c
 ID AEB15948 standard; RNA; 19 BP.

XX AC AEB15948;
XX DT 22-SEP-2005 (first entry)
XX DE Human telomerase-targeted siRNA strand SeqID439.
XX RNA interference; gene silencing; short interfering RNA; siRNA;
KM cytosolic; immunosuppressive; vasotropic; antimicrobial; cancer;
KM restenosis; transplant rejection; autoimmune disease; hyperproliferation;
KM aging; drug screening; diagnostic; genetic engineering; gene mapping; ss;
KM telomerase.
XX OS Homo sapiens.
XX PN US2005153916-A1.
XX PD 14-JUL-2005.
XX PF 20-AUG-2004; 2004US-00923330.
XX PR 18-MAY-2001; 2001US-0292217P.
PR 20-JUL-2001; 2001US-0306883P.
PR 13-AUG-2001; 2001US-0311865P.
PR 20-FEB-2002; 2002US-0358580P.
PR 06-MAR-2002; 2002US-0362016P.
PR 11-MAR-2002; 2002US-0363124P.
PR 20-MAY-2002; 2002WO-US015876.
PR 06-JUN-2002; 2002US-036782P.
PR 17-JUL-2002; 2002US-036600P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
PR 11-FEB-2003; 2003WO-US004088.
PR 20-FEB-2003; 2003WO-US005028.
PR 20-FEB-2003; 2003WO-US005346.
PR 30-APR-2003; 2003US-00427160.
PR 23-MAY-2003; 2003US-00444853.
PR 23-OCT-2003; 2003US-00693059.
PR 24-NOV-2003; 2003US-00720448.
PR 03-DEC-2003; 2003US-00727780.
PR 14-JAN-2004; 2004US-00757803.
PR 10-FEB-2004; 2004US-0543489P.
PR 13-FEB-2004; 2004US-00780447.
PR 16-APR-2004; 2004US-00826966.
PR 30-APR-2004; 2004WO-US013456.
PR 24-MAY-2004; 2004WO-US016390.
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX Mcawigen J, Belgelman L;
XX WPI; 2005-496858/50.
XX Novel chemically synthesized double-stranded short interfering nucleic
PT acid molecule directing cleavage of telomerase RNA by RNA interference,
PT useful for treating cancer and restenosis.
XX Claim 33; SEQ ID NO 439; 304pp; English.
XX The invention relates to chemically synthesized short interfering nucleic
CC acids (siRNAs) which downregulate expression of telomerase genes by RNA
CC interference. The siRNAs may or may not comprise ribonucleotides, can
CC contain deoxyribonucleotides, can be chemically modified and may be
CC double or single stranded. They further comprise sense and antisense
CC regions, or alternatively are assembled from a sense oligonucleotide and
CC an antisense oligonucleotide. Specifically, the siRNAs include short
CC interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short
CC hairpin RNA (shRNA). The invention also relates to pharmaceutical
CC compositions comprising an siRNA targeted to the human telomerase mRNA
CC which may have a cytosolic, immunosuppressive, vasotropic or
CC antimicrobial activity. The invention further discloses expression

CC vectors and host cells comprising an siRNA of the invention. The siRNAs are
CC used to modulate expression of the telomerase gene in cells, tissue
CC explants or organisms (for example by ex vivo gene therapy), or in grafts
CC and transplants for the treatment of a variety of conditions. They may be
CC used in the treatment of cancer, restenosis, transplant and/or tissue
CC rejection, and/or autoimmune, proliferative, infectious, and age-related
CC diseases, disorders or conditions. The siRNAs may also be used in drug
CC screening, diagnosis, therapeutic target identification and validation,
CC genetic engineering, pharmacogenomics, studying gene function, and gene
CC mapping (for example of single nucleotide polymorphisms). The present
CC sequence represents the antisense strand of a human telomerase-targeted
CC double-stranded siRNA.
XX SQ Sequence 19 BP; 4 A; 7 C; 2 G; 0 T; 6 U; 0 Other;
Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DY 463 AATACAGTGTGAACCTT 479
DB 17 AAGACAGTGTGAACCTT 1
RESULT 254
AED37961/C
ID AED37961 standard; RNA, 19 BP.
XX AC AED37961;
XX DT 15-DEC-2005 (first entry)
XX DE VEGF or VEGFR-specific siRNA sequence - SEQ ID 1762.
XX KM vascular endothelial growth factor;
KM respiratory-gen.; asthma; antihypertensive; allergic rhinitis; anti-allergic;
KM chronic obstructive pulmonary disease; gene silencing; siRNA;
KM short interfering RNA interference; gene silencing; siRNA;
XX OS Unidentified.
XX PN US2005222066-A1.
XX PD 06-OCT-2005.
XX PF 12-OCT-2004; 2004US-00962898.
XX PR 18-MAY-2001; 2001US-0292217P.
PR 20-JUL-2001; 2001US-0306883P.
PR 13-AUG-2001; 2001US-0311865P.
PR 20-FEB-2002; 2002US-0358580P.
PR 06-MAR-2002; 2002US-0362016P.
PR 11-MAR-2002; 2002US-0363124P.
PR 17-MAY-2002; 2002WO-US015876.
PR 06-JUN-2002; 2002US-036782P.
PR 03-JUL-2002; 2002US-036600P.
PR 29-JUL-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
PR 14-FEB-2003; 2003WO-US004088.
PR 20-FEB-2003; 2003WO-US005028.
PR 20-FEB-2003; 2003WO-US005346.
PR 20-FEB-2003; 2003WO-US005028.
PR 30-APR-2003; 2003US-00427160.
PR 23-MAY-2003; 2003US-00444853.
PR 16-SEP-2003; 2003US-00664767.
PR 16-SEP-2003; 2003US-00665255.
PR 23-SEP-2003; 2003US-00670011.
PR 23-OCT-2003; 2003US-00693059.

PR 24-NOV-2003; 2003US-00720448.
 PR 03-DEC-2003; 2003US-00722780.
 PR 14-JAN-2004; 2004US-00757803.
 PR 26-JAN-2004; 2004US-00764957.
 PR 10-FEB-2004; 2004US-0543480P.
 PR 13-FEB-2004; 2004US-00780447.
 PR 16-APR-2004; 2004US-00826966.
 PR 23-APR-2004; 2004US-00831620.
 PR 30-APR-2004; 2004US-05013456.
 PR 11-MAY-2004; 2004US-00844076.
 PR 24-MAY-2004; 2004US-00863973.
 PR 09-JUN-2004; 2004US-00863973.
 PR 20-AUG-2004; 2004US-00922675.
 PR 16-SEP-2004; 2004US-00944611.
 XX (SIRN-) SIRNA THERAPEUTICS INC.
 PA Richards I, Mcswiggen J;
 PI WPI; 2005-664178/68.
 DR
 XX
 PT New multifunctional siRNA molecule comprising a structure having Formula
 PT MF-III, useful for treating a respiratory disease selected from asthma,
 PT COPD, and allergic rhinitis.
 PS Example 13; SEQ ID NO 1762; 266pp; English.
 XX
 CC The invention comprises short interfering nucleic acid (siRNA) molecules
 CC which modulate vascular endothelial growth factor (VEGF) or VEGF receptor
 CC (VEGFR) gene expression. The siRNA molecules of the invention are useful
 CC for treating respiratory diseases (e.g. asthma, COPD, and allergic
 CC rhinitis). The present nucleic acid represents a VEGF/VEGFR-specific
 CC siRNA sequence that was used in an example of the invention.
 XX
 SQ Sequence 19 BP; 0 A; 8 C; 7 G; 0 T; 4 U; 0 Other;
 Query Match 0.9%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 2.1e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 139 AGCGCCGACGACAGGA 155
 DB 18 AGCGCCGACGACCGGA 2
 RESULT 255
 AED37714
 ID AED37714 standard; RNA; 19 BP.
 AC AED37714;
 XX
 DT 15-DEC-2005 (first entry)
 XX
 DE VEGF or VEGFR-specific siRNA sequence - SEQ ID 1515.
 XX
 XX vascular endothelial growth factor;
 KM vascular endothelial growth factor receptor; respiratory disease;
 KM respiratory-gen.; asthma; antiasthmatic;
 KM chronic obstructive pulmonary disease; allergic rhinitis; antiallergic;
 KM antiinflammatory; RNA interference; gene silencing; siRNA;
 KM short interfering RNA; ss.
 XX
 OS Unidentified.
 XX
 PN US2005222066-A1.
 XX
 PD 06-OCT-2005.
 XX
 PF 12-OCT-2004; 2004US-00962898.
 XX
 XX 18-MAY-2001; 2001US-0292217P.
 XX 20-JUL-2001; 2001US-0306883P.
 PR 13-AUG-2001; 2001US-0311865P.

PR 20-FEB-2002; 2002US-0358580P.
 PR 06-MAR-2002; 2002US-0362016P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 17-MAY-2002; 2002US-0365187P.
 PR 06-JUN-2002; 2002US-0367882P.
 PR 03-JUL-2002; 2002US-0393796P.
 PR 29-JUL-2002; 2002US-0399348P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409493P.
 PR 15-JAN-2003; 2003US-0440129P.
 PR 14-FEB-2003; 2003US-0004566P.
 PR 20-FEB-2003; 2003US-0005022P.
 PR 20-FEB-2003; 2003US-0005346P.
 PR 30-APR-2003; 2003US-0042716P.
 PR 23-MAY-2003; 2003US-0044485P.
 PR 16-SEP-2003; 2003US-00664767.
 PR 16-SEP-2003; 2003US-0066525P.
 PR 23-SEP-2003; 2003US-00670011.
 PR 23-OCT-2003; 2003US-00693059.
 PR 24-NOV-2003; 2003US-00720448.
 PR 03-DEC-2003; 2003US-00727780.
 PR 14-JAN-2004; 2004US-00757803.
 PR 26-JAN-2004; 2004US-00764957.
 PR 10-FEB-2004; 2004US-0543480P.
 PR 13-FEB-2004; 2004US-00780447.
 PR 16-APR-2004; 2004US-00826966.
 PR 30-APR-2004; 2004US-00831620.
 PR 11-MAY-2004; 2004US-00844076.
 PR 24-MAY-2004; 2004US-00863973.
 PR 09-JUN-2004; 2004US-00863973.
 PR 20-AUG-2004; 2004US-00922675.
 PR 16-SEP-2004; 2004US-00944611.
 XX
 XX (SIRN-) SIRNA THERAPEUTICS INC.
 PA Richards I, Mcswiggen J;
 PI WPI; 2005-664178/68.
 DR
 XX
 PT New multifunctional siRNA molecule comprising a structure having Formula
 PT MF-III, useful for treating a respiratory disease selected from asthma,
 PT COPD, and allergic rhinitis.
 PS Example 13; SEQ ID NO 1515; 266pp; English.
 XX
 CC The invention comprises short interfering nucleic acid (siRNA) molecules
 CC which modulate vascular endothelial growth factor (VEGF) or VEGF receptor
 CC (VEGFR) gene expression. The siRNA molecules of the invention are useful
 CC for treating respiratory diseases (e.g. asthma, COPD, and allergic
 CC rhinitis). The present nucleic acid represents a VEGF/VEGFR-specific
 CC siRNA sequence that was used in an example of the invention.
 XX
 SQ Sequence 19 BP; 4 A; 7 C; 8 G; 0 T; 0 U; 0 Other;
 Query Match 0.9%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 2.1e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 139 AGCGCCGACGACAGGA 155
 DB 2 AGCGCCGACGACCGGA 18
 RESULT 256
 AEF75485
 ID AEF75485 standard; RNA; 19 BP.
 XX
 AC AEF75485;
 XX
 DT 06-APR-2006 (first entry)

XX Human NOGO-A transcript target sequence/siRNA sense strand, SEQ:35.
DE
XX RNA interference; gene silencing; short interfering RNA; siRNA;
KM nervous system injury; spinal cord injury; neuroprotective; vulnery;
KM cerebrovascular ischemia; cerebroprotective; multiple sclerosis;
KM muscular dystrophy; muscular-gen.; neuropathy; motor neurone disease;
KM CNS-gen.; ataxia; Parkinsons disease; antiparkinsonian;
KM Huntingtons chorea; anticonvulsant; noctropic; dementia;
KM Creutzfeldt Jakob disease; Alzheimers disease; NOGO-A; KIAA0866;
KM reticulon 4; RTN4; ss.
XX
XX Homo sapiens.
OS
XX
XX US2005261212-A1.
PN
XX
XX 24-NOV-2005.
PD
XX
XX 26-JUL-2002; 2002US-00206693.
PF
XX
XX 11-FEB-2000; 2000US-0181797P.
PR
XX 09-FEB-2001; 2001US-00780533.
PR
XX 05-APR-2001; 2001US-00827395.
PR
XX 20-FEB-2002; 2002US-0358580P.
PR
XX 11-MAR-2002; 2002US-0363124P.
PR
XX 03-APR-2002; 2002WO-US010512.
PR
XX 06-JUN-2002; 2002US-0386782P.
PR
XX
XX (MCSW/) MCSWIGEN J A.
PA
XX
XX Mcswigen JA;
PI
XX
XX WPI; 2006-190836/20.
DR
XX
XX
XX New chemically modified double stranded short interfering nucleic acid
PT (siRNA) molecule that directs cleavage of a NOGO receptor (NOGOR) RNA via
PT RNA interference (RNAi), useful for modulating gene expression.
XX
XX
XX Disclosure; SEQ ID NO 35; 171pp; English.
PS
XX
XX The invention relates to chemically synthesized short interfering nucleic
CC acids (siNAs) which downregulate expression of a NOGO receptor gene by
CC RNA interference. The siNAs may or may not comprise ribonucleotides, can
CC contain deoxyribonucleotides, can be chemically modified and may be
CC double or single stranded. They further comprise sense and antisense
CC regions, or alternatively are assembled from a sense oligonucleotide and
CC an antisense oligonucleotide. Specifically, the siNAs include short
CC interfering RNA (shRNA), double-stranded RNA, micro-RNA (miRNA) and short
CC hairpin RNA (shRNA). The invention also relates to pharmaceutical
CC compositions comprising an siNA targeted to a NOGO receptor mRNA. It
CC further discloses siNAs targeted to a NOGO receptor gene, siNAs targeted
CC to a NOGO gene itself, and expression vectors and host cells comprising
CC an siNA of the invention. In particular, the invention discloses siRNAs
CC (AEF75903-AEF76100 and AEF76101-AEF76112) targeted to the human NOGO
CC receptor gene of GenBank accession number BC011787, and siRNAs (AEF75451-
CC AEF75902) targeted to the human NOGO-A (KIAA0866) gene of DDBJ accession
CC number AB020693. The siNAs are used to modulate expression of NOGO
CC receptor or NOGO genes in cells, tissue explants or organisms (e.g., by
CC ex vivo gene therapy), or in grafts and transplants for the treatment of
CC a variety of neurodegenerative conditions such as central nervous system
CC (CNS) injury (e.g., spinal cord injury or stroke), multiple sclerosis
CC (MS), muscular dystrophy, chemotherapy-induced neuropathy, amyotrophic
CC lateral sclerosis (ALS), ataxia, Parkinson's disease, Huntingtons
CC disease, dementia, Creutzfeldt-Jakob disease and especially Alzheimers
CC disease. The siNAs may also be used in drug screening, diagnosis,
CC therapeutic target identification and validation, genetic engineering,
CC pharmacogenetics, studying gene function, and gene mapping (e.g., of
CC single nucleotide polymorphisms). The present sequence represents the
CC sense strand of a human NOGO-A-targeted double-stranded siRNA, which is
CC identical to the NOGO-A transcript target sequence.
XX
XX
XX Sequence 19 BP; 1 A; 13 C; 4 G; 0 T; 1 U; 0 Other;
SQ

Query Match 0 9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. NO. 2.1e+02;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 619 CCCCTCCAGCCCGGCT 635
Db 1 CCCCCGACGCCGGCU 17
RESULT 257
AEF75711/c
ID AEF75711 standard; RNA; 19 BP.
XX
XX AC AEF75711;
XX
XX DT 06-APR-2006 (first entry)
XX
XX DE Human NOGO-A siRNA antisense strand, SEQ:261.
XX
XX RNA interference; gene silencing; short interfering RNA; siRNA;
KM nervous system injury; spinal cord injury; neuroprotective; vulnery;
KM cerebrovascular ischemia; cerebroprotective; multiple sclerosis;
KM muscular dystrophy; muscular-gen.; neuropathy; motor neurone disease;
KM CNS-gen.; ataxia; Parkinsons disease; antiparkinsonian;
KM Huntingtons chorea; anticonvulsant; noctropic; dementia;
KM Creutzfeldt Jakob disease; Alzheimers disease; NOGO-A; KIAA0866;
KM reticulon 4; RTN4; ss.
XX
XX
XX Homo sapiens.
OS
XX
XX US2005261212-A1.
PN
XX
XX 24-NOV-2005.
PD
XX
XX
XX 26-JUL-2002; 2002US-00206693.
PF
XX
XX 11-FEB-2000; 2000US-0181797P.
PR
XX 09-FEB-2001; 2001US-00780533.
PR
XX 05-APR-2001; 2001US-00827395.
PR
XX 20-FEB-2002; 2002US-0358580P.
PR
XX 11-MAR-2002; 2002US-0363124P.
PR
XX 03-APR-2002; 2002WO-US010512.
PR
XX 06-JUN-2002; 2002US-0386782P.
PR
XX
XX (MCSW/) MCSWIGEN J A.
PA
XX
XX Mcswigen JA;
PI
XX
XX WPI; 2006-190836/20.
DR
XX
XX
XX New chemically modified double stranded short interfering nucleic acid
PT (siRNA) molecule that directs cleavage of a NOGO receptor (NOGOR) RNA via
PT RNA interference (RNAi), useful for modulating gene expression.
XX
XX
XX Disclosure; SEQ ID NO 261; 171pp; English.
PS
XX
XX The invention relates to chemically synthesized short interfering nucleic
CC acids (siNAs) which downregulate expression of a NOGO receptor gene by
CC RNA interference. The siNAs may or may not comprise ribonucleotides, can
CC contain deoxyribonucleotides, can be chemically modified and may be
CC double or single stranded. They further comprise sense and antisense
CC regions, or alternatively are assembled from a sense oligonucleotide and
CC an antisense oligonucleotide. Specifically, the siNAs include short
CC interfering RNA (shRNA), double-stranded RNA, micro-RNA (miRNA) and short
CC hairpin RNA (shRNA). The invention also relates to pharmaceutical
CC compositions comprising an siNA targeted to a NOGO receptor mRNA. It
CC further discloses siNAs targeted to a NOGO receptor gene, siNAs targeted
CC to a NOGO gene itself, and expression vectors and host cells comprising
CC an siNA of the invention. In particular, the invention discloses siRNAs
CC (AEF75903-AEF76100 and AEF76101-AEF76112) targeted to the human NOGO
CC receptor gene of GenBank accession number BC011787, and siRNAs (AEF75451-
CC AEF75902) targeted to the human NOGO-A (KIAA0866) gene of DDBJ accession
CC number AB020693. The siNAs are used to modulate expression of NOGO

DT 05-JUN-1999 (first entry)
XX
XX Substance P receptor antisense oligonucleotide fragment.
XX
XX Antisense oligonucleotide; multiple target; antisense treatment;
XX impaired respiration; inflammation; lung disease;
XX pulmonary vasoconstriction; inflammation; allergic rhinitis;
XX acute asthma; allergy; asthma; impeded respiration;
XX respiratory distress syndrome; pain; cystic fibrosis;
XX pulmonary hypertension; pulmonary vasoconstriction; emphysema;
XX chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
XX colon cancer; breast cancer; lung cancer; pancreatic cancer;
XX hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
XX prostate cancer; ss.
XX
XX Synthetic.
XX
XX WO913886-A1.
XX
XX 25-MAR-1999.
XX
XX 17-SEP-1998; 98WO-US019419.
XX
XX 17-SEP-1997; 97US-0059160P.
XX 09-JUN-1998; 98US-00093972.
XX
XX (UYEC-) UNIV EAST CAROLINA.
XX
XX Myce JW;
XX
XX WPI; 1999-229400/19.
XX
XX New antisense oligonucleotides used in treatment of, e.g. pulmonary
XX vasoconstriction.
XX
XX Disclosure; Page 59; 120pp; English.
XX
XX The specification describes antisense oligonucleotides (AAK52869-X55271)
XX directed against at least 2 mRNAs selected from target genes, coding and
XX non-coding regions of RNAs corresponding to target genes, gene initiation
XX codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
XX -end and the juxta-section between coding and non-coding regions and all
XX segments of RNAs encoding proteins associated with one or more diseases,
XX conditions or mixtures. The antisense oligonucleotides may be derived
XX from sequences AAK55272-74. These multiple target oligonucleotides
XX (specifically AAK55180-271) can be used for the antisense treatment of
XX diseases and conditions. Typical diseases and conditions are those
XX associated with impaired respiration and inflammation, including lung
XX diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
XX acute asthma, allergies, asthma, impeded respiration, respiratory
XX distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
XX pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
XX disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
XX colon cancer, breast cancer, lung cancer, pancreatic cancer,
XX hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
XX well as all types of cancers which may metastasize or have metastasized
XX to the lungs, including breast and prostate cancer
XX
XX Sequence 15 BP; 0 A; 2 C; 6 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AC AAK54241;
XX
XX 05-JUN-1999 (first entry)
DT
XX Substance P receptor antisense oligonucleotide fragment.
DE
XX Antisense oligonucleotide; multiple target; antisense treatment;
XX impaired respiration; inflammation; lung disease;
XX pulmonary vasoconstriction; inflammation; allergic rhinitis;
XX acute asthma; allergy; asthma; impeded respiration;
XX respiratory distress syndrome; pain; cystic fibrosis;
XX pulmonary hypertension; pulmonary vasoconstriction; emphysema;
XX chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
XX colon cancer; breast cancer; lung cancer; pancreatic cancer;
XX hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
XX prostate cancer; ss.
XX
XX Synthetic.
XX
XX WO913886-A1.
XX
XX 25-MAR-1999.
XX
XX 17-SEP-1998; 98WO-US019419.
XX
XX 17-SEP-1997; 97US-0059160P.
XX 09-JUN-1998; 98US-00093972.
XX
XX (UYEC-) UNIV EAST CAROLINA.
XX
XX Myce JW;
XX
XX WPI; 1999-229400/19.
XX
XX New antisense oligonucleotides used in treatment of, e.g. pulmonary
XX vasoconstriction.
XX
XX Disclosure; Page 59; 120pp; English.
XX
XX The specification describes antisense oligonucleotides (AAK52869-X55271)
XX directed against at least 2 mRNAs selected from target genes, coding and
XX non-coding regions of RNAs corresponding to target genes, gene initiation
XX codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
XX -end and the juxta-section between coding and non-coding regions and all
XX segments of RNAs encoding proteins associated with one or more diseases,
XX conditions or mixtures. The antisense oligonucleotides may be derived
XX from sequences AAK55272-74. These multiple target oligonucleotides
XX (specifically AAK55180-271) can be used for the antisense treatment of
XX diseases and conditions. Typical diseases and conditions are those
XX associated with impaired respiration and inflammation, including lung
XX diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
XX acute asthma, allergies, asthma, impeded respiration, respiratory
XX distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
XX pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
XX disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
XX colon cancer, breast cancer, lung cancer, pancreatic cancer,
XX hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
XX well as all types of cancers which may metastasize or have metastasized
XX to the lungs, including breast and prostate cancer
XX
XX Sequence 15 BP; 0 A; 5 C; 6 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 261
AAK54241/c
ID AAK54241 standard; DNA; 15 BP.
XX

RESULT 262
AAK54241/c
ID AAK54241 standard; DNA; 15 BP.
XX

AAA33685 standard; DNA; 15 BP.
AAA33685;
28-JUL-2000 (first entry)
Low adenosine antisense oligonucleotide SEQ ID NO:1374.
Human; adenosine receptor; low adenosine antisense oligonucleotide;
phosphorothioate; impaired respiration; inflammation; allergy;
allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
antiallergic; antiasthmatic; cyostatic; analgesic; impaired airway;
lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
respiratory distress syndrome; pain; cystic fibrosis; emphysema;
pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
Homo sapiens.
WO200009525-A2.
24-FEB-2000.
03-AUG-1999; 99WO-US017712.
03-AUG-1998; 98US-0095212P.
(UYEC-) UNIV EAST CAROLINA.
Nyce JW;
UPI; 2000-205971/18.
New antisense oligonucleotides useful for treating e.g. pulmonary
vasoconstriction, inflammation, allergies, asthma, hypertension,
bronchitis, emphysema, respiratory distress syndrome, ischemia or
cancers.
Claim 18; Page 436; 1343pp; English.
The present invention describes a new composition comprising an antisense
oligonucleotide (ON) with low adenosine (up to 15%), which targets
nucleic acids involved in bronchoconstriction, allergies, and/or
inflammation. The ON can have antiinflammatory, antiallergic,
antiasthmatic, cyostatic and analgesic activities. The compositions are
useful for the treatment of diseases associated with inflammation,
impaired airways, including lung disease and diseases whose secondary
effects afflict the lungs of a subject. They can be used for treating
e.g. ischaemic conditions, respiratory distress syndrome, pain, cystic
fibrosis, pulmonary hypertension, emphysema, chronic obstructive
pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
carcinomas, and cancers which may metastasise to the lungs, including
the breast and prostate cancer. The reduction of the adenosine content of the
ONs reduces side effects. The A-containing ONs break down with the
release of deoxyadenosine which activates adenosine receptors causing
bronchoconstriction and inflammation. AAA3313 to AAA3512 represent the
nucleotide sequences given in the sequence listing from the present
invention, which correspond to SEQ ID NO:1 to 185, and then the last 185
sequences are also called SEQ ID NO:1 to 185, but the sequences differ
from the previously named sequences. SEQ ID NO:11 to 1680 (AAA3233 to
AAA3992) are specifically claimed ONs from the present invention. N.B.
Sequences given in the disclosure of the present invention do not match
up with their corresponding SEQ ID NO: sequences given in the sequence
listing
Sequence 15 BP; 0 A; 5 C; 6 G; 4 T; 0 U; 0 Other;
Query Match 0.8%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 15 CCAGACCCAGGCGAG 1
|||||||
RESULT 263
AAA33684/c
ID AAA33684 standard; DNA; 15 BP.
AAA33684;
28-JUL-2000 (first entry)
Low adenosine antisense oligonucleotide SEQ ID NO:1373.
Human; adenosine receptor; low adenosine antisense oligonucleotide;
phosphorothioate; impaired respiration; inflammation; allergy;
allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
antiallergic; antiasthmatic; cyostatic; analgesic; impaired airway;
lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
respiratory distress syndrome; pain; cystic fibrosis; emphysema;
pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
Homo sapiens.
WO200009525-A2.
24-FEB-2000.
03-AUG-1999; 99WO-US017712.
03-AUG-1998; 98US-0095212P.
(UYEC-) UNIV EAST CAROLINA.
Nyce JW;
UPI; 2000-205971/18.
New antisense oligonucleotides useful for treating e.g. pulmonary
vasoconstriction, inflammation, allergies, asthma, hypertension,
bronchitis, emphysema, respiratory distress syndrome, ischemia or
cancers.
Claim 18; Page 436; 1343pp; English.
The present invention describes a new composition comprising an antisense
oligonucleotide (ON) with low adenosine (up to 15%), which targets
nucleic acids involved in bronchoconstriction, allergies, and/or
inflammation. The ON can have antiinflammatory, antiallergic,
antiasthmatic, cyostatic and analgesic activities. The compositions are
useful for the treatment of diseases associated with inflammation,
impaired airways, including lung disease and diseases whose secondary
effects afflict the lungs of a subject. They can be used for treating
e.g. ischaemic conditions, respiratory distress syndrome, pain, cystic
fibrosis, pulmonary hypertension, emphysema, chronic obstructive
pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
carcinomas, and cancers which may metastasise to the lungs, including
the breast and prostate cancer. The reduction of the adenosine content of the
ONs reduces side effects. The A-containing ONs break down with the
release of deoxyadenosine which activates adenosine receptors causing
bronchoconstriction and inflammation. AAA3313 to AAA3512 represent the
nucleotide sequences given in the sequence listing from the present
invention, which correspond to SEQ ID NO:1 to 185, and then the last 185
sequences are also called SEQ ID NO:1 to 185, but the sequences differ
from the previously named sequences. SEQ ID NO:11 to 1680 (AAA3233 to
AAA3992) are specifically claimed ONs from the present invention. N.B.
Sequences given in the disclosure of the present invention do not match
up with their corresponding SEQ ID NO: sequences given in the sequence
listing
Sequence 15 BP; 0 A; 2 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 0.8%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 716 CAACCAAGAGACCA 730
 |||||
 Db 15 CAACCAAGAGACCA 1

RESULT 264
 AAF19807/C
 ID AAF19807 standard; DNA; 15 BP.
 XX
 AC AAF19807;
 XX
 DT 14-MAR-2001 (first entry)
 XX
 DE Human substance P receptor polynucleotide fragment #1374.

Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 human; airway disorder; bronchoconstriction; lung inflammation;
 surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 immunosuppressive; antiaesthetic; analgesic; hypotensive; cytoskeletal;
 respiratory obstruction; pulmonary obstruction; impeded respiration;
 surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 cancer; ss.

XX Homo sapiens.
 OS
 XX
 PN WO200062736-A2.
 XX
 PD 26-OCT-2000.
 XX
 PF 24-MAR-2000; 2000WO-US008020.
 XX
 PR 06-APR-1999; 99US-0127958P.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 PA (NYCE/) NYCE J W.
 XX
 PI Nyce JW;
 XX
 XX WPI; 2000-679539/66.
 DR
 XX
 PT Low adenosine (A) content antisense oligonucleotides which do not trigger
 PT adenosine receptors during metabolism, useful e.g. for treating cancers
 PT and respiratory obstructions.
 PS
 XX Claim 14; Page 245; 1592pp; English.

The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiaesthetic, hypotensive and cytoskeletal activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and/or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defense, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction

CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
 CC surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention
 CC
 XX
 SQ Sequence 15 BP; 0 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 0.8%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1236 CCAGACCCAGGCGAG 1250
 |||||
 Db 15 CCAGACCCAGGCGAG 1

RESULT 265
 AAF19806/C
 ID AAF19806 standard; DNA; 15 BP.
 XX
 AC AAF19806;
 XX
 DT 14-MAR-2001 (first entry)
 XX
 DE Human substance P receptor polynucleotide fragment #1373.

Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 human; airway disorder; bronchoconstriction; lung inflammation;
 surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 immunosuppressive; antiaesthetic; analgesic; hypotensive; cytoskeletal;
 respiratory obstruction; pulmonary obstruction; impeded respiration;
 surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 cancer; ss.

XX Homo sapiens.
 OS
 XX
 PN WO200062736-A2.
 XX
 PD 26-OCT-2000.
 XX
 PF 24-MAR-2000; 2000WO-US008020.
 XX
 PR 06-APR-1999; 99US-0127958P.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 PA (NYCE/) NYCE J W.
 XX
 PI Nyce JW;
 XX
 XX WPI; 2000-679539/66.
 DR
 XX
 PT Low adenosine (A) content antisense oligonucleotides which do not trigger
 PT adenosine receptors during metabolism, useful e.g. for treating cancers
 PT and respiratory obstructions.
 PS
 XX Claim 14; Page 245; 1592pp; English.

The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiaesthetic, hypotensive and cytoskeletal activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and/or activity of target polypeptides associated with

CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisease oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impaired respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisease oligonucleotides used in the exemplification of
CC the present invention

CC Sequence 15 BP; 0 A; 2 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 0.8%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 716 CAACCAAGAGACCA 730
DB 15 CAACCAAGAGACCA 1

RESULT 266
ABZ95501/c
ID ABZ95501 standard; DNA; 15 BP.

XX ABZ95501;

DT 17-OCT-2003 (first entry)

DE Human substance P receptor antisease fragment no.1365.

XX Human; antisease; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisease gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

PD 31-OCT-2002.

PF 23-APR-2002; 2002WO-US013135.

PR 24-APR-2001; 2001US-0286137P.

XX (EPIC-) EPIGENESIS PHARM INC.

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

DR WPI; 2003-229219/22.

PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisease to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.

PS Disclosure; SEQ ID NO 10743; 872bp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisease to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisease gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or
CC receptor, producing bronchodilation, increasing levels of adenosine
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

CC Sequence 15 BP; 0 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 0.8%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1236 CCAGCCCGAGGCGAG 1250
DB 15 CCAGCCCGAGGCGAG 1

RESULT 267
ABZ95500/c
ID ABZ95500 standard; DNA; 15 BP.

XX ABZ95500;

DT 17-OCT-2003 (first entry)

DE Human substance P receptor antisease fragment no.1364.

XX Human; antisease; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisease gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

PD 31-OCT-2002.

PF 23-APR-2002; 2002WO-US013135.

PR 24-APR-2001; 2001US-0286137P.

XX (EPIC-) EPIGENESIS PHARM INC.

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

DR WPI; 2003-229219/22.

PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisease to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.

PS Disclosure; SEQ ID NO 10742; 872pp; English.

XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX
XX Sequence 15 BP; 0 A; 2 C; 6 G; 7 T; 0 U; 0 Other:

Query Match 0.8%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 716 CAACCAAGAGACCA 730
Db 15 CAACCAAGAGACCA 1
|||||

RESULT 268
ABD19639/c
ID ABD19639 standard; DNA; 15 BP.

XX
XX ABD19639;
AC
XX
XX 29-JUL-2004 (first entry)
DT
XX
XX Human substance P receptor DNA fragment 1364.
DE
XX
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;
XX surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
XX analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
XX beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
XX respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
XX emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
XX pulmonary transplantation rejection; ds.

OS
XX
XX Homo sapiens.
XX
XX WO200285309-A2.
PN
XX
XX 31-OCT-2002.
PD
XX
XX 23-APR-2002; 2002WO-US013143.
PF
XX
XX 24-APR-2001; 2001US-0286036P.
PR
XX
XX (EPIG-) EPIGENESIS PHARM INC.
PA
XX
XX Nyce JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S,
XX
XX WPI; 2003-093058/08.
DR
XX
XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and

PT bronchodilating agent.

XX
XX Claim 15; SEQ ID NO 10742; 763pp; English.

PS
XX This invention describes a novel composition (a) a first active agent,
XX comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hyperextension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it

XX
XX Sequence 15 BP; 0 A; 2 C; 6 G; 7 T; 0 U; 0 Other:

Query Match 0.8%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 716 CAACCAAGAGACCA 730
Db 15 CAACCAAGAGACCA 1
|||||

RESULT 269
ABD19640/c
ID ABD19640 standard; DNA; 15 BP.

XX
XX ABD19640;
AC
XX
XX 29-JUL-2004 (first entry)
DT
XX
XX Human substance P receptor DNA fragment 1365.
DE
XX
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;
XX surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
XX analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
XX beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
XX respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
XX emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
XX pulmonary transplantation rejection; ds.

OS
XX
XX Homo sapiens.
XX
XX WO200285309-A2.
PN
XX
XX 31-OCT-2002.
PD
XX
XX 23-APR-2002; 2002WO-US013143.
PF
XX
XX

PR 24-APR-2001; 2001US-0286036P.
 XX (EPiG-) EPIGENESIS PHARM INC.
 PA NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX WPI; 2003-093058/08.
 DR
 XX Pharmaceutical composition for treating asthma, has antisense
 PT oligonucleotide containing less percentage of adenosine, targeted to
 PT nucleic acids associated with lung airway or lung dysfunction, and
 PT bronchodilating agent.
 PS
 XX Claim 15; SEQ ID NO 10743; 763bp; English.
 XX This invention describes a novel composition (a) a first active agent,
 CC comprising oligonucleotides, effective for alleviating
 CC bronchoconstriction, respiratory tract inflammation, allergies and
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
 CC surfactant depletion or hyposecretion, when administered to a mammal. The
 CC oligonucleotides are derived from a gene encoding or regulating
 CC expression of a target polypeptide associated with lung airway or lung
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
 CC The invention also describes a kit, that comprises: (a) a delivery
 CC device, in separate containers, (b) the oligonucleotides, (c)
 CC instructions for adding a carrier and for use of the kit. The composition
 CC of the invention has anti-allergic, anti-inflammatory, antispasmodic,
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
 CC beta-adrenergic agonist. The composition is useful for preventing or
 CC treating a respiratory, lung or malignant disease. The administered
 CC composition comprises oligo and is administered to reduce the production
 CC or availability, or to increase the degradation of the target mRNA or to
 CC reduce the amount of target polypeptide present in the lungs. The
 CC pulmonary obstruction, and/or surfactant hypoproduction and/or lung
 CC inflammation, allergies and/or surfactant hypoproduction are associated
 CC with a disease or condition such as pulmonary vasoconstriction,
 CC inflammation, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hyperextension, emphysema, chronic obstructive pulmonary disease, pulmonary
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
 CC prevent any unwanted effects due to it
 CC
 XX
 SQ Sequence 15 BP; 0 A; 5 C; 6 G; 4 T; 0 U; 0 Other;
 Query Match 0.8%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0;
 Oy 1236 CCAGAGCCAGGGCAG 1250
 DB 15 CCAGAGCCAGGGCAG 1
 RESULT 270
 ABK03403
 ID ABK03403 standard; RNA; 17 BP.
 AC ABK03403;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human CD20 G-cleaver #18.
 XX
 KM Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KM cerebroprotective; neuroprotective; antiparkinsonian;
 KM muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KM DNAzyme; Inozyme; G-cleaver; amberzyme; zinyne; lymphoma; leukaemia;
 KM B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;

KM human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KM MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
 KM inflammatory arthropathy; central nervous system injury; multiple sclerosis;
 KM cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KM chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KM Parkinson's disease; ataxia; Huntington's disease;
 KM Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200159103-A2.
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US004273.
 XX
 PR 11-FEB-2000; 2000US-0181797P.
 PR 28-FEB-2000; 2000US-0185516P.
 PR 06-MAR-2000; 2000US-0187128P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGEN J.
 PA (CHOW/) CHOWRIPA B M.
 PI Blatt L, Mcswigen J, Chowrira BM;
 XX WPI; 2001-607195/69.
 DR
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX
 XX Claim 30; Page 152; 200pp; English.
 XX The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acid may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNAzyme) an Inozyme (an endolytic nucleic acid cleaving a NN motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinyne (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition comprising the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is a G-cleaver molecule of the invention
 XX
 SQ Sequence 17 BP; 2 A; 2 C; 6 G; 0 T; 7 U; 0 Other;
 Query Match 0.8%; Score 15; DB 1; Length 17;
 Best Local Similarity 60.0%; Pred. No. 1.8e+02;


```
Matches 9; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 802 ATCTGTGACTGTG 816
   |||:|||||:|
Db 1 AUCUGUGACUGUG 15

RESULT 271
AAA54501/c
ID AAA54501 standard; DNA; 17 BP.
XX
AC AAA54501;
XX
DT 11-APR-2001 (first entry)
XX
DE Degenerate primer for amplifying fructan exohydrolase.
XX
KM Fructan exohydrolase; FEH; transgenic plant; recombination; transgene;
KM gene expression; detergent; detergent additive; oral care composition;
KM primer; ss.
XX
OS Synthetic.
XX
PN WO200068402-A1.
XX
PD 16-NOV-2000.
XX
PF 08-MAY-2000; 2000WO-EP004226.
XX
PR 06-MAY-1999; 99BE-00000329.
XX
PA (LEUV-) LEUVEN RES & DEV.
XX
PI Van Den Ende W, Van Laere A, De Roover J, Michiels A;
XX
DR WPI; 2001-007401/01.
XX
PT Novel DNA molecules encoding enzymes having fructan exohydrolase activity
PT for use in transgenic plant production, dental care compositions, and in
PT detergents.
XX
PS Example 1; Page 15; 45pp; English.
XX
CC Transgenic plants such as Cichorium intybus, Cynara scolymus, Helianthus
CC tuberosus, Scorzonera hispanica, Oryza sativa, Zea mays, Triticum
CC aestivum, Triticum durum, Hordeum vulgare, Secale cereale, Avena sativa,
CC Sorghum vulgare, Phleum pratense, Lolium temulentum, Dactylis glomerata,
CC Pennisetum americanum, Allium cepa, Agave americanum, Agave azul
CC tegulana, Sorghum bicolor and Panicum mliaceum, transformed with a vector
CC encoding a fructan exohydrolase (FEH) enzyme are useful for the
CC recombinant production of FEH or other polypeptides having FEH activity.
CC The FEH polypeptides produced are useful in detergents or as a detergent
CC additive and in oral care compositions. This degenerate primer was
CC constructed based on peptide fragments of FEH and was then used to
CC amplify the FEH coding sequence
XX
SQ Sequence 17 BP; 2 A; 4 C; 2 G; 4 T; 0 U; 5 Other;
Query Match 0.8%; Score 15; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 1.8e+02;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 1208 GCGTGAATGAATCC 1224
   |||:|||||:|
Db 17 GGYTGAARTGAAWCC 1

RESULT 272
ABN06976
ID ABN06976 standard; DNA; 17 BP.
XX
AC ABN06976;
XX
```

```
DT 23-MAY-2002 (first entry)
XX
DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:6968.
XX
KM Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KM muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KM skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
PN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
DR WPI; 2002-179446/23.
XX
PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
PS Disclosure; SEQ ID NO 6968; 214pp; English.
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 7 A; 4 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 0.8%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 28 CAGTGCATCCAGAG 42
|||||
Db 1 CAGTGCATCCAGAG 15

RESULT 273

ABN06974
ID ABN06974 standard; DNA; 17 BP.

AC ABN06974;

DT 29-MAY-2002 (first entry)

DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:6966.

XX Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KM muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.

XX Homo sapiens.

OS WO200192524-A2.

PN 06-DEC-2001.

PD 25-MAY-2001; 2001WO-US016981.

PF 26-MAY-2000; 2000US-0207456P.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

PR 30-JAN-2001; 2001WO-US000661.

PR 30-JAN-2001; 2001WO-US000662.

PR 30-JAN-2001; 2001WO-US000663.

PR 30-JAN-2001; 2001WO-US000664.

PR 30-JAN-2001; 2001WO-US000665.

PR 30-JAN-2001; 2001WO-US000667.

PR 30-JAN-2001; 2001WO-US000669.

PR 30-JAN-2001; 2001WO-US000670.

PR 05-FEB-2001; 2001US-0266860P.

XX (ABOM-) AEOMICA INC.

PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

DR WPI; 2002-179446/23.

XX New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.

XX Disclosure; SEQ ID NO 6966; 214pp; English.

XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and vaccine production. The hGDMLP-1
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterize and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognize hGDMLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption ionization, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localized to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the

CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 6 A; 5 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 0.8%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 CAGTGCATCCAGAG 42
|||||
Db 3 CAGTGCATCCAGAG 17

RESULT 274

ABN06975
ID ABN06975 standard; DNA; 17 BP.

AC ABN06975;

DT 29-MAY-2002 (first entry)

DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:6967.

XX Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KM muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.

XX Homo sapiens.

OS WO200192524-A2.

PN 06-DEC-2001.

PD 25-MAY-2001; 2001WO-US016981.

PF 26-MAY-2000; 2000US-0207456P.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

PR 30-JAN-2001; 2001WO-US000661.

PR 30-JAN-2001; 2001WO-US000662.

PR 30-JAN-2001; 2001WO-US000663.

PR 30-JAN-2001; 2001WO-US000664.

PR 30-JAN-2001; 2001WO-US000665.

PR 30-JAN-2001; 2001WO-US000667.

PR 30-JAN-2001; 2001WO-US000669.

PR 30-JAN-2001; 2001WO-US000670.

PR 05-FEB-2001; 2001US-0266860P.

XX (ABOM-) AEOMICA INC.

PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

DR WPI; 2002-179446/23.

XX New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.

XX Disclosure; SEQ ID NO 6967; 214pp; English.

XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and vaccine production. The hGDMLP-1
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterize and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for

CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX

Sequence 17 BP; 7 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 0.8%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+02; Mismatches 0; Gaps 0;
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 28 CAGTGCATCCAGAG 42
Db 2 CAGTGCATCCAGAG 16
|||||

RESULT 275
ACN70065
ID ACN70065 standard; DNA; 17 BP.
XX
XX ACN70065;
XX
XX 02-DEC-2004 (first entry)
XX
XX Human GDMLP-1 probe SEQ ID NO:6967.
XX
XX Human; ss; probe: myosin-like protein-1; hGDMLP-1;
XX hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
XX skeletal muscle function.
XX
XX Homo sapiens.
XX
XX US2004137589-A1.
XX
XX 15-JUL-2004.
XX
XX 26-NOV-2003; 2003US-00723361.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX 30-JAN-2001; 2001WO-US000661.
XX 30-JAN-2001; 2001WO-US000662.
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.
XX 30-JAN-2001; 2001WO-US000666.
XX 30-JAN-2001; 2001WO-US000667.
XX 30-JAN-2001; 2001WO-US000668.
XX 30-JAN-2001; 2001WO-US000669.
XX 30-JAN-2001; 2001WO-US000670.
XX 05-FEB-2001; 2001US-0266860P.
XX 25-MAY-2001; 2001US-00866108.
XX
XX (GUYY/) GU Y.
XX (JITY/) JT Y.
XX (PENN/) PENN S G.
XX (HANZ/) HANZEL D K.
XX (RANK/) RANK D.
XX (CHEN/) CHEN W.
XX (SHAN/) SHANNON M E.

XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
XX WPI; 2004-533378/51.
XX
XX Novel myosin-like protein-1, useful for treating or preventing disorder
XX associated with decreased expression or activity of human genome-derived
XX myosin-like protein-1 such as disorder of heart and/or skeletal muscle
XX function.
XX
XX Disclosure; SEQ ID NO 6967; 0pp; English.
XX
XX The invention relates to a novel polypeptide (I) comprising a sequence
XX (SI) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully
XX defined in the specification, a fragment of at least 8 amino acids of
XX (SI), 95% deviation from (SI) which are conservative substitutions, and
XX 65% identity to (SI). A polypeptide of the invention acts as a agonist or
XX antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A
XX pharmaceutical composition of the invention is useful for treating or
XX preventing a disorder associated with decreased expression or activity of
XX hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.
XX The present sequence represents a 17-mer nucleotide, used in the
XX invention for scanning the sequence represented in ACN63103
XX

Sequence 17 BP; 7 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 0.8%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+02; Mismatches 0; Gaps 0;
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 28 CAGTGCATCCAGAG 42
Db 2 CAGTGCATCCAGAG 16
|||||

RESULT 276
ACN70066
ID ACN70066 standard; DNA; 17 BP.
XX
XX ACN70066;
XX
XX 02-DEC-2004 (first entry)
XX
XX Human GDMLP-1 probe SEQ ID NO:6968.
XX
XX Human; ss; probe: myosin-like protein-1; hGDMLP-1;
XX hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
XX skeletal muscle function.
XX
XX Homo sapiens.
XX
XX US2004137589-A1.
XX
XX 15-JUL-2004.
XX
XX 26-NOV-2003; 2003US-00723361.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX 30-JAN-2001; 2001WO-US000661.
XX 30-JAN-2001; 2001WO-US000662.
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.
XX 30-JAN-2001; 2001WO-US000666.
XX 30-JAN-2001; 2001WO-US000667.
XX 30-JAN-2001; 2001WO-US000668.
XX 30-JAN-2001; 2001WO-US000669.
XX 30-JAN-2001; 2001WO-US000670.
XX 05-FEB-2001; 2001US-0266860P.
XX 25-MAY-2001; 2001US-00866108.
XX

XX (GUYY/) GU Y.
PA (JITY/) JI Y.
PA (PENN/) PENN S G.
PA (HANZ/) HANZEL D K.
PA (RANK/) RANK D.
PA (CHEN/) CHEN W.
PA (SHAN/) SHANNON M E.
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
PI WPI; 2004-533378/51.
XX Novel myosin-like protein-1, useful for treating or preventing disorder
PT associated with decreased expression or activity of human genome-derived
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT function.
XX Disclosure; SEQ ID NO 6968; Opp; English.
PS The invention relates to a novel polypeptide (I) comprising a sequence
XX (S1) of myosin-like protein-1 (hGDMPL-1) having 2568 amino acids fully
CC defined in the specification, a fragment of at least 8 amino acids of
CC (S1), 95% deviation from (S1) which are conservative substitutions, and
CC 65% identity to (S1). A polypeptide of the invention acts as a agonist or
CC antagonist of hGDMPL-1, or as an inhibitor of hGDMPL-1 activity. A
CC pharmaceutical composition of the invention is useful for treating or
CC preventing a disorder associated with decreased expression or activity of
CC hGDMPL-1, such as a disorder of heart and/or skeletal muscle function.
CC The present sequence represents a 17-mer nucleotide, used in the
CC invention for scanning the sequence represented in ACN63103
XX Sequence 17 BP; 7 A; 4 C; 4 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+02; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;
QY 28 CAGTGCATCCAGAAG 42
Db 1 CAGTGCATCCAGAAG 15
RESULT 277
ACN70064
ID ACN70064 standard; DNA; 17 BP.
XX ACN70064;
XX 02-DEC-2004 (first entry)
XX Human GDMPL-1 probe SEQ ID NO:6966.
XX Human; ss; probe; myosin-like protein-1; hGDMPL-1;
KW hGDMPL-1 agonist hGDMPL antagonist; hGDMPL inhibitor; heart disorder;
KW skeletal muscle function.
XX Homo sapiens.
XX US2004137589-A1.
XX 15-JUL-2004.
XX 26-NOV-2003; 2003US-00723361.
XX 26-MAY-2000; 2000US-0207456P.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX 30-JAN-2001; 2001WO-US000661.
XX 30-JAN-2001; 2001WO-US000662.
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.

PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 30-FEB-2001; 2001US-0266860P.
PR 25-MAY-2001; 2001US-00866108.
XX (GUYY/) GU Y.
PA (JITY/) JI Y.
PA (PENN/) PENN S G.
PA (HANZ/) HANZEL D K.
PA (RANK/) RANK D.
PA (CHEN/) CHEN W.
PA (SHAN/) SHANNON M E.
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
PI WPI; 2004-533378/51.
XX Novel myosin-like protein-1, useful for treating or preventing disorder
PT associated with decreased expression or activity of human genome-derived
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT function.
XX Disclosure; SEQ ID NO 6966; Opp; English.
PS The invention relates to a novel polypeptide (I) comprising a sequence
XX (S1) of myosin-like protein-1 (hGDMPL-1) having 2568 amino acids fully
CC defined in the specification, a fragment of at least 8 amino acids of
CC (S1), 95% deviation from (S1) which are conservative substitutions, and
CC 65% identity to (S1). A polypeptide of the invention acts as a agonist or
CC antagonist of hGDMPL-1, or as an inhibitor of hGDMPL-1 activity. A
CC pharmaceutical composition of the invention is useful for treating or
CC preventing a disorder associated with decreased expression or activity of
CC hGDMPL-1, such as a disorder of heart and/or skeletal muscle function.
CC The present sequence represents a 17-mer nucleotide, used in the
CC invention for scanning the sequence represented in ACN63103
XX Sequence 17 BP; 6 A; 5 C; 4 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+02; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;
QY 28 CAGTGCATCCAGAAG 42
Db 3 CAGTGCATCCAGAAG 17
RESULT 278
AAA99603
ID AAA99603 standard; DNA; 18 BP.
XX AAA99603;
XX 02-FEB-2001 (first entry)
XX Rat D4 receptor oligonucleotide primer ORD-403.
KW Rat; D4 dopamine receptor; cardiovascular system; retinal tissue;
KW vasoregulator; PCR primer; ss.
XX Rattus sp.
XX US6121015-A.
XX 19-SEP-2000.
XX 07-JUN-1995; 95US-00475742.
XX 28-JAN-1993; 93US-00014013.

```
PR 16-JUN-1994; 94US-00261293.
XX
XX (UNIW ) UNIV WASHINGTON.
XX
XX Todd RD, O'malley KL;
XX
XX WPI; 2000-655527/63.
XX
XX Screening for compounds that selectively bind to a rat D4 dopamine
XX receptor (DDR), useful for identifying dopamine (ant)agonists, comprises
XX exposing cells transfected with a nucleic acid encoding the DDR to
XX candidate compounds.
XX
XX Disclosure; Col 6; 29pp; English.
XX
XX The present sequence is an oligonucleotide which was used to screen a
XX lambda Dash rat spleen genomic library for D2-like receptor sequences.
XX The primer is derived from consensus sequences in rat D2 and D3 genes.
XX This method was used to isolate the rat D4 dopamine receptor gene. A cDNA
XX encoding the rat D4 dopamine receptor was expressed in transfected
XX mammalian cells and shown to preferentially bind dopamine antagonists
XX such as clozapine. The cDNA is useful for screening drugs which
XX specifically bind to the receptor and have selective effects on the
XX cardiovascular and retinal tissues through interactions with the
XX receptor. Such compounds may act as vasoregulators or may have ionotropic
XX effects. The D4 receptor protein may be used for the production of
XX polyclonal or monoclonal antibodies which recognise the D4 receptor
XX sequence but do not recognise other dopaminergic receptors. The
XX antibodies may be used in immunocytochemical studies and for
XX identification and isolation via flow sorting of D4 expressing cell types
XX
XX Sequence 18 BP; 0 A; 7 C; 4 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 15; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 988 TGCTGGCTGCCCTTC 1002
XX |||||
XX 1 TGCTGGCTGCCCTTC 15
XX
XX RESULT 279
XX ABX12223
XX ID ABX12223 standard; DNA; 18 BP.
XX
XX AC ABX12223;
XX
XX DT 16-MAY-2003 (first entry)
XX
XX DE Rat dopamine D2 and D3 receptors transmembrane domain VI primer. ORD-403.
XX
XX KM Rat; ss; primer; dopamine; D4; D4 receptor; D4 dopamine receptor probe;
XX clozapine; PCR; transmembrane domain VI.
XX
XX OS Rattus norvegicus.
XX
XX US6486310-B1.
XX
XX PD 26-NOV-2002.
XX
XX PF 16-JUN-1994; 94US-00261293.
XX
XX PR 28-JAN-1993; 93US-00014013.
XX
XX PA (UNIW ) UNIV WASHINGTON.
XX
XX PI O'malley KL, Todd RD;
XX
XX WPI; 2003-310438/30.
XX
XX Novel nucleic acid molecule encoding rat D4 dopamine receptor, useful as
XX a probe for related D4 dopamine receptors.
XX
```

```
XX
XX Example 1; Col 6; 33pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule encoding rat
XX D4 dopamine receptor. The rat D4 dopamine receptor binds dopamine
XX antagonists such as clozapine. The nucleic acid is useful as a probe for
XX related D4 dopamine receptors. The nucleic acid when expressed in cell
XX lines, is useful as an in vitro screen for drugs which specifically bind
XX to the receptor. Antibodies to the protein are useful in
XX immunocytochemical studies, identification and isolation via flow sorting
XX of D4 expressing cell types and in blocking or modifying the effects of
XX D4 agonists and/or antagonists. The present sequence represents the rat
XX dopamine D2 and D3 receptors transmembrane domain VI primer. ORD-403,
XX used to isolate the dopamine D4 receptor from a lambda Dash rat spleen
XX genomic library
XX
XX Sequence 18 BP; 0 A; 7 C; 4 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 15; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 988 TGCTGGCTGCCCTTC 1002
XX |||||
XX 1 TGCTGGCTGCCCTTC 15
XX
XX Db
XX
XX RESULT 280
XX ADF29051
XX ID ADF29051 standard; DNA; 18 BP.
XX
XX AC ADF29051;
XX
XX DT 12-FEB-2004 (first entry)
XX
XX DE Rat dopamine D4 receptor related primer seq id 5.
XX
XX KM cardiovascular; ophthalmological; rat; D4 dopamine receptor;
XX cardiovascular tissue; retinal tissue; neuronal morphology disorder;
XX neuronal connection disorder; PCR; primer; ss.
XX
XX OS Unidentified.
XX
XX US2003118506-A1.
XX
XX PD 26-JUN-2003.
XX
XX PF 11-SEP-2002; 2002US-00241313.
XX
XX PR 28-JAN-1993; 93US-00014013.
XX
XX PR 16-JUN-1994; 94US-00261293.
XX
XX PA (UNIW ) UNIV WASHINGTON.
XX
XX PI O'malley KL, Todd RD;
XX
XX WPI; 2004-009074/01.
XX
XX A new nucleic acid encoding a rat D4 dopamine receptor is useful to treat
XX disorders of the cardiovascular or retinal tissue or prevent or treat
XX disorders of neuronal morphology or connections.
XX
XX Example 1; SEQ ID NO 5; 30pp; English.
XX
XX The invention describes an isolated nucleic acid encoding a rat D4
XX dopamine receptor. The invention is useful to treat disorders of the
XX cardiovascular or retinal tissue or prevent or treat disorders of
XX neuronal morphology or connections. This sequence represents a primer
XX used to isolate DNA encoding the rat dopamine D4 receptor.
XX
XX Sequence 18 BP; 0 A; 7 C; 4 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 15; DB 1; Length 18;
XX
```

Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 988 TGCTGGCTGCCCTTC 1002
|||||
Db 1 TGCTGGCTGCCCTTC 15

RESULT 281

ADS41404/c
ID ADS41404 standard; DNA; 18 BP.

AC ADS41404;

DT 16-DEC-2004 (first entry)

DE Human autoimmune disease-related PCR primer - SEQ ID 6618.

XX single nucleotide polymorphism detection; SNP detection;

XX rheumatoid arthritis; type 1 diabetes; multiple sclerosis;

KW systemic lupus erythematosus; inflammatory bowel disease; psoriasis;

KW thyroiditis; celiac disease; pernicious anaemia; asthma; vitiligo;

KW glomerulonephritis; Grave's disease; myocarditis; Sjogren's disease;

KW primary systemic vasculitis; PCR; primer; ss.

XX Homo sapiens.

OS WO2004083403-A2.

XX 30-SEP-2004.

PF 18-MAR-2004; 2004WO-US008461.

XX 18-MAR-2003; 2003US-0455444P.

PR 25-APR-2003; 2003US-0465241P.

XX (APPL-) APPLERA CORP.

PI Cargill M, Begovich AB, Alexander HC;

XX WPI; 2004-728480/71.

PS Claim 21; SEQ ID NO 6618; 123pp; English.

XX The invention comprises amino acid and coding sequences containing

CC genetic polymorphisms associated with an altered risk of developing an

CC autoimmune disease (e.g. rheumatoid arthritis). The invention further

CC comprises a method of identifying an individual that has an altered risk

CC of developing an autoimmune disease, comprising detecting a single

CC nucleotide polymorphism (SNP) in a nucleic acid of the invention. The DNA

CC and protein sequences of the invention are useful for diagnosing and

CC treating autoimmune diseases, such as: rheumatoid arthritis, type 1

CC diabetes, multiple sclerosis, systemic lupus erythematosus, inflammatory

CC bowel diseases, psoriasis, thyroiditis, celiac disease, pernicious

CC anaemia, asthma, vitiligo, glomerulonephritis, Grave's disease, The

CC present DNA sequence represents a human autoimmune disease-related PCR

CC primer of the invention. NOTE: The present sequence is not shown in the

CC specification, but has been retrieved from the WIPO website.

XX Sequence 18 BP; 5 A; 3 C; 8 G; 2 T; 0 U; 0 Other;

Db 15 TCCTGGCTTCCTGC 1

RESULT 282

ADW71322

ID ADW71322 standard; DNA; 18 BP.

XX ADW71322;

AC 07-APR-2005 (first entry)

DT Human p53 target DNA 3 fragment.

DE High throughput screening; analyte detection; p53; ds.

XX Homo sapiens.

OS US2005014246-A1.

XX 20-JAN-2005.

PD 26-MAY-2004; 2004US-00854018.

XX 14-JUL-2003; 2003JP-00196178.

XX (HITA) HITACHI LTD.

PA Kohara Y, Okano K, Noda H;

PI WPI; 2005-111253/12.

DR High sample throughput device for chemical reaction and analysis

XX comprises a channel for receiving solution, a structure in channel having

PT a molecule immobilized on interior surface of channel.

PS Disclosure; SEQ ID NO 13; 20pp; English.

XX The present invention relates to a method of increasing the reaction

CC efficiency and to reduce the reaction time in the chemical reaction where

CC molecules immobilized on the solid phase are reacted with the molecules

CC in the solution or in the chemical analysis where molecules immobilized

CC on the solid phase capture the molecules in the solution by chemically

CC reacting with such molecules and the captured molecules are measured. The

CC invention is also helpful to improve the throughput to increase thereby

CC increase the reaction efficiency when the sample is the one at a low

CC concentration. The present sequence is human p53 target DNA fragment.

CC This sequence is used in DNA analysis using the DNA measurement device

CC 321.

XX Sequence 18 BP; 0 A; 5 C; 4 G; 9 T; 0 U; 0 Other;

XX Query Match 0.8%; Score 15; DB 1; Length 18;

XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;

XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1144 TTCCGCTCGGCTTC 1158
|||||
Db 2 TTCCGCTCGGCTTC 16

RESULT 283

ADW71312/c

ID ADW71312 standard; DNA; 18 BP.

XX ADW71312;

AC 07-APR-2005 (first entry)

DT Human p53 exon specific DNA probe 3.

XX High throughput screening; analyte detection; p53; probe; ss.

XX Homo sapiens.

XX US2005014246-A1.
PN
XX
PD 20-JAN-2005.
XX
PF 26-MAY-2004; 2004US-00854018.
XX
PR 14-JUL-2003; 2003JP-00196178.
XX
PA (HITA) HITACHI LTD.
XX
PI Kohara Y, Okano K, Noda H;
XX
DR WPI; 2005-111253/12.
XX
PT High sample throughput device for chemical reaction and analysis
PT comprises a channel for receiving solution, a structure in channel having
PT a molecule immobilized on interior surface of channel.
PS
XX Disclosure; SEQ ID NO 3; 20pp; English.
XX
XX The present invention relates to a method of increasing the reaction
CC efficiency and to reduce the reaction time in the chemical reaction where
CC molecules immobilized on the solid phase are reacted with the molecules
CC in the solution or in the chemical analysis where molecules immobilized
CC on the solid phase capture the molecules in the solution by chemically
CC reacting with such molecules and the captured molecules are measured. The
CC invention is also helpful to improve the throughput to increase thereby
CC increase the reaction efficiency when the sample is the one at a low
CC concentration. The present sequence is human p53 exon specific DNA probe.
CC This sequence is used in DNA analysis using the DNA measurement device
CC 321.
XX
SQ Sequence 18 BP; 9 A; 4 C; 5 G; 0 T; 0 U; 0 Other;
Query Match 0.8%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2,1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1144 TTCGCTCTGGGCTTC 1158
DB 17 TTCGCTCTGGGCTTC 3
RESULT 284
AAQ36431/c
ID AAQ36431 standard; DNA; 18 BP.
XX
AC AAQ36431;
XX
DT 25-MAR-2003 (revised)
DT 05-MAR-1993 (first entry)
XX
XX GRP-R primer (EXT 3).
XX
XX Gastrin releasing peptide; GRP; bombesin; neuromedin B; NMB; ranatensin;
KM RBP; bombesin-like peptide; R1BP; R2BP; receptor; agonist;
KM antagonist; ligand; antibody; cancer; ss.
XX
OS Synthetic.
OS
PN WO9216623-A2.
XX
XX 01-OCT-1992.
XX
XX 13-MAR-1992; 92WO-US002091.
XX
XX 15-MAR-1991; 91US-00670603.
PR 03-OCT-1991; 91US-00771332.
XX
XX (BERL-) BERLEX LAB INC.
PA (USSH) US DEPT HEALTH & HUMAN SERVICE.
XX

PI Batley JF, Corjay MH, Fathi Z, Feldman RI, Harkin RV;
PI Slatery TK, Wada B, Wu JM;
XX
XX WPI; 1992-349208/42.
DR
XX
XX Receptors for bombesin-like peptide(s) and their DNA - useful for
PT screening for agonists and antagonists of the receptor ligands, also for
PT treating or diagnosing cancer.
XX
XX
PS Example 12; Page 85-91; 173pp; English.
XX
XX The primers of AAQ36431-32 were used in the identification of cDNA clone
CC encoding the Swiss 3T3 GRP Receptor. EXT 3 (AAQ36431) was used as a gene-
CC specific primer for reverse transcription of Swiss 3T3 mRNA, and EXT 2
CC (AAQ36432) was used as a gene specific primer for Taq DNA polymerase
CC catalysed PCR. The DNA sequences encoding mouse R1BP; human R1BP; rat
CC R2BP; human R2BP and human R3BP are given in AAQ29158-62 respectively.
CC The receptor gene and encoded polypeptide are used for screening for
CC agonists and antagonists of the receptor ligands, for producing
CC diagnostic or therapeutic reagents, and for producing antibodies. Hosts
CC suffering from abnormal receptor function, e.g. proliferative cell
CC conditions such as cancer, may be treated. The mouse GRP receptor was
CC isolated from Swiss 3T3 fibroblasts and sequenced. The sequence was used
CC to design oligonucleotide probes to isolate DNA encoding mouse GRP
CC receptor from a Swiss 3T3 cDNA library. This DNA was then used as a probe
CC to isolate rat NMB receptor, human GRP receptor, human NMB receptor and
CC human R3BP (incompletely characterised homologous putative receptor) from
CC DNA libraries. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 18 BP; 5 A; 4 C; 9 G; 0 T; 0 U; 0 Other;
Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2,3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 982 GCCATCTGCTGGTGGCCC 999
DB 18 GCCTCTCTGCTGGTCCCC 1
RESULT 285
AAV34526/c
ID AAV34526 standard; DNA; 18 BP.
XX
AC AAV34526;
XX
DT 20-AUG-1998 (first entry)
XX
DE Chemokine receptor CXCR4 amplifying RT-PCR primer 2.
XX
XX Chemokine receptor; gp120; fusion protein; HIV; screening; AIDS;
KM CCR4 binding site; RT-PCR primer; ss.
XX
XX Synthetic.
OS Homo sapiens.
OS
XX WO9815569-A1.
PN
XX 16-APR-1998.
PD
XX 08-OCT-1997; 97WO-US018397.
PF
XX 09-OCT-1996; 96US-0027931P.
PR
XX (DAND) DANA FARBER CANCER INST INC.
PA (LEUK-) LEUKOSITE INC.
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Sodroski J, Newman W, Wu L, Gerard N, Gerard C;
XX
XX WPI; 1998-240778/21.
DR
XX Derivatives of gp120 containing modified chemokine receptor binding site
PT

PT - and complexes with soluble CD40, for inhibiting infectivity of human
PT immune deficiency virus and to screen for inhibitors.
XX
PS Example; Page 53; 92pp; English.
XX
CC This primer is used for the RT-PCR amplification of a chemokine receptor
CC CXCR4. The invention provides gp120 derivative having a conformational,
CC discontinuous chemokine receptor binding site defined by amino acids
CC residues present in the gp120 constant regions C2, C3 and C4, and the
CC variable region V3, and its conformation is similar to that of the
CC receptor binding site of wild-type gp120 complexed by CD4. Exposure of
CC the chemokine receptor binding site is increased by having at least part
CC of a variable or constant region of wild-type gp120 removed. A stabilised
CC complex of gp120 CD4 binding site with a soluble CD4 molecule is used to
CC inhibit infectivity of human immune deficiency virus (HIV). Labelled
CC gp120 derivatives are also used to screen for inhibitors of HIV
CC infectivity. The gp120 derivatives are used for diagnosing susceptibility
CC to HIV infection from increased levels of the chemokine receptors (at the
CC protein or nucleic acid levels). Transgenic animals expressing CD4 and
CC chemokine receptor are used as models for studying development of AIDS or
CC effect/safety of therapeutic agents
XX
SQ Sequence 18 BP; 4 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 988 TGCTGCTGCTGCTTCCAC 1005
DB 18 TGCTGCTGCTGCTTCCAC 1
RESULT 286
AAV49658/C
ID AAV49658 standard; DNA; 18 BP.
XX
AC AAV49658;
XX
DT 23-OCT-1998 (first entry)
XX
DE Human SRCR protein PCR primer 41nrl.
XX
XX Scavenger receptor cysteine rich domain; SRCR; diagnosis; treatment;
KM nervous system; medullo-blastoma; glioma; breast; detection;
KW autoantibody; PCR primer; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO9830687-A2.
XX
XX 16-JUL-1998.
XX
XX PD 09-JAN-1998; 98WO-DE000096.
XX
XX PF 09-JAN-1998; 98WO-DE000096.
XX
XX PR 09-JAN-1997; 97DE-01000519.
XX
XX PR 18-JUL-1997; 97DE-01030997.
XX
XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
XX PI Mollenhauer J, Poustka A;
XX
XX WPI; 1998-399136/34.
XX
XX DR Proteins containing scavenger receptor, cysteine rich domain - useful for
XX diagnosis and treatment of tumours.
XX
XX PT proteins containing scavenger receptor, cysteine rich domain - useful for
XX diagnosis and treatment of tumours.
XX
XX PS Example 1; Page 8; 54pp; German.
XX
XX CC AAV49657-V49660 are PCR primers used in the amplification of a gene which
XX encodes a human protein which contains a SRCR (scavenger receptor,
XX cysteine-rich) domain. The gene and encoded protein can be used to

CC diagnose or treat tumours, particularly of the nervous system (medullo-
CC blastoma or glioma) or breast. The DNA sequence and probes derived from
CC it, are used to identify genes that express SRCR-domain containing
CC proteins, to determine the form in which these proteins exist and to
CC assess the significance of individual forms on cellular properties. The
CC protein can be used to detect the presence of autoantibodies and
CC antibodies which regulate its expression
XX
SQ Sequence 18 BP; 2 A; 4 C; 8 G; 4 T; 0 U; 0 Other;
Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1263 CAGCCGCTCGAGACCAC 1280
DB 18 CAGCTGCTCGAGACCAC 1
RESULT 287
AAZ40901/C
ID AAZ40901 standard; DNA; 18 BP.
XX
AC AAZ40901;
XX
XX
DT 26-JAN-2000 (first entry)
XX
DE Human CD40 phosphorothioate antisense oligonucleotide SEQ ID NO:50.
XX
XX Identification; genetic target; gene modulation; human; probe;
KM antisense oligonucleotide; phosphorothioate; PCR primer;
KW nucleotide sequence-based technology; antisense drug discovery;
XX target validation; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO9953101-A1.
XX
XX 21-OCT-1999.
XX
XX PD 13-APR-1999; 99WO-US008268.
XX
XX PF 13-APR-1999; 98US-0081483P.
XX
XX PR 13-APR-1998; 98US-0081483P.
XX
XX PR 28-APR-1998; 98US-00067638.
XX
XX PA (ISIS-) ISIS PHARM INC.
XX
XX XX Cowser LM, Baker BF, Mcneil J, Freiler SM, Sasamor HM, Brooks DG;
XX PI Ohsai C, Wyatt JR, Borchers AH, Vickers TA;
XX
XX DR WPI, 1999-620446/53.
XX
XX PT Identifying compounds which modulate expression of nucleic acids, used to
XX provide compounds having defined physical, chemical or bioactive
XX properties, e.g. antisense activity.
XX
XX PS Example 8; Page 77; 264pp; English.
XX
XX CC A method has been developed of defining a set of compounds that modulate
XX the expression of a target nucleic acid (tNA) sequence via binding of the
XX compounds with the tNA sequence. The method comprises generating a
XX library of virtual compounds in silico according to defined criteria, and
XX evaluating in silico the binding of the virtual compounds with the tNA
XX according to defined criteria. Also described are: (1) a method of
XX defining a set of oligonucleotides (ONs) that modulate the expression of
XX a tNA sequence via binding of the ONs with the tNA sequence comprising
XX generating a library of virtual compounds in silico according to defined
XX criteria, and evaluating in silico the binding of the virtual ONs with
XX the tNA according to defined criteria; and (2) a method of defining a set
XX of compounds that modulate the expression of a tNA sequence via binding
XX of the compounds with the tNA. The methods can be used for the generation
XX and identification of synthetic compounds having defined physical,

CC chemical or bioactive properties. Information gathered from assays of
CC such compounds is used to identify nucleic acid sequences that are
CC tractable to a variety of nucleotide sequence-based technologies, e.g.
CC antisense drug discovery and target validation. AA240852 to AA41220, and
CC AA52701 to AA52706, represent sequences used in the exemplification of
CC the present invention

XX
SQ Sequence 18 BP; 7 A; 3 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1406 TCAGCTTCTCTCCATG 1423
Db 18 TCGGCTTCTCTCCATG 1

RESULT 288
AA247734/C
ID AA247734 standard; DNA; 18 BP.
XX
XX AA247734;
XX
XX 02-MAR-2000 (first entry)
XX
XX Human CD40 antisense oligonucleotide SEQ ID NO:50.
XX
XX Human; CD40; antisense oligonucleotide; phosphorothioate; modulation;
XX expression; immune disease; inflammatory disease; immunomodulatory;
XX anti-inflammatory; anti-arthritis; anti-asthmatic; antiproliferative;
XX anticancer; immuno-suppressive; anti-psoriasis; allograft rejection;
XX hyperproliferative disease; autoimmune disease; rheumatoid arthritis;
XX inflammatory bowel disease; asthma; psoriasis; cancer; tumour; ss.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX WO9957320-A1.
XX
XX 11-NOV-1999.
XX
XX 22-APR-1999; 99WO-US008765.
XX
XX 01-MAY-1998; 98US-00071433.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Cowser LM;
XX
XX WPI; 2000-062158/05.
XX
XX Antisense molecules directed against nucleic acid encoding human CD40,
XX for treating e.g. immune, inflammatory or hyperproliferative diseases.
XX
XX Example 9; Page 44; 102pp; English.

XX
XX AA247685 to AA247768 represent phosphorothioate antisense
XX oligonucleotides targeted to human CD40, which can be used to inhibit the
XX expression of human CD40. CD40 is involved in lymphocyte activation,
XX tumour growth and/or angiogenesis. Inhibition of CD40 is used to treat or
XX prevent immune-associated diseases (specifically guest vs. host disease,
XX allograft rejection or autoimmune diseases); inflammation (specifically
XX asthma, rheumatoid arthritis, allograft rejection, inflammatory bowel
XX disease or psoriasis) or hyperproliferation (specifically cancer and
XX tumours). The antisense oligonucleotides are also useful as diagnostic
XX and research reagents. AA247769 represents the human CD40 nucleotide
XX sequence. AA247770 to AA247772 represent human CD40 forward and reverse
XX PCR primers, and a human CD40 PCR probe, respectively. AA247773 to
XX AA247775 represent other PCR primers and a probe used in the
XX exemplification of the present invention

SQ Sequence 18 BP; 7 A; 3 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1406 TCAGCTTCTCTCCATG 1423
Db 18 TCGGCTTCTCTCCATG 1

RESULT 289
AAS06638
ID AAS06638 standard; DNA; 18 BP.
XX
XX AAS06638;
XX
XX 12-SEP-2001 (first entry)
XX
XX Human alpha1-antichymotrypsin PCR primer.
XX
XX Human; Estrogen response element; ERE; DDRT-PCR; ss; PCR primer;
XX differential display of reverse transcribed mRNAs by PCR;
XX testicular cancer; breast cancer; prostate cancer; endometrial cancer;
XX asthma; hypoplasia; cryptorchism; allergy; hormone replacement therapy;
XX HRT; endocrine system; alpha1-antichymotrypsin.
XX
XX Homo sapiens.
XX
XX WO200134834-A2.
XX
XX 17-MAY-2001.
XX
XX 10-NOV-2000; 2000WO-DK00628.
XX
XX 11-NOV-1999; 99DK-00001626.
XX
XX (RIGS-) RIGSHOSPITALLET.
XX
XX Leffers H, Jorgensen M, Skakkebaek NE;
XX
XX WPI; 2001-335941/35.
XX
XX Evaluating a cellular response to an environmental compound, for use in
XX toxicological analysis, involves determining or comparing the expression
XX levels of at least one endogenous gene.
XX
XX Example 2; Page 25; 77pp; English.

XX
XX The sequence represents a PCR primer from alpha1-antichymotrypsin used in
XX a DDRT-PCR experiment, demonstrating the method of the invention. The
XX method relates to evaluating a cellular response to an environmental
XX compound, comprising determining or comparing the expression levels of at
XX least one endogenous gene e.g by differential display of reverse
XX transcribed mRNAs by PCR (DDRT-PCR). The method can be adapted to
XX identify compounds that act on the level of endogenous gene expression
XX through activating nuclear receptors. The method is useful in
XX toxicological analysis, diagnostics, for diagnosing cancer (e.g.
XX testicular, breast, prostate and endometrium), asthma, hypoplasia,
XX cryptorchism and/or allergy, and for evaluating the efficiency of a
XX treatment for hormonal deficiency or hormonal replacement therapy, in a
XX human such as a post-menopausal female. The method is also useful for
XX identifying environmental chemicals or pharmaceutical compositions that
XX interact with endocrine systems, and for detecting chemicals that pose a
XX health threat. Expression levels of endogenous genes are determined
XX rapidly using a sensitive technique, and the expression of any gene can
XX be monitored. The assays are far more informative than the currently used
XX assay, and significantly reduces the number of animals required for the
XX testing, as it is expected that essentially all the animals in a test
XX group will respond to the compound

SQ Sequence 18 BP; 2 A; 7 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 0.8%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 105 CCTCTGTCGCTTTAG 122
1 CCTCTTCTGCTTAG 18
Db

RESULT 290
AAF76209/c
ID AAF76209 standard; DNA; 18 BP.

AC AAF76209;

DT 05-JUN-2001 (first entry)

DE Human/mouse NTRK3 RT-PCR primer, NTRK3human/mou-R.

XX Human; mouse; NTRK3; TRKC; neurotrophin-3 receptor; NTRK3-K14;
KW transgenic mouse; human chromosome 15q24-25; anxiety disorder;
KW panic disorder; noradrenergic neuron proliferation; agoraphobia;
KW social phobia; depression; bipolar disorder; eating disorder; anorexia;
KW bulimia; obesity; substance abuse; drug abuse; expression analysis;
KW reverse transcription-PCR; RT-PCR primer; ss.

OS Homo sapiens.
OS Mus sp.

PN WO200106848-A1.

PD 01-FEB-2001.

XX 21-JUL-2000; 2000WO-ES000267.

XX 23-JUL-1999; 99ES-00001674.

PR (PALI/) ESTIVILL PALLEJA X.

PI Estivill Palleja X, Gratacos Mayora M, Pujana Genestar MA;
PI Fillat Font C, Dierssen Sotos M;

DR WPI; 2001-182688/18.

PT Transgenic mice overexpressing the neurotrophin-3 receptor, useful e.g.
PT for studying and monitoring anxiety, depression and related disorders.

XX Example; Page 15; 38pp; Spanish.

XX The invention relates to transgenic mice which express the human
CC neurotrophin-3 receptor (NTRK3). The transgenic mice designated TgNTRK3
CC overexpress the wild-type NTRK3 (TRKC) gene, while those designated
CC TgNTRK3-K14 overexpress a form of NTRK3 which has a 14 amino acid
CC residue insert in the kinase domain. Both forms of the NTRK3 gene are
CC under the control of the PDGF (platelet-derived growth factor) promoter.
CC The NTRK3 gene is located in the region of human chromosome 15q24-25
CC which is duplicated in patients with anxiety disorders. Overexpression of
CC likely candidate for association with these disorders. Noradrenergic neurons,
CC NTRK3 has a trophic and proliferative effect on noradrenergic neurons,
CC increasing the response of the noradrenergic system. The transgenic mice
CC are used as models for studying the pathophysiology of anxiety disorders,
CC panic disorder, agoraphobia, social or simple phobias, major depression,
CC bipolar disorder, eating disorders (e.g., anorexia, bulimia, some cases
CC of obesity), and substance abuse (e.g., drug addiction). They may also be
CC used for identifying, monitoring and studying phenotypes of these
CC disorders, particularly during treatment; and for monitoring behavioural,
CC pharmaceutical or gene therapy-based treatments for these conditions.
CC Sequences AAF76208-AAF76209 represent NTRK3 reverse transcription-PCR
CC primers used in the exemplifications of the invention to study NTRK3
CC expression in transgenic mice of the invention and in control mice

Sequence 18 BP; 3 A; 4 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 0.8%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1335 CACACCTGTCCTCGA 1352
18 CACGCCCTGTCACCTGA 1
Db

RESULT 291
ABQ73036
ID ABQ73036 standard; DNA; 18 BP.

AC ABQ73036;

DT 24-SEP-2002 (first entry)

DE Human chloride channel related PCR primer SEQ ID NO:6.

XX Human; chloride channel; CLIC-N3A; CLIC-N3B; CFTR; cystic fibrosis;
KW cystic fibrosis transmembrane conductance regulator; CLIC-3B; respiration;
KW PCR primer; ss.

OS Homo sapiens.

PN WO200244369-A1.

PD 06-JUN-2002.

XX 30-NOV-2001; 2001WO-UP010499.

XX 30-NOV-2000; 2000JP-00365103.

PA (BANY) BANYU PHARM CO LTD.

PA (FURUKAWA T.

PI (OGURA T.

PI Furukawa T, Ogura T;

DR WPI; 2002-557541/59.

PT Human chloride channel CLIC-3B as outward rectifying chloride channel with
PT chloride selectivity and activated by forskolin in presence of cystic
PT fibrosis transmembrane conductance regulator, useful in diagnosis of
PT cystic fibrosis.

PS Disclosure; Page 12; 41pp; Japanese.

XX The present invention describes a human chloride channel protein (A). (A)
CC has respiratory activity. (A) can be used in the diagnosis of and
CC development of drugs for cystic fibrosis. (A) is a CLIC-3-selective
CC splicing subtype, which is an outward rectifying chloride channel with
CC chloride selectivity and is activated by forskolin in the presence of
CC cystic fibrosis transmembrane conductance regulator (CFTR). The present
CC sequence represents a PCR primer which is used in the exemplification of
CC the present invention

Sequence 18 BP; 5 A; 10 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.8%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 243 CTCGCCAACAATCTCCAC 260
1 CTCGCCAACAATCTCTC 18
Db

RESULT 292
ABS64461
ID ABS64461 standard; DNA; 18 BP.

AC ABS64461;

XX

PT	15-NOV-2002	(first entry)
DE	Human TGF-beta binding PCR primer SFL #2.	
XX		
XX	Human; NOX; neurodegenerative disease; Alzheimer's disease; anxiety;	
KW	Parkinson's disease; Huntington's disease; neurological disorder;	
KW	schizophrenia; manic depression; mental retardation; angina pectoris;	
KW	cardiovascular disease; acute heart failure; myocardial infarction;	
KW	muscular disease; muscular disorder; retinal disease; photoreception;	
KW	deafness; keratinisation disorder; cancer; ovarian cancer; melanoma;	
KW	immunological disorder; inflammatory disease; immune disease; diabetes;	
KW	bacterial infection; fungal infection; protozoal infection; obesity;	
KW	viral infection; reproductive system disorder; metabolic disturbance;	
KW	anorexia; wasting disorder; chronic disease; infectious disease;	
KW	dyslipidaemia; TGF-beta binding; cloning; PCR; primer; ss.	
XX		
OS	Homo sapiens.	
XX		
XX	WO200264791-A2.	
PN		
XX	22-AUG-2002.	
PD		
XX	10-DEC-2001; 2001MO-US048369.	
PE		
XX	08-DEC-2000; 2000US-0254329P.	
PR	14-DEC-2000; 2000US-0255648P.	
PR	15-MAY-2001; 2001US-0291037P.	
PR	08-JUN-2001; 2001US-0297173P.	
PR	28-JUN-2001; 2001US-0309258P.	
PR	09-AUG-2001; 2001US-0315639P.	
PR	01-OCT-2001; 2001US-0326393P.	
XX		
XX	(CURA-) CURAGEN CORP.	
PA		
PI	Alsbrook JP, Anderson DM, Burgess CE, Boldog FL, Caeman SJ;	
PI	Colman SD, Edinger SR, Ellerman K, Gerlach V, Gorman L, Grose NM,	
PI	Guo X, Herrman JL, Kekuda R, Lepley DW, Li L, Macdougall JR,	
PI	Miller I, Pena CE, Peyman JA, Raschell L, Rieger DK, Shinkets RA,	
PI	Smithson G, Szytek KA, Stone DJ, Tchernev VT, Vernet CM, Voss EZ,	
PI	Zerhusen BD, Zhong H, Zhong M;	
XX		
XX	WPI; 2002-643486/69.	
DR		
XX		
PT	New NOXV polypeptides and polynucleotides useful for creating or	
PT	preventing e.g. neurodegenerative diseases, neurological disorders,	
PT	cardiovascular diseases, muscular diseases and disorders, or	
PT	immunological diseases.	
XX		
XX	Example 3; page 288; 299pp; English.	
PS		
XX		
CC	The present invention relates to new NOXV polypeptides. The polypeptides	
CC	polynucleotides and antibodies are useful in the manufacture of a	
CC	medicament for treating or preventing neurodegenerative diseases (e.g.	
CC	Alzheimer's disease, Parkinson's disease, or Huntington's disease),	
CC	neurological disorders (e.g. anxiety, schizophrenia, manic depression or	
CC	mental retardation), cardiovascular disease (e.g. acute heart failure,	
CC	angina pectoris or myocardial infarction), muscular diseases and	
CC	disorders, retinal diseases (including those involving photoreception,	
CC	deafness and keratinisation disorders), cancer (e.g. ovarian cancer or	
CC	melanoma), immunological disorders, inflammatory and immune diseases,	
CC	bacterial, fungal, protozoal and viral infections, and reproductive	
CC	system disorders. The proteins of the invention may be used to screen	
CC	drugs or compounds that modulate the NOXV protein activity or expression,	
CC	as well as to treat disorders characterised by insufficient or excessive	
CC	production of NOXV protein or protein forms that have decreased or	
CC	aberrant activity compared to NOXV wild type protein, such as diabetes,	
CC	obesity, metabolic disturbances associated with obesity, anorexia and	
CC	wasting disorders associated with chronic diseases and various cancers,	
CC	infectious diseases and various dyslipidaemias. The nucleic acid	
CC	sequences of the invention may be used in chromosome mapping, identifying	
CC	an individual from minute biological samples (tissue typing), and in	
CC	forensic identification of a biological sample. The present nucleic acid	
CC	sequence represents a cloning PCR primer that was used in the methods of	

Query Match	0 8%;	Score 14.8;	DB 1;	Length 18;
Best Local Similarity	88.9%;	Pred. No. 2.3e+02;		
Matches 16;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0
315	GGCAGCTGCTACACGGT	332		
1	GGCAGCGCCCTACACGGT	18		
DB				
RESULT 293				
ADY75584/C				
ID	ADY75584	standard; DNA; 18 BP.		
XX				
AC	ADY75584;			
XX				
DT	02-JUN-2005	(first entry)		
XX				
DE	Antisense oligonucleotide targeting human CD40, SEQ ID 89.			
XX				
KM	2'-O-methoxyethyl; 2'-NOE; ss; diagnosis; drug discovery;			
XX	mass spectroscopy; phosphorothioate; antisense oligonucleotide; CD40.			
XX				
OS	Homo sapiens.			
XX				
PN	WO2005023986-A2.			
XX				
PD	17-MAR-2005.			
XX				
PF	07-SEP-2004; 2004WO-US028879.			
XX				
PR	04-SEP-2003; 2003US-0500723P.			
PR	04-SEP-2003; 2003US-0500724P.			
PR	04-SEP-2003; 2003US-0500730P.			
PR	04-SEP-2003; 2003US-0500732P.			
PR	04-SEP-2003; 2003US-0500824P.			
PR	11-SEP-2003; 2003US-0502007P.			
PR	11-SEP-2003; 2003US-0502076P.			
PR	17-SEP-2003; 2003US-0504495P.			
XX				
PA	(ISIS-) ISIS PHARM INC.			
PI	Griffey RH, Bennett CF, Ecker DJ, Ward DT, Freiler SM;			
XX				
DR	WPI; 2005-233282/24.			
XX				
PT	Selecting a target molecule having affinity for a ligand that is equal			
PT	to/greater than a baseline affinity by introducing a target molecule into			
PT	a ligand and standard target test mixture and identifying complex by mass			
PT	spectrometer.			
XX				
PS	Example 63; SEQ ID NO 89; 314pp; English.			
XX				
CC	The invention relates to selecting a target molecule that has an affinity			
CC	for a ligand that is equal to or greater than a baseline affinity, ligand			
CC	comprises introducing a target molecule into a test mixture of the ligand			
CC	and a standard target, introducing the test mixture into a mass			
CC	spectrometer and identifying any complexes of the target molecule and the			
CC	ligand. Also included are a method of detecting a ligand-target complex			
CC	having an affinity as expressed as a dissociation constant of nanomolar-			
CC	100 millimolar, a method for determining the relative interaction between			
CC	at least two molecules determining target a ligand, a method of			
CC	determining binding interaction (between a first target molecule and a			
CC	second target molecule with respect to a ligand), a method of determining			
CC	the relative proximity of binding sites for a first target molecule and a			
CC	second target molecule on a ligand, a method of determining the relative			
CC	orientation of a first target molecule to a second target molecule when			
CC	bound to a ligand, a method for screening target molecules having binding			
CC	affinity to a ligand, a method for modulating the binding affinity of a			
CC	target molecule for a ligand, a method for refining the binding of a			

RESULT 295
ID AEC52834 standard; DNA; 18 BP.
AC AEC52834;
XX
DT 17-NOV-2005 (first entry)
XX
DE Antisense oligonucleotide targeting human TGF-beta-3 #1232.
XX
KM Transforming growth factor beta; TGF-beta-3; antisense therapy;
KM antisense oligonucleotide; ss; cancer; cytostatic.
XX
OS Homo sapiens.
PN WO2005084712-A2.
PD 15-SEP-2005.
PF 28-FEB-2005; 2005WO-EP002101.
XX
PR 27-FEB-2004; 2004EP-00004478.
PR 01-APR-2004; 2004US-0558135P.
XX
PA (ANTI-) ANTISENSE PHARMA GMBH.
XX
PI Schlingensiepen K, Schlingensiepen R, Jachinczak P, Stauder G;
PI Bischof A, Hatner M, Egger T;
DR WPI; 2005-630685/64.
XX
XX New antisense oligonucleotides inhibiting the synthesis of proteins
PT involved in the formation of metastases such as transforming growth
PT factor-beta 1 (TGF-beta 1), TGF-beta 2 and TGF-beta 3, useful for
PT treating cancer.
XX
XX Claim 4; Page 72; 106pp; English.
XX
XX The invention relates to an antisense oligonucleotide or its active
CC derivative selected from AEC46374-AEC46395, targeting human interleukin-
CC 10 (IL-10). Also included are a process of manufacturing the antisense
CC oligonucleotide (or its active derivative, by adding consecutive
CC nucleosides and linker stepwise or by cutting the oligonucleotide out of
CC longer oligonucleotide chain), a pharmaceutical composition comprising a
CC composition for treating cancer. The oligonucleotide is an antisense
CC oligonucleotide inhibiting the synthesis of proteins involved in the
CC formation of metastases. The oligonucleotide is an antisense
CC oligonucleotide inhibiting the production of transforming growth factor
CC (TGF)-beta 1, TGF-beta 2, TGF-beta 3, cell-cell adhesion molecules
CC (CAMs), integrins, selectins, metalloproteases (MMPs), their tissue
CC inhibitors (TIMPs) and/or interleukins 10. The oligonucleotides are
CC useful for the preparation of a pharmaceutical composition for inhibiting
CC the formation of metastases in cancer treatment. The oligonucleotides are
CC useful for treating cancer, e.g. bile duct carcinoma, bladder carcinoma,
CC brain tumor, breast cancer, bronchogenic carcinoma, carcinoma of the
CC kidney, cervical cancer, choriocarcinoma, cystadenocarcinoma, cervical
CC carcinoma, colon carcinoma, colorectal carcinoma, embryonal carcinoma,
CC endometrial cancer, epithelial carcinoma, esophageal cancer, gall bladder
CC cancer, gastric cancer, head and neck cancer, hepatocellular cancer,
CC liver carcinoma, lung carcinoma, medullary carcinoma, non-small cell
CC bronchogenic/lung carcinoma, ovarian cancer, pancreas carcinoma, papillary
CC papillary carcinoma, papillary adenocarcinoma, prostate cancer, small
CC intestine carcinoma, rectal cancer, renal cell carcinoma, sebaceous gland
CC carcinoma, skin cancer, soft tissue cancer, squamous cell carcinoma,
CC testicular carcinoma, uterine cancer, acoustic neuromas, neurofibromas,
CC trachomas, and pyogenic granulomas; pre-malignant tumors, blastoma,
CC Bx/mg's tumor, craniopharyngioma, ependyoma, medulloblastoma,
CC hemangioblastoma, medulloblastoma, melanoma, mesothelioma, neuroblastoma,
CC neuroblastoma, pinealoma, retinoblastoma, sarcoma, seminoma, teratoma,
CC Wilms tumor and/or myeloma, multiple. The present sequence is an
XX antisense oligonucleotide targeting human TGF-beta-3.

SO Sequence 18 BP; 2 A; 10 C; 1 G; 5 T; 0 U; 0 Other;
Query Match 0.88; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 240 CCTCTCCCAAAATCTC 257
DB 1 CCTCTCCCAATGATCTC 18
RESULT 296
ID AEC51657 standard; DNA; 18 BP.
XX
AC AEC51657;
XX
DT 17-NOV-2005 (first entry)
XX
DE Antisense oligonucleotide targeting human TGF-beta-3 #55.
XX
KM Transforming growth factor beta; TGF-beta-3; antisense therapy;
KM antisense oligonucleotide; ss; cancer; cytostatic.
XX
OS Homo sapiens.
PN WO2005084712-A2.
PD 15-SEP-2005.
PF 28-FEB-2005; 2005WO-EP002101.
XX
PR 27-FEB-2004; 2004EP-00004478.
PR 01-APR-2004; 2004US-0558135P.
XX
PA (ANTI-) ANTISENSE PHARMA GMBH.
XX
PI Schlingensiepen K, Schlingensiepen R, Jachinczak P, Stauder G;
PI Bischof A, Hatner M, Egger T;
DR WPI; 2005-630685/64.
XX
XX New antisense oligonucleotides inhibiting the synthesis of proteins
PT involved in the formation of metastases such as transforming growth
PT factor-beta 1 (TGF-beta 1), TGF-beta 2 and TGF-beta 3, useful for
PT treating cancer.
XX
XX Claim 4; Page 70; 106pp; English.
XX
XX The invention relates to an antisense oligonucleotide or its active
CC derivative selected from AEC46374-AEC46395, targeting human interleukin-
CC 10 (IL-10). Also included are a process of manufacturing the antisense
CC oligonucleotide (or its active derivative, by adding consecutive
CC nucleosides and linker stepwise or by cutting the oligonucleotide out of
CC longer oligonucleotide chain), a pharmaceutical composition comprising a
CC composition for treating cancer. The oligonucleotide is an antisense
CC oligonucleotide inhibiting the synthesis of proteins involved in the
CC formation of metastases. The oligonucleotide is an antisense
CC oligonucleotide inhibiting the production of transforming growth factor
CC (TGF)-beta 1, TGF-beta 2, TGF-beta 3, cell-cell adhesion molecules
CC (CAMs), integrins, selectins, metalloproteases (MMPs), their tissue
CC inhibitors (TIMPs) and/or interleukins 10. The oligonucleotides are
CC useful for the preparation of a pharmaceutical composition for inhibiting
CC the formation of metastases in cancer treatment. The oligonucleotides are
CC useful for treating cancer, e.g. bile duct carcinoma, bladder carcinoma,
CC brain tumor, breast cancer, bronchogenic carcinoma, carcinoma of the
CC kidney, cervical cancer, choriocarcinoma, cystadenocarcinoma, cervical
CC carcinoma, colon carcinoma, colorectal carcinoma, embryonal carcinoma,
CC endometrial cancer, epithelial carcinoma, esophageal cancer, gall bladder
CC cancer, gastric cancer, head and neck cancer, hepatocellular cancer,
CC liver carcinoma, lung carcinoma, medullary carcinoma, non-small cell
CC bronchogenic/lung carcinoma, ovarian cancer, pancreas carcinoma,

CC papillary carcinoma, papillary adenocarcinoma, prostate cancer, small
CC intestine carcinoma, rectal cancer, renal cell carcinoma, sebaceous gland
CC carcinoma, skin cancer, soft tissue cancer, squamous cell carcinoma,
CC testicular carcinoma, uterine cancer, acoustic neuromas, neurofibromas,
CC trachomas, and pyogenic granulomas; pre-malignant tumors, blastoma,
CC Ewing's tumor, craniopharyngioma, ependyoma, medulloblastoma,
CC hemangioblastoma, medulloblastoma, melanoma, mesothelioma, neuroblastoma,
CC neurofibroma, pinealoma, retinoblastoma, sarcoma, seminoma, trachomas,
CC Wilms tumor and/or myeloma, multiple. The present sequence is an
CC antisense oligonucleotide targeting human TGF-beta-3.
XX
SQ Sequence 18 BP; 3 A; 4 C; 9 G; 2 T; 0 U; 0 Other;
Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Gy 15 GCGGCGACGCGCGCAGTG 32
Db 1 GCGGCGACTCAGCGCAGTG 18
RESULT 297
AEC52974
ID AEC52974 standard; DNA; 18 BP.
XX
AC AEC52974;
XX
DT 17-NOV-2005 (first entry)
XX
XX Antisense oligonucleotide targeting human TGF-beta-3 #1372.
XX
DE Transforming growth factor beta; TGF-beta-3; antisense therapy;
KW antisense oligonucleotide; ss; cancer; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2005084712-A2.
XX
PD 15-SEP-2005.
XX
PF 28-FEB-2005; 2005WO-BP002101.
XX
PR 27-FEB-2004; 2004BP-00004478.
PR 01-APR-2004; 2004US-0558135P.
XX
XX (ANTI-) ANTISENSE PHARMA GMBH.
PA Schlingensiepen K, Schlingensiepen R, Jachimczak P, Stauder G;
PI Bischof A, Halner M, Egger T;
XX
XX WPI; 2005-630685/64.
XX
DR New antisense oligonucleotides inhibiting the synthesis of proteins
XX involved in the formation of metastases such as transforming growth
XX factor-beta 1 (TGF-beta 1), TGF-beta 2 and TGF-beta 3, useful for
XX treating cancer.
XX
XX
XX Claim 4; Page 73; 106pp; English.
XX
XX The invention relates to an antisense oligonucleotide or its active
XX derivative selected from AEC46374-AEC46395, targeting human interleukin-
XX 10 (IL-10). Also included are a process of manufacturing the antisense
XX oligonucleotide (or its active derivative, by adding consecutive
XX nucleosides and linker stepwise or by cutting the oligonucleotide out of
XX longer oligonucleotide chain), a pharmaceutical composition comprising a
XX the antisense oligonucleotide and a TGF-beta 2 antagonist for preparing a
XX composition for treating cancer. The oligonucleotide is an antisense
XX oligonucleotide inhibiting the synthesis of proteins involved in the
XX formation of metastases. The oligonucleotide is an antisense
XX oligonucleotide inhibiting the production of transforming growth factor
XX (TGF)-beta 1, TGF-beta 2, TGF-beta 3, cell-cell adhesion molecules
XX (CAMs), integrins, selectins, metalloproteinases (MMPs), their tissue

CC inhibitors (TIMPs) and/or interleukins 10. The oligonucleotides are
CC useful for the preparation of a pharmaceutical composition for inhibiting
CC the formation of metastases in cancer treatment. The oligonucleotides are
CC useful for treating cancer, e.g. bile duct carcinoma, bladder carcinoma,
CC brain tumor, breast cancer, bronchogenic carcinoma, carcinoma of the
CC kidney, cervical cancer, choriocarcinoma, cystadenocarcinoma, cervical
CC carcinoma, colon carcinoma, colorectal carcinoma, embryonal carcinoma,
CC endometrial cancer, epithelial carcinoma, esophageal cancer, gall bladder
CC cancer, gastric cancer, head and neck cancer, hepatocellular cancer,
CC liver carcinoma, lung carcinoma, ovarian cancer, pancreas carcinoma,
CC bronchogenic/lung carcinoma, papillary adenocarcinoma, prostate cancer, small
CC intestine carcinoma, rectal cancer, renal cell carcinoma, sebaceous gland
CC carcinoma, skin cancer, soft tissue cancer, squamous cell carcinoma,
CC testicular carcinoma, uterine cancer, acoustic neuromas, neurofibromas,
CC trachomas, and pyogenic granulomas; pre-malignant tumors, blastoma,
CC Ewing's tumor, craniopharyngioma, ependyoma, medulloblastoma,
CC hemangioblastoma, medulloblastoma, melanoma, mesothelioma, neuroblastoma,
CC neurofibroma, pinealoma, retinoblastoma, sarcoma, seminoma, trachomas,
CC Wilms tumor and/or myeloma, multiple. The present sequence is an
CC antisense oligonucleotide targeting human TGF-beta-3.
XX
SQ Sequence 18 BP; 2 A; 10 C; 1 G; 5 T; 0 U; 0 Other;
Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Gy 241 CTCTCCCAACATCTCC 258
Db 1 CTCTCCCAATGATCTCC 18
RESULT 298
AEC27781/C
ID AEC27781 standard; DNA; 18 BP.
XX
AC AEC27781;
XX
DT 17-NOV-2005 (first entry)
XX
XX Human allele-specific oligonucleotide #3801.
XX
XX
XX Haplotype mapping; genetic marker; single nucleotide polymorphism; SNP;
XX major histocompatibility complex; MHC; HLA; human leukocyte antigen;
XX immune disorder; inflammation; inflammatory bowel disease;
XX ulcerative colitis; Crohns disease; rheumatoid arthritis; diabetes;
XX diabetes mellitus; myasthenia gravis; vitiligo; Graves disease;
XX Hashimoto's disease; Addison's disease; scleroderma; polymyositis;
XX rheumatism; systemic lupus erythematosus; scleroderma; polymyositis;
XX dermatomyositis; pernicious anemia; primary biliary cirrhosis;
XX idiopathic thrombocytopenia purpura; Sjogrens syndrome;
XX multiple sclerosis; Reiter's syndrome; psoriasis; anti-inflammatory;
XX gastrointestinal-gen.; antitumor; immunomodulator; immunosuppressive;
XX antiarthritic; antirheumatic; antidiabetic; muscular-gen.;
XX neuroprotective; dermatological; antihypertensive; hepatotropic; antianemic;
XX hemostatic; ophthalmological; uropathic; antiporiatic; ss;
XX SNP detection.
XX
XX
XX Homo sapiens.
XX
XX WO2005082110-A2.
XX
XX 09-SEP-2005.
XX
XX 28-FEB-2005; 2005WO-US006628.
XX
XX 26-FEB-2004; 2004US-0547823P.
XX
XX (ILDU-) ILUMINA INC.
XX
XX Oliphant A, Murray S;
XX

DR WPI; 2005-638856/65.

PT Identifying single nucleotide polymorphism (SNP) haplotype that
PT correlates with the HLA type, useful for diagnosing an immunological or
PT inflammatory condition, comprises providing SNPs in the major
PT histocompatibility complex region.

XX
XX
PS Example 1; SEQ ID NO 3801; 175bp; English.

CC The invention relates to a method of identifying the nucleotide for each
CC of a set of single nucleotide polymorphisms (SNPs) in the major
CC histocompatibility complex (MHC) region in a population of individuals,
CC comprising providing the HLA type for the individuals and identifying an
CC SNP haplotype in the population that correlates with the HLA type, where
CC the SNP haplotype comprises the SNPs in the MHC region. The invention
CC also relates to a method of predicting the HLA type of an individual, a
CC method of determining the presence or absence of an allelic variant of an
CC MHC gene in an individual, a method of identifying an SNP haplotype that
CC correlates with susceptibility to a disease or condition, and a method of
CC determining the susceptibility of an individual to a disease or
CC condition. The disease or condition is an immune disorder or inflammatory
CC condition selected from inflammatory bowel disease, ulcerative colitis,
CC Crohn's disease, rheumatoid arthritis, diabetes, diabetes mellitus,
CC myasthenia gravis, vitiligo, Graves disease, Hashimoto's disease, systemic
CC Addison's disease, gastritis, autoimmune hepatitis, rheumatism, systemic
CC lupus erythematosus, systemic sclerosis, polymyositis, dermatomyositis,
CC pernicious anemia, primary biliary cirrhosis, idiopathic thrombocytopenia
CC purpura, Sjogren's syndrome, multiple sclerosis, Reiter's syndrome and
CC psoriasis. This sequence represents a human allele-specific
CC oligonucleotide used in the scope of the invention.

XX
SQ Sequence 18 BP; 3 A; 9 C; 4 G; 2 T; 0 U; 0 Other;

CC Query Match 0.8%; Score 14.8; DB 1; Length 18;
CC Best Local Similarity 88.9%; Pred.No. 2.3e+02;
CC Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1292 TGGTGGGGGCCCCAGAG 1309
DB 18 TGGTGGAGGCGCTCGAG 1
|||||
|||||

RESULT 299
ABK12174
ID ABK12174 standard; DNA; 15 BP.
XX
AC ABK12174;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human Tachykinin Receptor 1 allele specific oligonucleotide probe #4.
XX
XX Human; 88; probe; TACR1; Tachykinin receptor 1; chromosome 2; SNP;
KM single nucleotide polymorphism; gene therapy; haplotype; genotype; pain;
KM depression; vomiting; acute inflammatory diarrhoea; ASO;
KM opiate addiction; drug screening; allele specific oligonucleotide.
XX
OS Homo sapiens.
XX
PN WO200216399-A2.
XX
PD 28-FEB-2002.
XX
PF 27-AUG-2001; 2001WO-US026663.
XX
PR 25-AUG-2000; 2000US-0227815P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
XX Anaestasio AE, Kazemi A;
XX
DR WPI; 2002-280907/32.

PT Novel isolated polynucleotide which is a polymorphic variant of
PT tachykinin receptor 1 (TACR1) gene useful for expressing TACR1 protein
PT isoform used in screening drug candidates to treat pain, depression,
PT vomiting.

XX
XX
PS Claim 17; Page 14; 89pp; English.

CC The invention relates to an isolated polynucleotide sequence which
CC comprises a tachykinin receptor 1 (TACR1) isogene (SG) that is any one of
CC 16 SG as given in specification, where each SG comprises specific regions
CC of the TACR1 genomic DNA appearing as ABK12169, and is defined by
CC polymorphisms at positions (p) 3164, 3319, 3906, 4339, 4444, 92915,
CC 94601, 94821, 94892, 94960. Also included are fragments of the TACR1
CC isogenes and TACR1 cDNA, a transgenic non-human animal transformed with
CC the TACR1 isogene or coding region, haplotyping (or genotyping) the TACR1
CC of an individual by determining either the haplotype of one or both
CC copies of the TACR1 gene, predicting the haplotype pair for the TACR1
CC gene of an individual, identifying an association between a trait and a
CC haplotype pair, an isolated oligonucleotide for detecting the
CC polymorphisms, a computer system for storing and analysing polymorphism
CC data and a genome anthology for TACR1 gene. The TACR1 isogene is useful
CC for studying expression and function of TACR1 and expressing TACR1
CC protein for use in screening for candidate drugs to treat diseases
CC related to TACR1 activity. The polymorphism and haplotype data is useful
CC for validating whether TACR1 is a suitable target for drugs to treat
CC pain, depression, vomiting, acute inflammatory diarrhoea and opiate
CC addiction. Screening for such drugs and reducing bias in clinical trials
CC of such drugs. The genotyping method is useful for determining whether an
CC individual has one of the haplotype pairs. The haplotyping method is
CC useful for improving efficiency and outcome of several steps in discovery
CC and development of drugs for treating the diseases. The haplotyping
CC method is also useful for validating TACR1 as a candidate target for
CC treating a specific condition or disease predicted to be associated with
CC TACR1 activity. The method is also useful for screening compounds to
CC treat a specific condition or disease predicted to be associated with
CC TACR1 activity. The methods are useful for identifying an association
CC between susceptibility to a disease, straging of a disease, or response to
CC a drug. The gene for TACR1 is located on human chromosome 2. The present
CC sequence is an allele specific oligonucleotide (ASO) probe used to detect
CC polymorphisms in the TACR1 gene

XX
SQ Sequence 15 BP; 2 A; 6 C; 1 G; 5 T; 0 U; 1 Other;

CC Query Match 0.8%; Score 14.6; DB 1; Length 15;
CC Best Local Similarity 93.3%; Pred.No. 1.5e+02;
CC Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 536 ACTCTTCCCATCG 550
DB 1 ACTCTTCCCATCG 15
|||||
|||||

RESULT 300
ABK12178
ID ABK12178 standard; DNA; 15 BP.
XX
AC ABK12178;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human Tachykinin Receptor 1 allele specific oligonucleotide probe #8.
XX
XX Human; 88; probe; TACR1; Tachykinin receptor 1; chromosome 2; SNP;
KM single nucleotide polymorphism; gene therapy; haplotype; genotype; pain;
KM depression; vomiting; acute inflammatory diarrhoea; ASO;
KM opiate addiction; drug screening; allele specific oligonucleotide.
XX
OS Homo sapiens.
XX
XX WO200216399-A2.
XX
PN 28-FEB-2002.
XX
PD

PF 27-AUG-2001; 2001WO-US026663.
 XX 25-AUG-2000; 2000US-0227815P.
 XX (GENA-) GENNAISSANCE PHARM INC.
 PA Anastasio AE, Kazemi A;
 XX WPI; 2002-280907/32.
 DR
 XX Novel isolated polynucleotide which is a polymorphic variant of
 PT tachykinin receptor 1 (TACR1) gene useful for expressing TACR1 protein
 PT isoform used in screening drug candidates to treat pain, depression,
 PT vomiting.
 XX
 XX Claim 17; Page 14; 89pp; English.
 PS
 XX The invention relates to an isolated polynucleotide sequence which
 CC comprises a tachykinin receptor 1 (TACR1) isogene (SG) that is any one of
 CC 16 SG as given in specification, where each SG comprises specific regions
 CC of the TACR1 genomic DNA appearing as ABK12169, and is defined by
 CC polymorphisms at positions (p) 3164, 3319, 3906, 4339, 4444, 92915,
 CC 94501, 94821, 94892, 94960. Also included are fragments of the TACR1
 CC isogenes and TACR1 cDNA, a transgenic non-human animal transformed with
 CC the TACR1 isogene or coding region, haplotyping (or genotyping) the TACR1
 CC of an individual by determining either the haplotype of one or both
 CC copies of the TACR1 gene, predicting an association between a trait and a
 CC gene of an individual, identifying an association between a trait and a
 CC haplotype pair, an isolated oligonucleotide for detecting the
 CC polymorphisms, a computer system for storing and analysing polymorphism
 CC data and a genome anthology for TACR1 gene. The TACR1 isogene is useful
 CC for studying expression and function of TACR1 and expressing TACR1
 CC protein for use in screening for candidate drugs to treat diseases
 CC related to TACR1 activity. The polymorphism and haplotype data is useful
 CC for validating whether TACR1 is a suitable target for drugs to treat
 CC pain, depression, vomiting, acute inflammatory diarrhoea and opiate
 CC addiction, screening for such drugs and reducing bias in clinical trials
 CC of such drugs. The genotyping method is useful for determining whether an
 CC individual has one of the haplotype pairs. The haplotyping method is
 CC useful for improving efficiency and outcome of several steps in discovery
 CC and development of drugs for treating the diseases. The haplotyping
 CC method is also useful for validating TACR1 as a candidate target for
 CC treating a specific condition or disease predicted to be associated with
 CC TACR1 activity. The method is also useful for screening compounds to
 CC treat a specific condition or disease predicted to be associated with
 CC TACR1 activity. The methods are useful for identifying an association
 CC between susceptibility to a disease, staging of a disease, or response to
 CC a drug. The gene for TACR1 is located on human chromosome 2. The present
 CC sequence is an allele specific oligonucleotide (ASO) probe used to detect
 CC polymorphisms in the TACR1 gene
 CC
 XX
 SQ Sequence 15 BP; 3 A; 3 C; 3 G; 5 T; 0 U; 1 Other;
 Query Match 0.8%; Score 14.6; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 1.5e+02;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1628 ATGCTGTGACTCA 1642
 DB 1 ATGCTGTGACTCA 15
 XX
 RESULT 301
 ABK12184
 ID ABK12184 standard; DNA; 15 BP.
 XX
 XX ABK12184;
 AC
 XX 18-JUN-2002 (first entry)
 DT
 XX Human Tachykinin Receptor 1 allele specific oligonucleotide primer #5.
 DE Human; ss; primer; TACR1; Tachykinin receptor 1; chromosome 2; PCR; SNP;
 KW

KW single nucleotide polymorphism; gene therapy; haplotype; genotype; pain;
 KW depression; vomiting; acute inflammatory diarrhoea; ASO;
 KW opiate addiction; drug screening; allele specific oligonucleotide.
 XX
 OS Homo sapiens.
 XX WO200216399-A2.
 PN
 XX 28-FEB-2002.
 PD
 XX 27-AUG-2001; 2001WO-US026663.
 PF 25-AUG-2000; 2000US-0227815P.
 XX (GENA-) GENNAISSANCE PHARM INC.
 PA Anastasio AE, Kazemi A;
 XX WPI; 2002-280907/32.
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 XX Novel isolated polynucleotide which is a polymorphic variant of
 PT tachykinin receptor 1 (TACR1) gene useful for expressing TACR1 protein
 PT isoform used in screening drug candidates to treat pain, depression,
 PT vomiting.
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 XX Claim 17; Page 14; 89pp; English.
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 CC polymorphisms at positions (p) 3164, 3319, 3906, 4339, 4444, 92915,
 CC 94501, 94821, 94892, 94960. Also included are fragments of the TACR1
 CC isogenes and TACR1 cDNA, a transgenic non-human animal transformed with
 CC the TACR1 isogene or coding region, haplotyping (or genotyping) the TACR1
 CC of an individual by determining either the haplotype of one or both
 CC copies of the TACR1 gene, predicting an association between a trait and a
 CC gene of an individual, identifying an association between a trait and a
 CC haplotype pair, an isolated oligonucleotide for detecting the
 CC polymorphisms, a computer system for storing and analysing polymorphism
 CC data and a genome anthology for TACR1 gene. The TACR1 isogene is useful
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 CC protein for use in screening for candidate drugs to treat diseases
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 CC pain, depression, vomiting, acute inflammatory diarrhoea and opiate
 CC addiction, screening for such drugs and reducing bias in clinical trials
 CC of such drugs. The genotyping method is useful for determining whether an
 CC individual has one of the haplotype pairs. The haplotyping method is
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 CC and development of drugs for treating the diseases. The haplotyping
 CC method is also useful for validating TACR1 as a candidate target for
 CC treating a specific condition or disease predicted to be associated with
 CC TACR1 activity. The method is also useful for screening compounds to
 CC treat a specific condition or disease predicted to be associated with
 CC TACR1 activity. The methods are useful for identifying an association
 CC between susceptibility to a disease, staging of a disease, or response to
 CC a drug. The gene for TACR1 is located on human chromosome 2. The present
 CC sequence is an allele specific oligonucleotide (ASO) PCR primer used to
 CC detect polymorphisms in the TACR1 gene
 CC
 XX
 SQ Sequence 15 BP; 1 A; 8 C; 1 G; 4 T; 0 U; 1 Other;
 Query Match 0.8%; Score 14.6; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 1.5e+02;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 100 TTCCACCCCTCTGTC 114
 DB 1 TTCCACCCCTCTGTC 15
 XX
 RESULT 302

ABK12192
ID ABK12192 standard; DNA; 15 BP.
XX
AC ABK12192;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human Tachykinin Receptor 1 ASO primer #13.
XX
KW Human; 89; primer; TACR1; Tachykinin receptor 1; chromosome 2; PCR; SNP;
KM single nucleotide polymorphism; gene therapy; haplotype; genotype; pain;
KW depression; vomiting; acute inflammatory diarrhoea; ASO;
XX opiate addiction; drug screening; allele specific oligonucleotide.
OS Homo sapiens.
XX
PN WO200216399-A2.
XX
PD 28-FEB-2002.
XX
PF 27-AUG-2001; 2001WO-US026663.
XX
PR 25-AUG-2000; 2000US-0227815P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Anastasio AE, Kazemi A;
XX
XX WPI; 2002-280907/32.
XX
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PT tachykinin receptor 1 (TACR1) gene useful for expressing TACR1 protein
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PT vomiting.
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CC polymorphisms at positions (P) 3164, 3319, 3906, 4339, 4444, 92915,
CC 94601, 94821, 94892, 94960. Also included are fragments of the TACR1
CC isogenes and TACR1 cDNA, a transgenic non-human animal transformed with
CC the TACR1 isogene or coding region, haplotyping (or genotyping) the TACR1
CC of an individual by determining either the haplotype of one or both
CC copies of the TACR1 gene, predicting an association between a trait and a
CC haplotype pair, an isolated oligonucleotide for detecting the
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CC TACR1 activity. The method is also useful for screening compounds to
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CC TACR1 activity. The method are useful for identifying an association
CC between susceptibility to a disease, staging of a disease, or response to
CC a drug. The gene for TACR1 is located on human chromosome 2. The present
CC sequence is an allele specific oligonucleotide (ASO) PCR primer used to
CC detect polymorphisms in the TACR1 gene
XX
XX Sequence 15 BP; 3 A; 7 C; 2 G; 2 T; 0 U; 1 Other; '

Query Match 0.8%; Score 14.6; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.5e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1331 AGGCCACACCTCTCGT 1345
DB 1 AGGCCACACCTCTCCT 15
RESULT 303
ABK12193/c
ID ABK12193 standard; DNA; 15 BP.
XX
AC ABK12193;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human Tachykinin Receptor 1 ASO primer #14.
XX
KW Human; 89; primer; TACR1; Tachykinin receptor 1; chromosome 2; PCR; SNP;
KM single nucleotide polymorphism; gene therapy; haplotype; genotype; pain;
KW depression; vomiting; acute inflammatory diarrhoea; ASO;
XX opiate addiction; drug screening; allele specific oligonucleotide.
OS Homo sapiens.
XX
XX WO200216399-A2.
XX
PD 28-FEB-2002.
XX
PF 27-AUG-2001; 2001WO-US026663.
XX
PR 25-AUG-2000; 2000US-0227815P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
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PI Anastasio AE, Kazemi A;
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XX WPI; 2002-280907/32.
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CC 94601, 94821, 94892, 94960. Also included are fragments of the TACR1
CC isogenes and TACR1 cDNA, a transgenic non-human animal transformed with
CC the TACR1 isogene or coding region, haplotyping (or genotyping) the TACR1
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CC copies of the TACR1 gene, predicting an association between a trait and a
CC haplotype pair, an isolated oligonucleotide for detecting the
CC polymorphisms, a computer system for storing and analysing polymorphism
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CC treat a specific condition or disease predicted to be associated with
CC TACR1 activity. The methods are useful for identifying an association
CC between susceptibility to a disease, staging of a disease, or response to
CC a drug. The gene for TACR1 is located on human chromosome 2. The present
CC sequence is an allele specific oligonucleotide (ASO) PCR primer used to
CC detect polymorphisms in the TACR1 gene
XX
SQ Sequence 15 BP; 3 A; 3 C; 6 G; 2 T; 0 U; 1 Other;
Query Match 0.8%; Score 14.6; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.5e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1343 CGTCCCTGACCTGA 1357
15 CRTCCCTGACCTGA 1
Db
RESULT 304
ABK12194
ID ABK12194 standard; DNA; 15 BP.
XX
AC ABK12194;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human Tachykinin Receptor 1 ASO primer #15.
XX
XX Human; ss; primer; TACR1; Tachykinin receptor 1; chromosome 2; PCR; SNP;
KW single nucleotide polymorphism; gene therapy; haplotype; genotype; pain;
KW depression; vomiting; acute inflammatory diarrhoea; ASO;
KW opiate addiction; drug screening; allele specific oligonucleotide.
XX
XX Homo sapiens.
XX
XX WO200216399-A2.
XX
XX 28-FEB-2002.
XX
PF 27-AUG-2001; 2001WO-US026663.
XX
PR 25-AUG-2000; 2000US-0227815P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
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PI Anastasio AE, Kazemi A;
XX
DR WPI; 2002-280907/32.
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PT isoform used in screening drug candidates to treat pain, depression,
PT vomiting.
XX
XX Claim 17, Page 14; 89pp; English.
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CC of the TACR1 genomic DNA appearing as ABK12169, and is defined by
CC polymorphisms at positions (P) 3164, 3319, 3906, 4339, 4444, 92915,
CC 94601, 94821, 94892, 94960. Also included are fragments of the TACR1
CC isogenes and TACR1 cDNA, a transgenic non-human animal transformed with
CC the TACR1 isogene or coding region, haplotyping (or genotyping) the TACR1
CC of an individual by determining either the haplotype of one or both
CC copies of the TACR1 gene, predicting an association between a trait and a
CC haplotype pair, identifying an association between a trait and a
CC polymorphisms, a computer system for storing and analysing polymorphism
CC data and a genome anthology for TACR1 gene. The TACR1 isogene is useful
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CC related to TACR1 activity. The polymorphism and haplotype data is useful
CC for validating whether TACR1 is a suitable target for drugs to treat
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CC of such drugs. The genotyping method is useful for determining whether an
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CC TACR1 activity. The methods are useful for identifying an association
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CC a drug. The gene for TACR1 is located on human chromosome 2. The present
CC sequence is an allele specific oligonucleotide (ASO) PCR primer used to
CC detect polymorphisms in the TACR1 gene
XX
SQ Sequence 15 BP; 2 A; 5 C; 2 G; 5 T; 0 U; 1 Other;
Query Match 0.8%; Score 14.6; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.5e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1622 ACCCTCATGCTGTGT 1636
1 ACCCTCATGCTGT 15
Db
RESULT 305
ABK12195/c
ID ABK12195 standard; DNA; 15 BP.
XX
AC ABK12195;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human Tachykinin Receptor 1 ASO primer #15.
XX
XX Human; ss; primer; TACR1; Tachykinin receptor 1; chromosome 2; PCR; SNP;
KW single nucleotide polymorphism; gene therapy; haplotype; genotype; pain;
KW depression; vomiting; acute inflammatory diarrhoea; ASO;
KW opiate addiction; drug screening; allele specific oligonucleotide.
XX
XX Homo sapiens.
XX
XX WO200216399-A2.
XX
XX 28-FEB-2002.
XX
PF 27-AUG-2001; 2001WO-US026663.
XX
PR 25-AUG-2000; 2000US-0227815P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Anastasio AE, Kazemi A;
XX
DR WPI; 2002-280907/32.
XX
XX Novel isolated polynucleotide which is a polymorphic variant of
PT tachykinin receptor 1 (TACR1) gene useful for expressing TACR1 protein
PT isoform used in screening drug candidates to treat pain, depression,
PT vomiting.
XX
XX Claim 17, Page 14; 89pp; English.
XX
XX The invention relates to an isolated polynucleotide sequence which
CC comprises a tachykinin receptor 1 (TACR1) isogene (SG) that is any one of
CC 16 SG as given in specification, where each SG comprises specific regions
CC of the TACR1 genomic DNA appearing as ABK12169, and is defined by
CC polymorphisms at positions (P) 3164, 3319, 3906, 4339, 4444, 92915,
CC 94601, 94821, 94892, 94960. Also included are fragments of the TACR1

isogenes and TACR1 cDNA, a transgenic non-human animal transformed with the TACR1 isogene or coding region, haplotyping (or genotyping) the TACR1 of an individual by determining either the haplotype of one or both copies of the TACR1 gene, predicting the haplotype pair for the TACR1 gene of an individual, identifying an association between a trait and a haplotype pair, an isolated oligonucleotide for detecting the polymorphisms, a computer system for storing and analysing polymorphism data and a genome anthology for TACR1 gene. The TACR1 isogene is useful for studying expression and function of TACR1 and expressing TACR1 protein for use in screening for candidate drugs to treat diseases related to TACR1 activity. The polymorphism and haplotype data is useful for validating whether TACR1 is a suitable target for drugs to treat pain, depression, vomiting, acute inflammatory diarrhoea and opiate addiction, screening for such drugs and reducing bias in clinical trials of such drugs. The genotyping method is useful for determining whether an individual has one of the haplotype pairs. The haplotyping method is useful for improving efficiency and outcome of several steps in discovery and development of drugs for treating the diseases. The haplotyping method is also useful for validating TACR1 as a candidate target for treating a specific condition or disease predicted to be associated with TACR1 activity. The method is also useful for screening compounds to treat a specific condition or disease predicted to be associated with TACR1 activity. The methods are useful for identifying an association between susceptibility to a disease, staging of a disease, or response to a drug. The gene for TACR1 is located on human chromosome 2. The present sequence is an allele specific oligonucleotide (ASO) PCR primer used to detect polymorphisms in the TACR1 gene

Sequence 15 BP; 3 A; 1 C; 4 G; 6 T; 0 U; 1 Other;

Query Match Best Local Similarity 93.3%; Score 14.6; DB 1; Length 15; Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1634 TGTGACTCAACCAA 1648
|:|||||
15 TKTGACTCAACCAA 1

RESULT 306
ABK12187/c
ID ABK12187 standard; DNA; 15 BP.
XX
AC ABK12187;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human Tachykinin Receptor 1 allele specific oligonucleotide primer #8.
XX
KW Human; ss; primer; TACR1; Tachykinin receptor 1; chromosome 2; PCR; SNP; single nucleotide polymorphism; gene therapy; haplotype; genotype; pain; depression; vomiting; acute inflammatory diarrhoea; ASO;
KM opiate addiction; drug screening; allele specific oligonucleotide.
XX
OS Homo sapiens.
XX
PN W0200216399-A2.
XX
PD 28-FEB-2002.
XX
PF 27-AUG-2001; 2001WO-US026663.
XX
PR 25-AUG-2000; 2000US-0227815P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Anaestasio AB, Kazemi A;
XX
DR WPI; 2002-280907/32.
XX
PT Novel isolated polynucleotide which is a polymorphic variant of tachykinin receptor 1 (TACR1) gene useful for expressing TACR1 protein isoform used in screening drug candidates to treat pain, depression,

vomiting.

Claim 17, Page 14; 89pp; English.

The invention relates to an isolated polynucleotide sequence which comprises a tachykinin receptor 1 (TACR1) isogene (SG) that is any one of 16 SG as given in specification, where each SG comprises specific regions of the TACR1 genomic DNA appearing as ABK12169, and is defined by polymorphisms at positions (p) 3164, 3319, 3906, 4339, 4444, 92915, 94601, 94821, 94892, 94960. Also included are fragments of the TACR1 isogenes and TACR1 cDNA, a transgenic non-human animal transformed with the TACR1 isogene or coding region, haplotyping (or genotyping) the TACR1 of an individual by determining either the haplotype of one or both copies of the TACR1 gene, predicting the haplotype pair for the TACR1 gene of an individual, identifying an association between a trait and a haplotype pair, an isolated oligonucleotide for detecting the polymorphisms, a computer system for storing and analysing polymorphism data and a genome anthology for TACR1 gene. The TACR1 isogene is useful for studying expression and function of TACR1 and expressing TACR1 protein for use in screening for candidate drugs to treat diseases related to TACR1 activity. The polymorphism and haplotype data is useful for validating whether TACR1 is a suitable target for drugs to treat pain, depression, vomiting, acute inflammatory diarrhoea and opiate addiction, screening for such drugs and reducing bias in clinical trials of such drugs. The genotyping method is useful for determining whether an individual has one of the haplotype pairs. The haplotyping method is useful for improving efficiency and outcome of several steps in discovery and development of drugs for treating the diseases. The haplotyping method is also useful for validating TACR1 as a candidate target for treating a specific condition or disease predicted to be associated with TACR1 activity. The method is also useful for screening compounds to treat a specific condition or disease predicted to be associated with TACR1 activity. The methods are useful for identifying an association between susceptibility to a disease, staging of a disease, or response to a drug. The gene for TACR1 is located on human chromosome 2. The present sequence is an allele specific oligonucleotide (ASO) PCR primer used to detect polymorphisms in the TACR1 gene

Sequence 15 BP; 3 A; 3 C; 7 G; 1 T; 0 U; 1 Other;

Query Match Best Local Similarity 93.3%; Score 14.6; DB 1; Length 15; Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

542 TTCCCATGCCGCTG 556
|:|||||
15 TYCCCATGCCGCTG 1

RESULT 307
ABK12177
ID ABK12177 standard; DNA; 15 BP.
XX
AC ABK12177;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human Tachykinin Receptor 1 allele specific oligonucleotide probe #7.
XX
KW Human; ss; probe; TACR1; Tachykinin receptor 1; chromosome 2; SNP; single nucleotide polymorphism; gene therapy; haplotype; genotype; pain; depression; vomiting; acute inflammatory diarrhoea; ASO;
KM opiate addiction; drug screening; allele specific oligonucleotide.
XX
OS Homo sapiens.
XX
PN W0200216399-A2.
XX
PD 28-FEB-2002.
XX
PF 27-AUG-2001; 2001WO-US026663.
XX
PR 25-AUG-2000; 2000US-0227815P.

XX (GENA-) GENAISSANCE PHARM INC.
 PA Anastasio AE, Kazemi A;
 PI WPI; 2002-280907/32.
 DR
 XX
 XX Novel isolated polynucleotide which is a polymorphic variant of
 PT tachykinin receptor 1 (TACR1) gene useful for expressing TACR1 protein
 PT isoform used in screening drug candidates to treat pain, depression,
 PT vomiting.
 XX
 XX Claim 17; Page 14; 89pp; English.
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 XX The invention relates to an isolated polynucleotide sequence which
 XX comprises a tachykinin receptor 1 (TACR1) isogene (SG) that is any one of
 CC 16 SG as given in specification, where each SG comprises specific regions
 CC of the TACR1 genomic DNA appearing as ABK12169, and is defined by
 CC polymorphisms at positions (p) 3164, 3319, 3906, 4339, 4444, 92915,
 CC 94601, 94821, 94892, 94960. Also included are fragments of the TACR1
 CC isogenes and TACR1 cDNA, a transgenic non-human animal transformed with
 CC the TACR1 isogene or coding region, haplotyping (or genotyping) the TACR1
 CC copies of an individual by determining either the haplotype pair for the TACR1
 CC gene of an individual, identifying an association between a trait and a
 CC haplotype pair, an isolated oligonucleotide for detecting the
 CC polymorphisms, a computer system for storing and analysing polymorphism
 CC data and a genome anthology for TACR1 gene. The TACR1 isogene is useful
 CC for studying expression and function of TACR1 and expressing TACR1
 CC protein for use in screening for candidate drugs to treat diseases
 CC related to TACR1 activity. The polymorphism and haplotype data is useful
 CC for validating whether TACR1 is a suitable target for drugs to treat
 CC pain, depression, vomiting, acute inflammatory diarrhoea and opiate
 CC addiction, screening for such drugs and reducing bias in clinical trials
 CC of such drugs. The genotyping method is useful for determining whether an
 CC individual has one of the haplotype pairs. The haplotyping method is
 CC useful for improving efficiency and outcome of several steps in discovery
 CC and development of drugs for treating the diseases. The haplotyping
 CC method is also useful for validating TACR1 as a candidate target for
 CC treating a specific condition or disease predicted to be associated with
 CC TACR1 activity. The method is also useful for screening compounds to
 CC treat a specific condition or disease predicted to be associated with
 CC TACR1 activity. The methods are useful for identifying an association
 CC between susceptibility to a disease, staging of a disease, or response to
 CC a drug. The gene for TACR1 is located on human chromosome 2. The present
 CC sequence is an allele specific oligonucleotide (ASO) probe used to detect
 CC polymorphisms in the TACR1 gene
 CC
 XX
 XX Sequence 15 BP; 1 A; 8 C; 2 G; 3 T; 0 U; 1 Other;
 SQ
 XX
 XX Query Match 0.8%; Score 14.6; DB 1; Length 15;
 XX Best Local Similarity 93.3%; Pred. No. 1.5e+02;
 XX Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1337 CACCCTGCTCCCTGG 1351
 Db 1 CACCCTGCTCCCTGG 15
 RESULT 308
 ABK12186
 ID ABK12186 standard; DNA; 15 BP.
 XX
 XX ABK12186;
 AC
 XX
 DT 18-JUN-2002 (first entry)
 XX
 XX Human Tachykinin Receptor 1 allele specific oligonucleotide primer #7.
 DB
 XX Human; ss; primer; TACR1; Tachykinin receptor 1; chromosome 2; PCR; SNP;
 KW single nucleotide polymorphism; gene therapy; haplotype; genotype; pain;
 KW depression; vomiting; acute inflammatory diarrhoea; ASO;
 KW opiate addiction; drug screening; allele specific oligonucleotide.

XX Homo sapiens.
 OS
 XX WO200216399-A2.
 XX
 XX
 XX 28-FEB-2002.
 XX
 XX
 XX 27-AUG-2001; 2001WO-US026663.
 PF
 XX 25-AUG-2000; 2000US-0227815P.
 PR
 XX (GENA-) GENAISSANCE PHARM INC.
 PA Anastasio AE, Kazemi A;
 PI WPI; 2002-280907/32.
 DR
 XX
 XX Novel isolated polynucleotide which is a polymorphic variant of
 PT tachykinin receptor 1 (TACR1) gene useful for expressing TACR1 protein
 PT isoform used in screening drug candidates to treat pain, depression,
 PT vomiting.
 XX
 XX Claim 17; Page 14; 89pp; English.
 PS
 XX The invention relates to an isolated polynucleotide sequence which
 CC comprises a tachykinin receptor 1 (TACR1) isogene (SG) that is any one of
 CC 16 SG as given in specification, where each SG comprises specific regions
 CC of the TACR1 genomic DNA appearing as ABK12169, and is defined by
 CC polymorphisms at positions (p) 3164, 3319, 3906, 4339, 4444, 92915,
 CC 94601, 94821, 94892, 94960. Also included are fragments of the TACR1
 CC isogenes and TACR1 cDNA, a transgenic non-human animal transformed with
 CC the TACR1 isogene or coding region, haplotyping (or genotyping) the TACR1
 CC copies of an individual by determining either the haplotype pair for the TACR1
 CC gene of an individual, identifying an association between a trait and a
 CC haplotype pair, an isolated oligonucleotide for detecting the
 CC polymorphisms, a computer system for storing and analysing polymorphism
 CC data and a genome anthology for TACR1 gene. The TACR1 isogene is useful
 CC for studying expression and function of TACR1 and expressing TACR1
 CC protein for use in screening for candidate drugs to treat diseases
 CC related to TACR1 activity. The polymorphism and haplotype data is useful
 CC for validating whether TACR1 is a suitable target for drugs to treat
 CC pain, depression, vomiting, acute inflammatory diarrhoea and opiate
 CC addiction, screening for such drugs and reducing bias in clinical trials
 CC of such drugs. The genotyping method is useful for determining whether an
 CC individual has one of the haplotype pairs. The haplotyping method is
 CC useful for improving efficiency and outcome of several steps in discovery
 CC and development of drugs for treating the diseases. The haplotyping
 CC method is also useful for validating TACR1 as a candidate target for
 CC treating a specific condition or disease predicted to be associated with
 CC TACR1 activity. The method is also useful for screening compounds to
 CC treat a specific condition or disease predicted to be associated with
 CC TACR1 activity. The methods are useful for identifying an association
 CC between susceptibility to a disease, staging of a disease, or response to
 CC a drug. The gene for TACR1 is located on human chromosome 2. The present
 CC sequence is an allele specific oligonucleotide (ASO) PCR primer used to
 CC detect polymorphisms in the TACR1 gene
 CC
 XX
 XX Sequence 15 BP; 3 A; 6 C; 0 G; 5 T; 0 U; 1 Other;
 SQ
 XX
 XX Query Match 0.8%; Score 14.6; DB 1; Length 15;
 XX Best Local Similarity 93.3%; Pred. No. 1.5e+02;
 XX Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 530 TCCACACTTCTTC 544
 Db 1 TCCACACTTCTTC 15
 RESULT 309
 ADU94981
 ID ADU94981 standard; RNA; 16 BP.
 XX

AC ADU94981;
XX
DT 10-FEB-2005 (first entry)
XX
XX Human TERT G-cleaver ribozyme substrate sequence #279.
DE
XX Enzymatic nucleic acid molecule; gene expression; down regulation;
KM protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;
KM MeAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
KM beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
KM C-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
KM hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
KM amberyne; zinzyne; DNazyme; cancer; breast cancer; Alzheimer's disease;
KM diabetes; obesity; cardiac disease; heart disease; age-related disease;
KM hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
KM ss.
XX
XX Homo sapiens.
XX
XX WO200116312-A2.
XX
PD 08-MAR-2001.
XX
PF 30-AUG-2000; 2000MO-US023998.
XX
XX 31-AUG-1999; 99US-0151713P.
PR 27-SEP-1999; 99US-00406643.
PR 27-SEP-1999; 99US-0156236P.
PR 27-SEP-1999; 99US-0156467P.
PR 08-NOV-1999; 99US-00436430.
PR 06-DEC-1999; 99US-0169100P.
PR 29-DEC-1999; 99US-00474432.
PR 29-DEC-1999; 99US-0173612P.
PR 30-DEC-1999; 99US-00476387.
PR 04-FEB-2000; 2000US-00498824.
PR 20-MAR-2000; 2000US-00531025.
PR 14-APR-2000; 2000US-0197769P.
PR 23-MAY-2000; 2000US-00578323.
PR 09-AUG-2000; 2000US-00635853.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Mcswiggen J, Usman N, Biact L, Belgelman L, Burghin A, Chowrira B;
PI Karpelsky A, Metulic-Adamic J, Sweedler D, Draper K, Zimin S, Sproat BS;
PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;
XX
XX WPI; 2001-244406/25.
XX
XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules
PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
PT obesity and heart disease.
XX
XX Example 1; Page 308; 717pp; English.
XX
XX The present invention relates to the use of enzymatic nucleic acid
CC molecules (e.g. ribozymes) to modulate gene expression. The invention
CC also methods for their use to down regulate or inhibit the expression of
CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine
CC aminopeptidase (MeAP-2), human telomerase (hTERT), protein kinase C
CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
CC receptor-2 (HER2/C-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
CC nucleic acid molecules used to inhibit the expression of the said genes
CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberyne,
CC zinzyne, and/or DNazyme motifs. The methods of the invention are useful
CC for treating cancer, in particular breast cancer, Alzheimer's disease,
CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related
CC diseases, hepatitis B infections, and hepatitis and hepatocellular
CC carcinoma. The enzymatic nucleic acid molecules can also be used as
CC diagnostic tools to examine genetic drift and mutations within diseased
CC cells and to detect the presence of specific RNA in a cell. The present
CC sequence represents a substrate/target sequence for a ribozyme used in
CC the examples of the present invention. Note: Some SEQ ID Nos are repeated

CC more than once in the specification, but these have different sequences
CC associated with them.
XX
XX Sequence 16 BP; 5 A; 2 C; 5 G; 0 T; 4 U; 0 Other;
SQ
Query Match 0.84; Score 14.4; DB 1; Length 16;
Best Local Similarity 68.84; Pred. No. 1.9e+02;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 464 ATACAGTGTGAACCTT 479
Db 1 AGACAGGCGGACACU 16
|||||:|||||:
|:|:|:|:|:
RESULT 310
ABK63842/c
ID ABK63842 standard; DNA; 16 BP.
XX
AC ABK63842;
XX
DT 18-JUN-2002 (first entry)
XX
XX Neurokinin 1 receptor (NK-1) antisense oligonucleotide #6.
DE
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;
KM immune disorder; autoimmune disorder; cardiovascular disorder;
KM vascular disorder; airway disorder; neuropathic disorder; pain;
KM psychiatric disorder; central nervous system disorder; inflammation;
KM respiratory condition; ophthalmic condition; intestinal condition;
KM demyelinating disease; small cell lung cancer; depression;
KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
KM neuro-pathological disorder; stress; antisense; primer; ss.
XX
XX Homo sapiens.
XX
XX WO200213799-A2.
XX
XX 21-FEB-2002.
XX
XX 17-AUG-2001; 2001MO-IB001510.
XX
XX 18-AUG-2000; 2000US-0226086P.
XX
XX (UTMC-) UNIV MCGILL.
XX
XX Henry JL, Cahill CM, Yashpal K;
PI WPI; 2002-241835/29.
XX
XX Claim 24; Page 65; 100pp; English.
PS
XX The invention relates to a method of treating a pathological condition
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)
CC receptor, especially treating, attenuating or preventing pain or
CC inflammatory condition. The method comprises administering to a mammal, a
CC compound chosen from an oligonucleotide, its analogue, and a disruptor
CC which interferes with function or production of NK-1 receptor. The
CC method is useful for treating a pathological condition characterised by
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,
CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,
CC psychiatric and central nervous system disorders (e.g. anxiety,
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or
CC peripheral aspects of chronic or acute pain, and for treating,
CC attenuating or preventing pain or inflammation such as peripheral,
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or
CC pain relating to psychiatric disorders and central nervous system
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia

PR 11-FEB-2000; 2000US-0181797P.
 PR 28-FEB-2000; 2000US-0185516P.
 PR 06-MAR-2000; 2000US-0187128P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 PI Blatt L, Mcswiggen J, Chowrira BM;
 XX
 DR WPI; 2001-607195/69.
 XX
 PT Nucleic acid molecules, e.g., enzymatic, nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX
 XX
 PS Claim 30; Page 154; 200pp; English.
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOCO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g., a ribozyme or a
 CC DNazyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NGN motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapiers. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopenia, and inflammatory arthropathy. The NOCO-
 CC targeting nucleic acid is used to cleave RNA of the NOCO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOCO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOCO. The treatment may further comprise the use of one or more
 CC therapiers. In particular, the NOCO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOCO expression. The present
 CC sequence is a zinzyme molecule of the invention
 XX
 SQ Sequence 17 BP; 3 A; 5 C; 4 G; 0 T; 5 U; 0 Other;
 XX
 Query Match 0.8%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 62.5%; Pred. No. 2.3e+02;
 Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

KW Human; ss; antisense therapy; cyrostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian; ribozyme;
 KW muscular; CD20; neurite growth inhibitor gene; NOCO; hammerhead ribozyme;
 KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 PN WO200159103-A2.
 XX
 XX 16-AUG-2001.
 PD
 XX
 PF 09-FEB-2001; 2001WO-US004273.
 XX
 PF 11-FEB-2000; 2000US-0181797P.
 XX
 PR 28-FEB-2000; 2000US-0185516P.
 PR 06-MAR-2000; 2000US-0187128P.
 XX
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 PI Blatt L, Mcswiggen J, Chowrira BM;
 XX
 DR WPI; 2001-607195/69.
 XX
 PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX
 XX
 PS Claim 88; Page 81; 200pp; English.
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOCO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g., a ribozyme or a
 CC DNazyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NGN motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapiers. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopenia, and inflammatory arthropathy. The NOCO-
 CC targeting nucleic acid is used to cleave RNA of the NOCO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOCO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOCO. The treatment may further comprise the use of one or more
 CC therapiers. In particular, the NOCO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOCO expression. The present
 CC sequence is an inozyme of the invention

```
XX SQ Sequence 17 BP; 2 A; 11 C; 4 G; 0 T; 0 U; 0 Other;
Query Match 0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 619 CCCCTCCAGCCCGGC 634
    |||||
Db 2 CCCCGCAGCCCGGC 17

RESULT 314
ADV06518/c
ID ADV06518 standard; RNA; 17 BP.
XX AC
XX AC ADV06518;
XX DT 10-FEB-2005 (first entry)
XX DE Human BACE DNAzyme substrate sequence #478.
XX KW Enzymatic nucleic acid molecule; gene expression; down regulation;
XX KW protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;
XX KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
XX KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
XX KW c-erbB2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
XX KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
XX KW amberyzyme; zinzyme; DNAzyme; cancer; breast cancer; Alzheimer's disease;
XX KW diabetes; obesity; cardiac disease; heart disease; age-related disease;
XX KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
XX KW ss.
XX OS Homo sapiens.
XX PN WO200116312-A2.
XX PD 08-MAR-2001.
XX PF 30-AUG-2000; 2000WO-US023998.
XX PW 31-AUG-1999; 99US-0151713P.
XX PR 27-SEP-1999; 99US-00406643.
XX PR 27-SEP-1999; 99US-0156236P.
XX PR 27-SEP-1999; 99US-0156467P.
XX PR 08-NOV-1999; 99US-00436430.
XX PR 06-DEC-1999; 99US-0169100P.
XX PR 29-DEC-1999; 99US-00474432.
XX PR 29-DEC-1999; 99US-0173612P.
XX PR 30-DEC-1999; 99US-00476387.
XX PR 04-FEB-2000; 2000US-00498824.
XX PR 20-MAR-2000; 2000US-00531025.
XX PR 14-APR-2000; 2000US-0197769P.
XX PR 23-MAY-2000; 2000US-00578223.
XX PR 09-AUG-2000; 2000US-00636385.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI McSwiggen J, Usman N, Blatt L, Beigelman L, Burgin A;
XX PI Karpelsky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
XX PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;
XX DR WPI; 2001-244406/25.
XX PT Enzymatic nucleic acid molecules able to cleave separate RNA molecules
XX PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
XX PT obesity and heart disease.
XX PS Example 4; Page 386; 717pp; English.
XX CC The present invention relates to the use of enzymatic nucleic acid
XX CC molecules (e.g. ribozymes) to modulate gene expression. The invention
XX CC also methods for their use to down regulate or inhibit the expression of
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CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine
CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
CC receptor-2 (HER2/c-erbB2/neu), phospholamban (PLN), presenilin-1 (ps-1),
CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
CC nucleic acid molecules used to inhibit the expression of the said genes
CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberyzyme,
CC zinzyme, and/or DNAzyme motifs. The methods of the invention are useful
CC for treating cancer, in particular breast cancer, Alzheimer's disease,
CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related
CC diseases, hepatitis B infections, and hepatitis and hepatocellular
CC carcinoma. The enzymatic nucleic acid molecules can also be used as
CC diagnostic tools to examine genetic drift and mutations within diseased
CC cells and to detect the presence of specific RNA in a cell. The present
CC sequence represents a substrate/target sequence for a DNAzyme used in the
CC examples of the present invention. Note: Some SEQ ID Nos are repeated
CC more than once in the specification, but these have different sequences
CC associated with them.
XX SQ Sequence 17 BP; 3 A; 1 C; 8 G; 0 T; 5 U; 0 Other;
Query Match 0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1275 GACCACATCTCCACA 1290
    |||||
Db 17 GTCCACCATCTCCACA 2

RESULT 315
ADU86311
ID ADU86311 standard; DNA; 17 BP.
XX AC
XX AC ADU86311;
XX DT 10-FEB-2005 (first entry)
XX DE Human TERT hammerhead ribozyme substrate sequence #342.
XX KW Enzymatic nucleic acid molecule; gene expression; down regulation;
XX KW protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;
XX KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
XX KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
XX KW c-erbB2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
XX KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
XX KW amberyzyme; zinzyme; DNAzyme; cancer; breast cancer; Alzheimer's disease;
XX KW diabetes; obesity; cardiac disease; heart disease; age-related disease;
XX KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
XX KW ds.
XX OS Homo sapiens.
XX PN WO200116312-A2.
XX PD 08-MAR-2001.
XX PF 30-AUG-2000; 2000WO-US023998.
XX PW 31-AUG-1999; 99US-0151713P.
XX PR 27-SEP-1999; 99US-00406643.
XX PR 27-SEP-1999; 99US-0156236P.
XX PR 27-SEP-1999; 99US-0156467P.
XX PR 08-NOV-1999; 99US-00436430.
XX PR 06-DEC-1999; 99US-0169100P.
XX PR 29-DEC-1999; 99US-00474432.
XX PR 29-DEC-1999; 99US-0173612P.
XX PR 30-DEC-1999; 99US-00476387.
XX PR 04-FEB-2000; 2000US-00498824.
XX PR 20-MAR-2000; 2000US-00531025.
XX PR 14-APR-2000; 2000US-0197769P.
XX PR 23-MAY-2000; 2000US-00578223.
XX PR 09-AUG-2000; 2000US-00636385.
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XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Mcswiggen J, Usman N, Blact L, Beigelman L, Burgin A;
PI Karpelsky A, Metulic-Adamic J, Sweedler D, Draper K, Chowrira B;
PI Stinchcomb D, Beaudry A, Zinnen S, Lugwig J, Sproat BS;
XX WPI; 2001-244406/25.
XX
XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules
PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
PT obesity and heart disease.
XX
XX Example 1; Page 274; 717pp; English.
XX
XX The present invention relates to the use of enzymatic nucleic acid
CC molecules (e.g. ribozymes) to modulate gene expression. The invention
CC also methods for their use to down regulate or inhibit the expression of
CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine
CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
CC receptor-2 (HER2/C-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
CC nucleic acid molecules used to inhibit the expression of the said genes
CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,
CC zinczyme, and/or DNAzyme motifs. The methods of the invention are useful
CC for treating cancer, in particular breast cancer, Alzheimer's disease,
CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related
CC diseases, hepatitis B infections, and hepatitis and hepatocellular
CC carcinoma. The enzymatic nucleic acid molecules can also be used as
CC diagnostic tools to examine genetic drift and mutations within diseased
CC cells and to detect the presence of specific RNA in a cell. The present
CC sequence represents a substrate/target sequence for a ribozyme used in
CC the examples of the present invention. Note: Some SEQ ID Nos are repeated
CC more than once in the specification, but these have different sequences
CC associated with them.
XX
XX Sequence 17 BP; 2 A; 7 C; 3 G; 5 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1687 GACCAGCTTTTCTCA 1702
DB 1 GGCACGCTTTCCTCA 16
RESULT 316
ABK63841/C
ID ABK63841 standard; DNA; 17 BP.
XX
XX ABK63841;
XX
XX 18-JUN-2002 (first entry)
XX
XX Neurokinin 1 receptor (NK-1) antisense oligonucleotide #5.
XX
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;
KM immune disorder; autoimmune disorder; cardiovascular disorder; pain;
KM vascular disorder; airway disorder; neuropathic disorder; inflammation;
KM psychiatric disorder; central nervous system disorder; intestinal condition;
KM respiratory condition; opthalmic condition; intestinal condition;
KM demyelinating disease; small cell lung cancer; depression;
KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
KM neuro-pathological disorder; stress; antisense; primer; ss.
XX
XX Homo sapiens.
XX
XX ACAG07747
XX PN W0200213799-A2.
XX
XX 21-FEB-2002.

XX 17-AUG-2001; 2001WO-IB001510.
XX
XX 18-AUG-2000; 2000US-0226086P.
XX
XX (UVMC-) UNIV MCGILL.
XX
XX Henry JL, Cahill CM, Yashpal K;
PI WPI; 2002-241835/29.
XX
XX
XX Treating pathological condition involving neurokinin receptor-1, e.g.
PT pain or inflammation, by administering oligonucleotide or a non-
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
PT pathway.
XX
XX Claim 24; Page 65; 100pp; English.
XX
XX The invention relates to a method of treating a pathological condition
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)
CC receptor, especially treating, attenuating or preventing pain or
CC inflammatory condition. The method comprises administering to a mammal, a
CC compound chosen from an oligonucleotide, its analogue, and a disruptor
CC which interferes with function or production of NK-1 receptors. The
CC method is useful for treating a pathological condition characterised by
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,
CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,
CC psychiatric and central nervous system disorders (e.g. anxiety,
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or
CC peripheral aspects of chronic or acute pain, and for treating,
CC attenuating or preventing pain or inflammation such as peripheral,
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or
CC pain relating to psychiatric disorders and central nervous system
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
CC in a mammal, in particular human. NK-1 receptor related disorders,
CC diseases, or pathological conditions treatable by this method include
CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and
CC Crohn's disease), cardiovascular conditions (stroke), chronic
CC gastrointestinal tract inflammation, and inflammatory diseases such as
CC inflammatory bowel diseases. Other disorders and diseases include
CC cardiovascular pathologies including stroke, chronic inflammatory
CC diseases such as rheumatoid arthritis, demyelinating diseases such as
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
CC disorders such as allergies and poison ivy, vasospastic diseases such as
CC angina, addiction disorders such as alcoholism, neurodegenerative
CC disorders such as acquired immune deficiency syndrome (AIDS) related
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
CC disorders such as peripheral neuropathy, oedema, stress related and
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
CC effectively treat chronic conditions and other pathological states
CC without the co-administration of substance P, and reduce the number of
CC activated receptors while not reducing the number of quiescent NK-1
CC receptors. Receptors not chronically stimulated are less affected.
CC reducing side effects of treatment. ABK63841-ABK63906 represent NK-1
CC receptor coding sequences and oligonucleotides of the invention
XX
XX Sequence 17 BP; 3 A; 3 C; 4 G; 7 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 207 CGAATGATGATGATC 222
DB 16 CAAATGATGATGATC 1
RESULT 317
ACA07747
ID ACA07747 standard; RNA; 17 BP.
XX

AC ACA07747;
 XX
 DT 03-JUN-2003 (first entry)
 XX
 DE NFKB sub-unit modulating zincyme substrate #146.
 XX
 KM Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinczyme;
 KM G-cleaver; amberyase; cancer; REL-A activity; breast cancer; human;
 KM lung cancer; prostate cancer; colorectal cancer; brain cancer;
 KM oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
 KM cervical cancer; head and neck cancer; ovarian cancer; melanoma;
 KM lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
 KM chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
 KM cyclophosphamide; doxorubicin; fluorouracil carboplatin; edatrexate;
 KM gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
 KM rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
 KM gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
 KM transplant/graft rejection; reperfusion injury; glomerulonephritis;
 KM allergic airway inflammation; inflammatory bowel disease; infection; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2002177568-A1.
 XX
 PD 28-NOV-2002.
 XX
 PF 23-MAY-2001; 2001US-00864785.
 XX
 PR 07-DEC-1992; 92US-00987132.
 PR 18-MAY-1994; 94US-00245466.
 PR 15-AUG-1994; 94US-00291932.
 PR 23-DEC-1996; 96US-00777916.
 XX
 PA (STIN/) STINGCOMB D T.
 PA (MCSW/) MCSWIGGEN J.
 PA (DRAP/) DRAPER K G.
 XX
 PI Stinchcomb DT, Mcswiggen J, Draper KG;
 XX
 DR WPI; 2003-340953/32.
 XX
 PT Novel enzymatic nucleic acid molecules which down regulates expression of
 PT a sequence encoding a subunit of nuclear factor kappa B useful for
 PT treating cancer, inflammatory disorders and autoimmune diseases.
 XX
 PS Claim 3; Page 39; 72pp; English.
 XX
 XX The invention describes an enzymatic nucleic acid molecule (I) which down
 CC regulates expression of a sequence encoding a subunit of nuclear factor
 CC kappa B (NFKB), where (I) is an inozyme, zinczyme, G-cleaver or amberyase
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat
 CC cancer and is useful for down-regulating REL-A activity in a cell, for
 CC treating a patient having a condition associated with the level of REL-A.
 CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
 CC the presence of a divalent cation, especially Mg²⁺. The enzymatic and
 CC antisense nucleic acid molecules are useful for treating breast, lung,
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
 CC multidrug resistant cancer. The method involves use of other drug
 CC chemotherapies such as monoclonal antibodies, REL-A-specific inhibitors or
 CC cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate,
 CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic
 CC acid molecules are also useful for treating inflammatory disease such as
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
 CC rejection, gene therapy applications, ischaemia/reperfusion injury,
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or
 CC infection. This sequence represents the substrate of a novel enzymatic
 CC nucleic acid molecule
 XX
 SQ Sequence 17 BP; 2 A; 9 C; 4 G; 0 T; 2 U; 0 Other;

Query Match 0.8%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.3e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 134 GCCCGAGGCCGAGCC 149
 DB 2 GCCCGAGGCCGAGCC 17
 ID ABZ61190 standard; RNA; 17 BP.
 XX ABZ61190/c
 XX ABZ61190;
 AC ABZ61190;
 XX
 DT 21-MAR-2003 (first entry)
 XX
 DE Human K-Ras DNAzyme substrate #1302.
 XX
 KM Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
 KM enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytoskeletal; anti-HIV;
 KM anti-rheumatic; cancer; AIDS; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200297114-A2.
 XX
 PD 05-DEC-2002.
 XX
 PF 29-MAY-2002; 2002WO-US016840.
 XX
 PR 29-MAY-2001; 2001US-0294140P.
 PR 06-JUN-2001; 2001US-0296249P.
 PR 10-SEP-2001; 2001US-0318471P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Mcswiggen J;
 XX
 DR WPI; 2003-140484/13.
 XX
 PT Novel short interfering RNA and enzymatic nucleic acid useful for
 PT treating cancer, modulates the expression of a nucleic acid encoding
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
 XX
 PS Claim 58; Page 110; 185pp; English.
 XX
 XX The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 CC acid molecule of the invention has cytoskeletal, anti-HIV, and anti-
 CC rheumatic activity. The nucleic acid molecules are useful for reducing
 CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
 CC also useful for treating breast, ovarian, colorectal, lung, prostate,
 CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
 CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ6520 - ABZ6524,
 CC ABZ6530 - ABZ6585 represent substrate/target sequences for the human
 CC ribozymes of the invention
 XX
 SQ Sequence 17 BP; 4 A; 6 C; 5 G; 0 T; 2 U; 0 Other;
 QY Query Match 0.8%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.3e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 DB 834 CCTGCTGGTGAATTGCG 849
 17 CCTGCTGGTGAATTGCG 2
 RESULT 319

ADK13263/C
ID ADK13263 standard; DNA; 17 BP.
XX
AC ADK13263;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human glioma endothelial marker (GEM) long tag SEQ ID NO:441.
XX
KM glioma; brain tissue; neoplastic; glioma endothelial marker; GEM;
KM anticancer; antiglioma; immune response; cytosolic;
KM multi-drug sensitive glioma; human; long tag; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN MO2004016758-A2.
PD
PD 26-FEB-2004.
XX
PF 15-AUG-2003; 2003WO-US025614.
XX
PR 15-AUG-2002; 2002US-0403390P.
PR 01-APR-2003; 2003US-0458978P.
XX
PA (GENZ) GENZYME CORP.
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Madden SJ, Wang CJ, Cook BP, Laterra J, Walter K;
XX
DR WPI; 2004-247973/23.
XX
PT Diagnosing glioma by detecting expression product of any one of 255
PT genes, glioma endothelial markers, in brain tissue sample suspected of
PT being neoplastic, and comparing the expression with expression in normal
PT brain tissue sample.
XX
XX
PS Example 2; SEQ ID NO 441; 114pp; English.
XX
CC The present invention describes a method (M1) for aiding in the diagnosis
CC of glioma. (M1) involves detecting an expression product of at least one
CC gene (I) in a first brain tissue sample (T) suspected of being
CC neoplastic, where (I) is chosen from any one of 255 genes (glioma
CC endothelial markers (GEMs)) as given in specification, and comparing the
CC expression of (I) in (T) with expression of (I) in a second normal brain
CC tissue sample (R), where increased expression of (I) in (T) relative to
CC (R), identifies (T) as likely to be neoplastic. Also described: (1)
CC treating (M2) glioma involves contacting cells of the glioma with an
CC antibody that specifically binds to a extracellular epitope; (2)
CC identifying (M3) a test compound as potential anticancer or antiglioma
CC drug involves contacting a test compound with the cell which expresses
CC (I), monitoring an expression product of the at least one gene and
CC identifying test compound as a potential anticancer drug if it decreases
CC the expression of at least one gene; (3) identifying (M4) a test compound
CC as potential anticancer or antiglioma drug involves contacting a test
CC compound with the cell which expresses mRNA of at least one gene
CC identified by a tag as described above, monitoring mRNA of the gene, and
CC identifying the test compound as a potential anticancer drug if it
CC decreases the expression of at least one gene; and (4) inducing (M5) an
CC immune response to glioma involves administering to a mammal, a protein
CC or (I). (I) have cytostatic activities, and can be used to trigger immune
CC destruction of glioma cells, and as immune response inducers. (M1) is
CC useful for aiding in diagnosing glioma. (M2) is useful for treating multi-
CC drug sensitive glioma in a human. (M5) is useful for inducing an immune
CC response to a glioma in a mammal having glioma or in a mammal who has had
CC a glioma surgically removed. The present sequence represents a human GEM
CC long tag oligonucleotide, which is used in the exemplification of the
CC present invention.
XX
SQ Sequence 17 BP; 5 A; 1 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.3e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1415 CCTCCCAATGTCCTCTC 1430
|||
Db 16 CCTCCCAATGTCCTCTC 1
|||
RESULT 320
ADN00720
ID ADN00720 standard; DNA; 17 BP.
XX
AC ADN00720;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human SLT related PCR primer, SEQ ID 19.
XX
KM Anorectic; nootropic; neuroprotective; antidiabetic; transgenic animal;
KM SLT; obesity; eating disorder; insulin resistance; puberty disturbance;
KM memory damage; sexual function disorder; anorexia; anaemia; human; PCR;
KM primer; ss.
XX
OS Synthetic.
XX
PN MO2004023870-A1.
PD
PD 25-MAR-2004.
XX
PF 09-SEP-2003; 2003WO-JP011501.
XX
PR 10-SEP-2002; 2002JP-00264054.
XX
PA (TAKEDA) TAKEDA CHEM IND LTD.
XX
PI Mori M, Sugo T, Nishida M, Kaeuga H, Takeomi S;
XX
DR WPI; 2004-269810/25.
XX
XX
XX Human SLT transgenic animals for evaluating SLT inhibitors and screening
XX drugs for obesity, eating hyperactivity, insulin resistance, disturbances
XX during puberty, memory damage or disorder of sexual function.
XX
PS Example 2; SEQ ID NO 19; 79pp; Japanese.
XX
CC The present invention relates to a transgenic SLT animal. The transgenic
CC animal is useful for evaluating SLT inhibitors and screening drugs for
CC obesity, eating hyperactivity, insulin resistance, disturbances during
CC puberty, memory damage or disorder of sexual function, or preventives or
CC remedies for anorexia, anaemia accompanying anorexia or hypoproteinemia,
CC including clarification of pathological mechanism of these diseases. The
CC present sequence is a PCR primer, used to illustrate the invention.
XX
SQ Sequence 17 BP; 1 A; 6 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 309 CCTTTGGGACAGCTGCC 324
|||
Db 2 CCTTTGGGACAGCTTCC 17
|||
RESULT 321
AD230264/C
ID AD230264 standard; RNA; 17 BP.
XX
AC AD230264;
XX
DT 30-JUN-2005 (first entry)
XX
DE Human K-Ras substrate RNA sequence SEQ ID NO:1302.
XX

KW short interfering RNA; siRNA, RNA interference; gene silencing;
KM cytosolic; cancer; Ras gene; substrate; ss.
XX Homo sapiens.
PN US2005080031-A1.
XX 14-APR-2005.
XX 26-NOV-2003; 2003US-00724270.
XX 18-MAY-2001; 2001US-0292217P.
PR 29-MAY-2001; 2001US-0294140P.
PR 06-JUN-2001; 2001US-0296249P.
PR 20-JUL-2001; 2001US-0306883P.
PR 13-AUG-2001; 2001US-0311865P.
PR 10-SEP-2001; 2001US-0318471P.
PR 20-FEB-2002; 2002US-0358580P.
PR 06-MAR-2002; 2002US-0362016P.
PR 11-MAR-2002; 2002US-0363124P.
PR 20-MAY-2002; 2002US-0363124P.
PR 29-MAY-2002; 2002US-00157580.
PR 06-JUN-2002; 2002US-00163552.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0408378P.
PR 05-SEP-2002; 2002US-0409293P.
PR 09-SEP-2002; 2002US-00238700.
PR 10-SEP-2002; 2003US-00422704.
PR 15-JAN-2003; 2003US-0440129P.
PR 20-FEB-2003; 2003US-00505028.
PR 20-FEB-2003; 2003US-00505346.
PR 16-APR-2003; 2003US-00417012.
PR 24-APR-2003; 2003US-00422704.
PR 30-APR-2003; 2003US-00448853.
PR 23-MAY-2003; 2003US-00448853.
PR 29-AUG-2003; 2003US-00652791.
PR 23-OCT-2003; 2003US-00693059.
XX (SIRN-) SIRNA THERAPEUTICS INC.
PA Mcswiggen J;
PI WPI; 2005-331166/34.
XX Novel double-stranded short interfering RNA molecule having first
PT nucleotide sequence complementary to RNA encoding HER2 or its portion,
PT and second nucleotide sequence having complementarity to first sequence,
PT useful for treating cancer.
XX Example 1; SEQ ID NO 1302; 143pp; English.
XX The invention relates to a double-stranded short interfering RNA (siRNA)
CC molecule (I) comprising a first nucleotide sequence having 19-23
CC nucleotides complementary to an RNA sequence encoding HER2 or its
CC portion, and a second nucleotide sequence having 19-23 nucleotides
CC exhibiting complementarity to the first sequence, and including at least
CC one nucleotide that is not a 2'-OH containing ribonucleotide. Also
CC described is a method of producing a class of nucleic acid-based gene
CC modulating agents that exhibit a high degree of specificity for RNA of a
CC desired target. (I) is useful for modulating HER2 activity in a cell, and
CC for treating diseases or conditions related to levels of HER2 gene
CC expression. (I) is useful for treating cancer, such as pancreatic cancer,
CC bladder cancer, lung cancer, breast cancer or prostate cancer. The
CC present sequence represents a human K-Ras substrate RNA sequence for a
CC DNAzyme (ribozyme), which is used in an example from the present
CC invention for the identification of potential target sites in human Ras
CC RNA.
XX Sequence 17 BP; 4 A; 6 C; 5 G; 0 T; 2 U; 0 Other;
SQ Query Match 0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.3e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 834 CCTGCTGGTGAATGGC 849
Db 17 CCTGCTGGTGAATGGC 2
RESULT 322
AED88220/c
ID AED88220 standard; DNA; 17 BP.
XX AED88220;
AC AED88220;
XX 26-JUN-2006 (first entry)
DT Human Leukocyte Antigen B allele identification probe, SEQ ID 103.
XX HLA; Leukocyte; Antigen; transplant rejection; histocompatibility;
KM preclinical testing; cancer; cytosolic; diabetes mellitus; antidiabetic;
KW probe; ss.
XX Homo sapiens.
OS JP2005185172-A.
XX 14-JUL-2005.
PD 25-DEC-2003; 2003JP-00430554.
PF 25-DEC-2003; 2003JP-00430554.
PR 25-DEC-2003; 2003JP-00430554.
PR (CANO) CANON KK.
PA Tsukada M;
PI WPI; 2006-013379/02.
XX Probe set for specific identification of an HLA-B allele in a sample,
PT useful e.g. in matching transplant donors and recipients, and in
PT determining suitable treatment for patients with conditions such as
PT cancer and diabetes mellitus.
XX Claim 2; SEQ ID NO 103; 152pp; Japanese.
XX The invention relates to a novel probe set for the identification of a
CC Human Leukocyte Antigen (HLA)-B allele in a sample. The invention further
CC includes a method for identifying an HLA-B allele using the probe set.
CC The probe set and method are useful for identifying an HLA-B allele in a
CC sample. The information gained is useful, for example, in matching organ
CC donors and recipients, and in guiding clinical decisions in the treatment
CC of diseases such as cancer and diabetes mellitus. This oligo sequence
CC represents a probe used in the identification of a Human Leukocyte
CC Antigen B allele of the invention.
XX Sequence 17 BP; 4 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
SQ Query Match 0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 438 CGCGAGGCGCTCCATG 453
Db 17 CGCGAGGCGCTCCATG 2
RESULT 323
AAQ85449/c
ID AAQ85449 standard; DNA; 18 BP.
XX AAQ85449;
AC AAQ85449;
XX 25-MAR-2003 (revised)
DT 05-OCT-1995 (first entry)

```
XX PCR primer for HARDS clone p3H226.
DE
XX
XX Hantavirus-Associated Respiratory Distress Syndrome; epitope;
KW immunodiagnostic; vaccine; antigenic; amplification; ss.
XX
XX Synthetic.
OS
XX
XX W09506250-A1.
PN
XX
XX 02-MAR-1995.
PD
XX
XX 25-AUG-1994; 94WO-US009416.
PF
XX
XX 25-AUG-1993; 93US-00111519.
PR 13-SEP-1993; 93US-00120096.
PR 26-OCT-1993; 93US-00141035.
PR 22-MAR-1994; 94US-00210762.
XX
XX (UYNE-) UNIV NEW MEXICO STATE.
PA
XX
XX Hjelte B, Jenison S;
PI
XX
XX WPI; 1995-106942/14.
DR
XX
XX Recombinant antigens of HARDS virus - useful in immuno-diagnostic(s),
PT prophylactics and therapeutics for HARDS virus.
XX
XX
XX Example; Page 14; 78pp; English.
PS
XX
XX The sequence is that of a PCR primer used to amplify clone p3H226 from
CC Hantavirus-Associated Respiratory Distress Syndrome virus. See also
CC AA085436-50, AA086100-10. (Updated on 25-MAR-2003 to correct PW field.)
CC
XX
XX Sequence 18 BP; 2 A; 2 C; 9 G; 3 T; 0 U; 2 Other;
SQ
Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 129 CCTGAGCCCGCAGGCCCA 146
Db 18 CCTGARCCTCCATGCMCCA 1
RESULT 324
AAT41606
ID AAT41606 standard; DNA; 18 BP.
XX
XX AAT41606;
AC
XX
XX 04-JUN-1997 (first entry)
DT
XX
XX Oligonucleotide containing core DNA regulatory element.
DE
XX
XX Regulatory element; STAT; protein; cytokine; responsive; host cell;
KW transfection; agonist; antagonist; mediated; STAT5; transcription;
KW modulation; signalling pathway; STAT6; Oligonucleotide;
KW electrophoretic mobility shift assay; EMSA; ds.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH 5.18
FT misc_feature /tag= a
FT /note= "core DNA regulatory element"
XX
XX W09630515-A1.
PN
XX
XX 03-OCT-1996.
PD
XX
XX 25-MAR-1996; 96WO-US004012.
PF
XX
```

```
PR 27-MAR-1995; 95US-00411020.
XX
XX (LIGA-) LIGAND PHARM INC.
PA
XX
XX Seidel HM, Lamb IP, Tian Chan S;
PI
XX
XX WPI; 1996-455362/45.
DR
XX
XX DNA construct for screening modulators of cytokine-mediated transcription
PT - contg. regulatory element and a cytokine-sensitive promoter operably
PT linked to a heterologous gene.
XX
XX
XX Example 1; Page 26; 72pp; English.
PS
XX
XX A novel DNA construct comprises the present oligonucleotide (ON), which
CC contains a core a regulatory element, operably linked to a promoter,
CC which is operably linked to a heterologous gene (preferably a marker
CC gene). The gene is under the transcriptional control of the promoter and
CC the ON sequence when the ON is bound by a STAT protein activated in
CC response to IL-2, IL-3, G-CSF, GM-CSF, erythropoietin, thrombopoietin, or
CC preferably IL-4, IL-7, IL-9, IL-13 or IL-15. Cytokine responsive host
CC cells transfected with the DNA construct can be used to measure the
CC ability of a compound to act as an agonist or antagonist of cytokine
CC mediated gene transcription. In particular, they can be used to screen
CC for cytokine modulators involved in the STAT5 and/or STAT6 protein
CC signalling pathway. Following an electrophoretic mobility shift assay the
CC DNA construct was found to bind IL-4 moderately and IL-13 not determined
CC
XX
XX Sequence 18 BP; 5 A; 3 C; 4 G; 6 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1717 TCCATTCTCGAAGTG 1732
Db 3 TCCATTCTCGAATG 18
RESULT 325
AAW73505/C
ID AAW73505 standard; RNA; 18 BP.
XX
XX AAW73505;
AC
XX
XX 28-JUL-1999 (first entry)
DT
XX
XX Mouse flk-1 VEGF receptor hairpin ribozyme substrate #52.
DE
XX
XX Vascular endothelial growth factor receptor; VEGF receptor; flk-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
XX
XX Mus SP.
OS
XX
XX W09715662-A2.
PN
XX
XX 01-MAY-1997.
PD
XX
XX 25-OCT-1996; 96WO-US017480.
PF
XX
XX 26-OCT-1995; 95US-0005974P.
PR 11-JAN-1996; 96US-00584040.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (CHIR) CHIRON CORP.
XX
XX Pavco P, McSwiggen J, Stinchcomb D, Escobedo J;
PI
XX
XX WPI; 1997-259017/23.
DR
XX
```

PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
PS Claim 4; Page 152; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (Flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
CC
XX
SQ Sequence 18 BP; 7 A; 5 C; 3 G; 0 T; 3 U; 0 Other;

Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 662 TCTGTGTCATCTGGT 677
Db 18 TCTGTGTCATCTGAGT 3

RESULT 326
AAX84480
ID AAX84480 standard; DNA; 18 BP.
XX
AC AAX84480;
XX
DT 10-SEP-1999 (first entry)
XX
DE PCR primer for Human EDIRF II coding sequence.
XX
XX Embryo derived interleukin related factor; diagnosis; detection; therapy;
XX EDIRF-related disorder; immune disorder; haematopoietic disorder;
XX developmental disorder; inflammatory disease; arthritis; psoriasis;
XX EDIRF II; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN MO9932632-A1.
XX
PD 01-JUL-1999.
XX
XX 18-DEC-1998; 98MO-US027068.
XX
XX 19-DEC-1997; 97US-00994890.
XX
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
XX Holtzman DA;
XX
XX WPI; 1999-418929/35.
XX
PT Nucleic acid encoding embryo-derived interleukin-related factors.
XX
PS Example 2; Page 75; 116pp; English.
XX
CC This sequence is a PCR primer for DNA encoding the embryo-derived
CC interleukin-related factor (EDIRF) of the invention, designated human
CC EDIRF II. The EDIRF DNA and protein sequences (and their homologues),
CC antibodies (Ab) specific for EDIRF, and other modulators are used; (i) in
CC screening and detection assays, e.g. for chromosome mapping, tissue
CC typing or forensic studies; (ii) in diagnosis, prognosis or monitoring
CC clinical trials; and (iii) for treating or preventing EDIRF-related
CC diseases (especially immune, haematopoietic, differentiative,
CC developmental or inflammatory disease, including arthritis and psoriasis.

CC The EDIRF coding sequence, or its fragments, are also useful as probes
CC and primers (for detecting related sequences and disease-associated
CC mutations, also for mutagenesis), for expressing recombinant EDIRF and as
CC source of antisense, ribozyme and peptide nucleic acids for inhibiting
CC translation of EDIRF-derived mRNA. EDIRF is used to raise Ab (useful for
CC detecting EDIRF, including forms with aberrant post-translational
CC modification, for affinity purification and therapeutically) and to
CC screen for specific modulators (e.g. peptides or peptidomimetics)
CC
XX
SQ Sequence 18 BP; 4 A; 6 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1450 GCAGGTGACGCCCA 1465
Db 2 GCAGGTGACGCCCA 17

RESULT 327
AAA07036/c
ID AAA07036 standard; DNA; 18 BP.
XX
AC AAA07036;
XX
DT 03-JUL-2000 (first entry)
XX
DE Human integrin beta 3 antisense oligonucleotide, SEQ ID NO:9.
XX
XX Integrin beta 3; human endothelial glycoprotein; GP3A, GPIIb; ITGB3;
XX C6b1; platelet glycoprotein 3a; cellular adhesion; vitronectin receptor;
XX fibronectin receptor; expression inhibition; antisense; tumour formation;
XX cancer invasion; bleeding disorder; inflammation; ss.
XX
OS Homo sapiens.
OS
PN US6037176-A.
XX
PD 14-MAR-2000.
XX
XX 25-JUN-1999; 99US-00344520.
XX
XX 25-JUN-1999; 99US-00344520.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Cowseert LM, Monia BP;
XX
XX WPI; 2000-246189/21.
XX
XX New antisense compound that inhibits human integrin beta3, useful e.g.
XX for treating or preventing infection, inflammation and tumors.
XX
PS Claim 1; Col 39; 33pp; English.
XX
CC Sequences AAA07035-A07074 represent antisense oligonucleotides targeted
CC to the human integrin beta 3 gene, which inhibit its expression. The
CC antisense oligonucleotides were designed to target different regions of
CC the human integrin beta 3 RNA, and were analysed for their effect on
CC integrin beta 3 mRNA levels by quantitative real-time PCR. GAPDH
CC (glyceraldehyde-3-phosphate) mRNA levels were measured as a control.
CC Integrins constitute one of four classes of cellular adhesion molecules,
CC and play an important role in cell migration, cell anchorage to
CC substrates and cytoadhesion signalling pathways. They are heterodimeric
CC cation-dependent membrane glycoproteins composed of an alpha and beta
CC subunit. Integrin beta 3 (also known as human endothelial glycoprotein,
CC GP3A, GPIIb, ITGB3, C6b1 and platelet glycoprotein 3a) is the common
CC beta subunit partner of the members of the beta-3 subfamily of integrins.
CC This family consists of the vitronectin receptor (alpha-v-beta-3) and the
CC fibronectin receptor (alpha-1b-beta-3). Cells expressing this class of
CC integrin can adhere to various matrix proteins and participating in various
CC cytoadhesion-driven cellular responses. Integrin beta 3 is implicated in

CC conditions such as vascular stenosis, excessive bone resorption,
CC angiogenesis (in melanoma), tumour invasion, platelet aggregation and
CC Glanzmann's thrombasthenia. The oligonucleotides of the invention are
CC useful for diagnosis, prevention and treatment of conditions associated
CC with integrin beta 3 expression, such as tumour formation, inflammation,
CC infections and the diseases mentioned above
XX
SQ Sequence 18 BP; 5 A; 8 C; 4 G; 1 T; 0 U; 0 Other;
Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 804 CTGTCGACTGCTGCTG 819
Db 18 CTGGGTGACTGCTGCTG 3
RESULT 328
AAZ48483
ID AAZ48483 standard; DNA; 18 BP.
XX
AC AAZ48483;
XX
DT 31-MAR-2000 (first entry)
XX
DE Human TNFR1 mRNA inhibiting antisense oligo ISIS# 18876.
XX
KW Tumour necrosis factor receptor type 1; TNFR1; antisense; infection;
KW inflammation; tumour formation; TNFR1; anticancer; ss.
XX
OS Synthetic.
XX
OS Homo sapiens.
XX
PN US6007995-A.
XX
PD 28-DEC-1999.
XX
PF 26-JUN-1998; 98US-00106038.
XX
PR 26-JUN-1998; 98US-00106038.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Baker BF, Cowsebert LM;
XX
DR WPI; 2000-105333/09.
XX
PT Antisense inhibition of tumor necrosis factor type 1 expression for
PT diagnosis, treatment and prevention of disease, particularly tumors.
XX
PS Example 10; Col 24; 34pp; English.
XX
CC The invention provides antisense compounds targeted to human tumour
CC necrosis factor receptor type 1 (TNFR1) RNA. These antisense compounds
CC can be used in a method of inhibiting the expression of TNFR1 human cells
CC or tissues. The antisense compounds specifically hybridize with one or
CC more nucleic acids encoding TNFR1 modulating the function of nucleic acid
CC molecules encoding TNFR1, ultimately modulating the amount of TNFR1
CC produced. The antisense compounds and method are useful as research
CC reagents and diagnostics, and in the treatment and prophylaxis of
CC infection, inflammation or tumour formation. Sequences AAZ48482-565
CC represent antisense oligos used for inhibition of the human TNFR1 mRNA
XX
SQ Sequence 18 BP; 0 A; 9 C; 1 G; 8 T; 0 U; 0 Other;
Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 105 CCCTCTCTCTCTGCTTT 120
Db 3 CCCTCTCTCTCTGCTTT 18

RESULT 329
AAZ59805/C
ID AAZ59805 standard; DNA; 18 BP.
XX
AC AAZ59805;
XX
DT 19-APR-2000 (first entry)
XX
DE Human Smad3 phosphorothioate antisense oligonucleotide, SEQ ID NO:17.
XX
KW Smad3; MADH3; JVI5-2; TGF-beta signalling pathway;
KW transcription factor; expression inhibition; antisense therapy;
KW tumour formation; inflammation; antisense; ss.
XX
OS Homo sapiens.
XX
PN US6013788-A.
XX
PD 11-JAN-2000.
XX
PF 09-APR-1999; 99US-00289376.
XX
PR 09-APR-1999; 99US-00289376.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Cowsebert LM;
XX
DR WPI; 2000-126072/11.
XX
PT Antisense inhibition of the human Smad3 gene, useful for diagnosing,
PT preventing and treating conditions associated with Smad3 expression e.g.
PT inflammation.
XX
PS Claim 11; Col 38; 31pp; English.
XX
CC Sequences AAZ49796-259835 represent antisense oligonucleotides targeted
CC to the human Smad3 gene, which inhibit its expression. The antisense
CC oligonucleotides were designed to target different regions of the human
CC Smad3 RNA, and were analysed for their effect on Smad3 mRNA levels by
CC quantitative real-time PCR. The Smad proteins are a family of cytosolic
CC proteins which are involved in TGF-beta superfamily signal transduction.
CC On ligand binding, TGF-beta superfamily proteins (such as bone
CC morphogenetic protein (BMP), activin and TGF-betas themselves)
CC phosphorylate Smad proteins, which then homo- or heterodimerise and
CC translocate to the nucleus to activate target gene transcription. Smad3
CC (also known as MADH3, hMAD3 and JVI5-2) is a member of a subgroup of Smad
CC family transcription factors, the pathway-restricted Smads, which are
CC regulated by TGF-beta and activins. It can heterodimerise with Smad4
CC (US6013787-A, AAY69622), the complex being able to activate TGF-beta
CC inducible transcription. The oligonucleotides of the invention are useful
CC for diagnosis, prevention and treatment of conditions associated with
CC Smad3 expression, such as tumour formation, inflammation and certain
CC infections
XX
SQ Sequence 18 BP; 6 A; 3 C; 7 G; 2 T; 0 U; 0 Other;
Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1118 TCATCTACTGCTGCTT 1133
Db 18 TCATCTACTGCTGCTT 3
RESULT 330
AAZ76614
ID AAZ76614 standard; DNA; 18 BP.
XX
AC AAZ76614;

XX 10-SEP-2001 (first entry)
 XX Human biallelic marker downstream amplification primer SEQ ID NO:10970.
 DE
 XX Human genome; biallelic marker; high density disequilibrium map;
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
 KW haplotyping; hybridisation; identification; characterisation;
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;
 KW diagnosis; ss.
 XX
 XX Homo sapiens.
 OS
 XX MO9954500-A2.
 PN
 XX 28-OCT-1999.
 PD
 XX 21-APR-1999; 99WO-IB000822.
 PP
 XX 21-APR-1998; 98US-0082614P.
 PR 23-NOV-1998; 98US-0109732P.
 PR
 XX (GBST) GENSET.
 PA
 XX Cohen D, Blumenfeld M, Chumakov I,
 PI WPI, 2000-013267/01.
 DR
 XX Novel biallelic markers used to construct a high density disequilibrium
 PT map of the human genome.
 XX
 PS Claim 9, Page 2569; 2745BP; English.
 XX
 CC AA26564 to AA269578 represent human biallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AA269579 to AA277440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the invention
 CC have a variety of uses: they can be used for high density mapping of the
 CC human genome, and in complex association studies and haplotyping studies
 CC which are useful in determining the genetic basis for disease states.
 CC Compositions and methods of the invention can also be useful for the
 CC identification of the targets for the development of pharmaceutical
 CC agents and diagnostic methods, as well as the characterisation of the
 CC differential efficacious responses to and side effects from
 CC pharmaceutical agents acting on a disease as well as other treatment.
 CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
 CC 3367, are not actually given a sequence in the Sequence listing from the
 CC present invention
 CC
 SQ Sequence 18 BP; 1 A; 9 C; 0 G; 8 T; 0 U; 0 Other;
 XX
 XX
 Query Match 0.8%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1404 CTTGACCTTCTCTCC 1419
 |||||
 DB 2 CTTGACCTTCTCTCC 17
 |||||

RESULT 331
 AAH37701/C
 ID AAH37701 standard; DNA; 18 BP.

AAH37701;

14-AUG-2001 (first entry)

SNP specific upper PCR primer SEQ ID 497.

Single nucleotide polymorphism; SNP; single nucleotide primer extension;
 KW genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
 KW Leech-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;

KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
 KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
 KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.
 OS
 XX Homo sapiens.
 XX
 PN MO200129262-A2.
 PD
 XX 26-APR-2001.
 PP
 XX 13-OCT-2000; 2000WO-US028436.
 PR 15-OCT-1999; 99US-0160096P.
 PR
 XX (ORCH-) ORCHID BIOSCIENCES INC.
 PA
 XX Picoult-Newburg L, Pohl M;
 PI WPI, 2001-290930/30.
 DR
 XX New genotyping oligonucleotide, useful for detecting the presence,
 PT absence or identity of single polynucleotide polymorphism in a nucleic
 PT acid sample.
 XX
 PS Claim 1; Page 52; 83BP; English.
 XX

CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
 CC primer extension (SNP) primers, and the sequences of regions flanking
 CC sites of single nucleotide polymorphisms SNPs. The present invention
 CC includes kits for determining the presence or absence of a SNP, using the
 CC oligonucleotides of the invention. The PCR primers are used to amplify a
 CC SNP flanking sequence, the SNP primer is used as a genotyping primer.
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by
 CC performing a single-nucleotide primer extension reaction. The
 CC oligonucleotides are useful for determining the presence, absence or
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
 CC assess by association analysis the genotype of an individual or group of
 CC individuals, having a pathological phenotypic trait suspected of being
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
 CC agammaglobulinaemia, diabetes insipidus, Leech-Nyhan syndrome, muscular
 CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
 CC traits also include symptoms of or susceptibility to multifactorial
 CC disease of which a component is or may be genetic such as autoimmune
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,
 CC inflammation, cancer, nervous system diseases and infection by pathogenic
 CC microorganism. The method is also useful in forensic investigations and
 CC paternity analysis. The present sequence represents a PCR primer specific
 CC for a human SNP containing DNA sequence
 CC
 SQ Sequence 18 BP; 4 A; 4 C; 8 G; 2 T; 0 U; 0 Other;
 XX
 XX

Query Match 0.8%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1223 CCACCCGGGTATCTCA 1238
 |||||
 DB 18 CCACCCGGGTATCTCA 3
 |||||

RESULT 332
 ABT04979
 ID ABT04979 standard; DNA; 18 BP.

ABT04979;

11-OCT-2002 (first entry)

TNFR1 expression modulation related antisense oligo SEQ ID No 9.

Antisense compound; tumour necrosis factor receptor 1; liver disease;
 KW TNFR1; hepatitis; liver injury; hyperproliferative disorder; cancer;

KX human; ds.
XX
OS Homo sapiens.
XX
PN WO200248168-A1.
XX
PD 20-JUN-2002.
XX
PF 22-OCT-2001; 2001WO-US051224.
XX
PR 24-OCT-2000; 2000US-00695451.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Baker BF, Cowse LM, Zhang H, Dean NM;
XX
DR WPI; 2002-583481/62.
XX
PT Novel antisense compound targeted to nucleic acid molecule encoding tumor
PT necrosis factor receptor 1 (TNFR1), useful for treating humans having
PT disease associated with TNFR1 e.g. hepatitis, liver injury, liver cancer.
XX
PS Example 10; Page 44; 121pp; English.
XX
CC The invention relates to an antisense compound 8 to 30 nucleotides in
CC length targeted to nucleic acid molecule encoding tumour necrosis factor
CC receptor 1 (TNFR1), where the antisense compound inhibits expression of
CC TNFR1. The antisense compound is useful for inhibiting the expression of
CC TNFR1 in cells or tissues. The antisense compound is also useful for
CC treating an animal (preferably human) having a disease or condition
CC associated with TNFR1, e.g. a liver disease (such as hepatitis, or liver
CC injury) or a hyperproliferative disorder such as cancer, by inhibiting
CC the expression of TNFR1. The antisense compound is useful for
CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC This polynucleotide sequence represents a human oligonucleotide relating
CC to the TNFR1 of the invention
XX
SQ Sequence 18 BP; 0 A; 9 C; 1 G; 8 T; 0 U; 0 Other;
Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 105 CCCCTCGTCTGCTT 120
Db 3 CCCCTCTCTCTGCTT 18
RESULT 333
ABK63840/c
ID ABK63840 standard; DNA; 18 BP.
XX
AC ABK63840;
XX
DT 18-JUN-2002 (first entry)
XX
DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #4.
XX
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;
XX immune disorder; autoimmune disorder; cardiovascular disorder;
XX vascular disorder; airway disorder; neuropathic disorder; pain;
XX psychiatric disorder; central nervous system disorder; inflammation;
XX respiratory condition; ophthalmic condition; intestinal condition;
XX demyelinating disease; small cell lung cancer; depression;
XX hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
XX neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
XX neuro-pathological disorder; stress; antisense; primer; ss.
OS Homo sapiens.
XX
XX ADD40778/c
XX WO200213799-A2.
XX
XX 21-FEB-2002.

XX
PF 17-AUG-2001; 2001WO-IB001510.
XX
PR 18-AUG-2000; 2000US-0226086P.
XX
XX (UYMC-) UNIV MCGILL.
XX
PA Henry JL, Cahill CM, Yashpal K;
XX
PI WPI; 2002-241835/29.
XX
DR
XX
XX Treating pathological condition involving neurokinin receptor-1, e.g.
PT pain or inflammation, by administering oligonucleotide or a non-
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
PT pathway.
XX
PS Claim 24; Page 65; 100pp; English.
XX
XX The invention relates to a method of treating a pathological condition
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)
CC receptor, especially treating, attenuating or preventing pain or
CC inflammatory condition. The method comprises administering to a mammal, a
CC compound chosen from an oligonucleotide, its analogue, and a disruptor
CC which interferes with function or production of NK-1 receptors. The
CC method is useful for treating a pathological condition characterised by
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,
CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,
CC psychiatric and central nervous system disorders (e.g. anxiety,
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or
CC peripheral aspects of chronic or acute pain, and for treating,
CC attenuating or preventing pain or inflammation such as peripheral,
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or
CC pain relating to psychiatric disorders and central nervous system
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
CC in a mammal, in particular human. NK-1 receptor related disorders,
CC diseases, or pathological conditions treatable by this method include
CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and
CC Crohn's disease), cardiovascular conditions (stroke), chronic
CC gastrointestinal tract inflammation, and inflammatory diseases such as
CC inflammatory bowel diseases. Other disorders and diseases include
CC cardiovascular pathologies including stroke, chronic inflammatory
CC diseases such as rheumatoid arthritis, demyelinating diseases such as
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
CC disorders such as allergies and poison ivy, vasospastic diseases such as
CC angina, addiction disorders such as alcoholism, neurodegenerative
CC disorders such as acquired immune deficiency syndrome (AIDS) related
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
CC disorders such as peripheral neuropathy, edema, stress related and
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
CC effectively treat chronic conditions and other pathological states
CC without the co-administration of substance P, and reduce the number of
CC activated receptors while not reducing the number of quiescent NK-1
CC receptors. Receptors not chronically stimulated are less affected.
CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1
CC receptor coding sequences and oligonucleotides of the invention
XX
SQ Sequence 18 BP; 3 A; 3 C; 5 G; 7 T; 0 U; 0 Other;
Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 207 CGAATGATTAACGTC 222
Db 16 CAAATGATTAACGTC 1
RESULT 334
ADD40778/c
ID ADD40778 standard; DNA; 18 BP.
XX

```

AC ADD40778;
XX
XX 15-JAN-2004 (first entry)
XX
XX Human tenascin-W PCR primer #6.
XX
XX Tenascin-W; stem cell marker; cancer; thrombosis; wound healing;
XX atherosclerosis; osteogenesis; bone healing; osteoporosis;
XX excessive bone growth; cytosatic; osteopathic; anticoagulant;
XX thrombolytic; vulnerary; antiarteriosclerotic;
XX extracellular matrix molecule; metastatic tumour; periosteum; human; PCR;
XX primer; ss.
XX
XX Homo sapiens.
XX
XX WO2003080663-A2.
XX
XX 02-OCT-2003.
XX
XX 26-MAR-2003; 2003WO-EP003150.
XX
XX 27-MAR-2002; 2002GB-00007224.
XX
XX (NOVS ) NOVARTIS FORSCHUNGSSTIFTUNG ZWEIGNIEDERL.
XX
XX Chiquet-Ehrismann R, Scherberich A;
XX
XX WPI; 2003-876907/81.
XX
XX New tenascin-W polypeptide and nucleic acid molecule, useful for
XX manufacturing a medicament for the prophylaxis or treatment of cancer, or
XX a condition requiring increased tenascin-W levels, e.g. wound healing or
XX atherosclerosis.
XX
XX Example 3; SEQ ID NO 22; 84bp; English.
XX
XX The present invention relates to tenascin-W proteins (ADD40758 and
XX ADD40760) and their coding sequences (ADD40757 and ADD40759). Tenascin-W
XX is an extracellular matrix molecule that is specifically expressed in
XX metastatic tumour cells and in the peritoneum, the stem cell compartment
XX for osteogenesis. Tenascin-W is useful as a stem cell marker and are
XX useful for the treatment of cancer, including metastatic cancer (e.g. a
XX solid tumour, glioblastoma, prostate, lung, colorectal, osteo- or breast
XX carcinoma), any disease or condition requiring increased tenascin-W
XX levels (e.g. thrombosis, wound healing or atherosclerosis), a condition
XX ameliorated by the promotion of osteogenesis (e.g. bone healing or
XX osteoporosis) or a bone disease resulting from excessive bone growth. The
XX present sequence is a PCR primer, which was used to isolate the coding
XX sequence for human tenascin-W.
XX
XX Sequence 18 BP; 2 A; 1 C; 11 G; 4 T; 0 U; 0 Other;
XX
XX
XX Query Match 0.8%; Score 14.4; DB 1; Length 18;
XX Best Local Similarity 93.8%; Pred. No. 2.6e+02;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1276 ACCACCATCTCCACAG 1291
XX |||||
XX Db 16 ACCACCTCTCCACAG 1
XX
XX RESULT 335
XX ADEI3426/c
XX ID ADEI3426 standard; DNA; 18 BP.
XX
XX ADEI3426;
XX
XX 29-JAN-2004 (first entry)
XX
XX HLA class I allele specific primer #42.
XX
XX ss; primer; PCR; human; Human Leukocyte Antigen; HLA; genotype.
XX

```

```

OS Homo sapiens.
XX
XX US2003165884-A1.
XX
XX 04-SEP-2003.
XX
XX 25-APR-2002; 2002US-00133779.
XX
XX 20-DEC-1999; 99US-0172768P.
XX
XX 20-DEC-2000; 2000US-00747391.
XX
XX (STEM-) STEMCTYE INC.
XX
XX Chow R, Tonaï R;
XX
XX WPI; 2003-874916/81.
XX
XX Identifying class I or II Human Leukocyte Antigen genotypes using
XX hybridization and amplification assays.
XX
XX Claim 7; SEQ ID NO 42; 66bp; English.
XX
XX The invention relates to a method of identifying a class I or II Human
XX Leukocyte Antigen (HLA) genotype of a subject using hybridisation and
XX amplification assay. The method is used for determining the HLA genotype
XX of a subject. The present sequence represents a HLA class I allele
XX specific primer.
XX
XX Sequence 18 BP; 5 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
XX
XX
XX Query Match 0.8%; Score 14.4; DB 1; Length 18;
XX Best Local Similarity 93.8%; Pred. No. 2.6e+02;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 438 CGCGAGGCGCTTCATG 453
XX |||||
XX Db 18 CGCGAGGCGCTTCATG 3
XX
XX RESULT 336
XX ADL09276/c
XX ID ADL09276 standard; DNA; 18 BP.
XX
XX ADL09276;
XX
XX 06-MAY-2004 (first entry)
XX
XX HLA locus-specific capture oligonucleotide #42.
XX
XX ss; primer; human leukocyte antigen; HLA; HLA genotyping; human; PCR.
XX
XX Homo sapiens.
XX
XX US6670124-B1.
XX
XX 30-DEC-2003.
XX
XX 20-DEC-2000; 2000US-00747391.
XX
XX 20-DEC-1999; 99US-0172768P.
XX
XX (STEM-) STEMCTYE INC.
XX
XX Chow R, Tonaï R;
XX
XX WPI; 2004-068584/07.
XX
XX Identifying an HLA genotype of a subject by hybridizing the amplification
XX products with an HLA locus-specific capture oligonucleotide and detecting
XX the detectable complexes to identify the HLA genotype of the subject.
XX
XX Example 1; SEQ ID NO 42; 66bp; English.
XX

```

CC The invention describes a method of identifying a human leukocyte antigen
CC (HLA) genotype of a subject comprising: obtaining a sample comprising a
CC template nucleic acid from the subject; amplifying the template nucleic
CC acid with HLA allele-specific forward primers and HLA allele-specific
CC reverse primers to form amplification products; hybridizing the
CC amplification products with an HLA locus-specific capture oligonucleotide
CC ; and detecting the detectable complexes to identify the HLA genotype of
CC the subject. The present sequence represents one of 276 HLA locus-
CC specific capture oligonucleotides of the invention.

XX Sequence 18 BP; 5 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 0.8%; Score 14.4; DB 1; Length 18;

Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 438 CGCGAGGCGCTTCATG 453
|||
Db 18 CGCGAGGCGCTTCATG 3

RESULT 337

ADN35828
ID ADN35828 standard; DNA; 18 BP.

XX
AC ADN35828;

XX
DT 01-JUL-2004 (first entry)

XX
DE Human NSCLC gene antisense-S oligonucleotide #44.

XX
KW ss; cytosratic; gene therapy; vaccine; non-small cell lung cancer; NSCLC;

XX
KW diagnosis; cancer; URLC1; antisense.

XX
OS Homo sapiens.

XX
PN WO2004031413-A2.

XX
PD 15-APR-2004.

XX
PE 22-SEP-2003; 2003WO-JP012072.

XX
PR 30-SEP-2002; 2002US-0414673P.

XX
PR 28-FEB-2003; 2003US-0451374P.

XX
PR 28-APR-2003; 2003US-046100P.

XX
PA (ONCO-) ONCOTHERAPY SCI INC.

XX
PA (UITY) UNIV TOKYO.

XX
PI Nakamura Y, Daigo Y, Nakatsuru S;

XX
DR WPI; 2004-330206/30.

XX
PT Diagnosing, preventing and treating non-small cell lung cancer (NSCLC)
PT comprises determining an expression level of an NSCLC-associated gene in
PT a sample.

XX
PS Disclosure; SEQ ID NO 509; 394bp; English.

XX
CC The invention relates to a method of diagnosing non-small cell lung
CC cancer (NSCLC) or a predisposition to developing NSCLC in a subject by
CC determining the expression level of a NSCLC-associated gene in a
CC biological sample derived from the subject, where an increase or decrease
CC of the level compared to a normal control level of the gene indicates
CC that the subject suffers from or is at risk of developing NSCLC. The
CC method is useful in diagnosing NSCLC or a predisposition to developing
CC NSCLC in a subject. The compound, polynucleotide and the encoded
CC polypeptide and composition are useful in treating or preventing NSCLC.
CC This sequence corresponds to an antisense oligonucleotide of genes that
CC are differentially expressed in NSCLC cells.

XX
XX Sequence 18 BP; 4 A; 8 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1277 CCACCATCTCCACAGT 1292
|||
Db 3 CGGCATCTCCACAGT 18

RESULT 338

ADRO6011
ID ADRO6011 standard; DNA; 18 BP.

XX
AC ADRO6011;

XX
DT 21-OCT-2004 (first entry)

XX
DE Human TNFR1 antisense oligonucleotide seqid 9.

XX
KW cytosratic; gene therapy; apoptosis inhibitor;

XX
KW radiation-induced apoptosis; tumour necrosis factor receptor 1; TNFR1;

XX
KW human; antisense oligonucleotide; antisense technology; ss.

XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers

FT modified_base 1..18

FT /*tag= b

FT /mod_base= OTHER

FT /note= "OTHER= Phosphorothioate backbone"

FT modified_base 1..4

FT /*tag= a

FT /mod_base= OTHER

FT /note= "OTHER= Optionally 2'-O-Methoxyethyl (2'-MOE)

FT nucleotides"

FT /*tag= c

FT /mod_base= OTHER

FT /note= "OTHER= Optionally 2'-O-Methoxyethyl (2'-MOE)

FT nucleotides"

FT US2004147471-A1.

XX
XX 29-JUL-2004.

XX
XX PD 06-NOV-2003; 2003US-00702817.

XX
XX PE 26-JUN-1998; 98US-00106038.

XX
XX PR 17-JUN-1999; 99WO-US013763.

XX
XX PR 24-OCT-2000; 2000US-00695451.

XX
XX (ZHAN/) ZHANG H.

XX
XX Zhang H;

XX
XX WPI; 2004-561407/54.

XX
XX PT Inhibiting radiation-induced apoptosis in a cell or tissue comprises
XX administering to the cell or tissue an antisense oligonucleotide targeted
XX to a nucleic acid molecule encoding tumor necrosis factor receptor 1.

XX
XX PS Example 10; SEQ ID NO 9; 24bp; English.

XX
XX CC The invention describes a method of inhibiting radiation-induced
XX apoptosis in a cell or tissue comprising administering to the cell or
XX tissue an antisense oligonucleotide of 8-30 nucleotides in length
XX targeted to a nucleic acid molecule encoding tumor necrosis factor
XX receptor 1 (TNFR1). The method and antisense oligonucleotides are useful
XX for inhibiting radiation-induced apoptosis in a cell or tissue, and for
XX treating diseases associated with the expression of TNFR1. This sequence
XX represents a human tumour necrosis factor receptor 1 (TNFR1) antisense
XX oligonucleotide.

SQ Sequence 18 BP; 0 A; 9 C; 1 G; 8 T; 0 U; 0 Other;

Query Match 0.8%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 105 CCCTCCTGCTGCTTT 120
 |||||
 DB 3 CCCTCCTGCTGCTTT 18

RESULT 339
 ADX58092/c
 ID ADX58092 standard; DNA; 17 BP.
 XX
 AC ADX58092;
 XX
 DT 21-APR-2005 (first entry)
 XX
 DE Primer Gamma 15 for single chain antibody heavy chain variable fragment.
 XX
 XX virucide; vaccine; single chain antibody; HSV; glycoprotein;
 KM glycoprotein D; herpes simplex virus; HSV infection; RT-PCR; primer; ss;
 KM heavy chain.
 XX
 OS Synthetic.
 XX
 PN WO2005011580-A2.
 XX
 PD 10-FEB-2005.
 XX
 PP 26-JUL-2004; 2004WO-US024013.
 XX
 PR 25-JUL-2003; 2003US-0489984P.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Simmons A, Chen J;
 XX
 DR WPI; 2005-142827/15.
 XX
 PT New single chain antibody that specifically binds to a Herpes Simplex
 PT Virus (HSV) glycoprotein, useful in preparing a composition for
 PT preventing or treating a HSV infection.
 XX
 PS Example 1; SEQ ID NO 30; 99PD; English.
 XX
 CC The specification describes a single chain antibody that specifically
 CC binds to a herpes simplex virus (HSV) glycoprotein, e.g. glycoprotein D.
 CC The single chain antibody of the invention is useful for preparing a
 CC composition for preventing or treating a HSV infection. C region RT-PCR
 CC primer ADX58077 with gamma degenerate signal sequence RT-PCR primers
 CC ADX58078-ADX58094 were used to amplify cDNA encoding single chain
 CC antibody heavy chain variable fragments. The amplicons were used to
 CC generate single chain antibodies of the invention.
 CC
 XX Sequence 17 BP; 5 A; 4 C; 5 G; 1 T; 0 U; 2 Other;
 SQ

Query Match 0.8%; Score 14.2; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 2.4e+02;
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 310 CTTTGGGAGCTGCC 324
 |||||
 DB 17 CTTTGGGAGCTGCC 3

RESULT 340
 AAT76447/c
 ID AAT76447 standard; DNA; 14 BP.
 XX
 AC AAT76447;
 XX

DT 16-SEP-1997 (first entry)
 XX
 DE Substance P receptor antisense oligonucleotide.
 XX
 XX Asthma; airway epithelium; adenovine free; cystic fibrosis;
 KM chronic obstructive pulmonary disease; bronchitis; ss.
 XX
 OS Synthetic.
 XX
 PN WO9640162-A1.
 XX
 PD 19-DEC-1996.
 XX
 PP 06-JUN-1996; 96WO-US009306.
 XX
 PR 07-JUN-1995; 95US-00474497.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 PI Nyce JW, Metzger WJ;
 XX
 DR WPI; 1997-051871/05.
 XX
 PT Treatment of airway diseases such as asthma - by topically applying
 PT adenosine-free antisense oligo:nucleotide to airway epithelium of
 PT subject.
 XX
 PS Example 5; Page 40; 71PP; English.
 XX
 CC A method for treating airway disease in a subject has been produced,
 CC which involves the topical administration of an essentially adenosine
 CC free antisense oligonucleotide (ON) to the airway epithelium of the
 CC subject. The present sequence is an antisense oligonucleotide specific
 CC for the substance P receptor. The method can be used to treat airway
 CC diseases such as cystic fibrosis, asthma, chronic obstructive pulmonary
 CC disease, bronchitis and other airway diseases characterised by an
 CC inflammatory response. By eliminating adenosine from the antisense ON,
 CC its liberation upon antisense degradation is prevented, thereby
 CC preventing adenosine-induced bronchoconstriction in patients with hyper-
 CC reactive airways
 XX
 SQ Sequence 14 BP; 0 A; 2 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 0.8%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 384 AGCCGACAAAGAA 397
 |||||
 DB 14 AGCCGACAAAGAA 1

RESULT 341
 AAX54238/c
 ID AAX54238 standard; DNA; 14 BP.
 XX
 AC AAX54238;
 XX
 DT 05-JUL-1999 (first entry)
 XX
 DE Substance P receptor antisense oligonucleotide fragment.
 XX
 XX Antisense oligonucleotide; multiple target; antisense treatment;
 XX impaired respiration; inflammation; lung disease;
 XX pulmonary vasoconstriction; inflammation; allergic rhinitis;
 KM acute asthma; allergy; asthma; impeded respiration;
 KM respiratory distress syndrome; pain; cystic fibrosis;
 KM pulmonary hypertension; pulmonary vasoconstriction; emphysema;
 KM chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
 KM colon cancer; breast cancer; lung cancer; pancreatic cancer;
 KM hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
 KM prostate cancer; ss.
 XX

OS Synthetic.
XX
PN W09913886-A1.
XX
PD 25-MAR-1999.
XX
PF 17-SEP-1998; 98WO-US019419.
XX
PR 17-SEP-1997; 97US-0059160P.
PR 09-JUN-1998; 98US-00093972.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 1999-229400/19.
XX
PT New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT vasoconstriction.
XX
PS Disclosure; Page 59; 120pp; English.
XX
PS The specification describes antisense oligonucleotides (AA52869-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target genes, gene initiation
CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-
CC end and the junction between coding and non-coding regions and all
CC segments of RNAs encoding proteins associated with one or more diseases,
CC conditions or mixtures. The antisense oligonucleotides may be derived
CC from sequences AA55272-74. These multiple target oligonucleotides
CC (specifically AA55180-271) can be used for the antisense treatment of
CC diseases and conditions. Typical diseases and conditions are those
CC associated with impaired respiration and inflammation, including lung
CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
CC acute asthma, allergies, asthma, impaired respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
CC colon cancer, breast cancer, lung cancer, pancreatic cancer,
CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
CC well as all types of cancers which may metastasize or have metastasized
CC to the lungs, including breast and prostate cancer
XX
SQ Sequence 14 BP; 0 A; 2 C; 4 G; 8 T; 0 U; 0 Other;
Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 384 AGCCCAAAAAGAA 397
Db 14 AGCCCAAAAAGAA 1
RESULT 342
AA533682/C
ID AA533682 standard; DNA; 14 BP.
XX
AC AA533682;
XX
DT 28-JUL-2000 (first entry)
XX
DE Low adenosine antisense oligonucleotide SEQ ID NO:1371.
XX
KM Human; adenosine receptor; low adenosine antisense oligonucleotide;
KM phosphorocholate; impaired respiration; inflammation; allergy;
KM allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KM antiallergic; antiaesthetic; cyostatic; analgesic; impaired airway;
KM lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KM respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KM pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KM cancer; leukemia; lymphoma; carcinoma; metastasis; ss.
XX

OS Homo sapiens.
XX
PN W0200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US017712.
XX
PR 03-AUG-1998; 98US-0095212P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers.
XX
PS Claim 18; Page 436; 1343pp; English.
XX
PS The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiaesthetic, cyostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impaired respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC carcinomas, and cancers which may metastasize to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AA52313 to AA5312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AA52323 to
CC AA53922) are specifically claimed ONs from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO: sequences given in the sequence
CC listing
XX
SQ Sequence 14 BP; 0 A; 2 C; 4 G; 8 T; 0 U; 0 Other;
Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 384 AGCCCAAAAAGAA 397
Db 14 AGCCCAAAAAGAA 1
RESULT 343
AA289118
ID AA289118 standard; DNA; 14 BP.
XX
AC AA289118;
XX
DT 02-JUN-2000 (first entry)
XX
DE Rice OPR17 PCR primer #1.
XX
KM Molecular marker; rice; PCR primer; PABD marker; SCAR marker; ss.
XX
OS Oryza sativa.

XX CN1237328-A.
 PN 08-DEC-1999.
 XX 10-APR-1999; 99CN-00103764.
 XX 10-APR-1999; 99CN-00103764.
 XX (ANHU-) ANHU ACAD AGRIC SCI.
 XX Yang J, Wang X, Li L;
 PI WPI; 2000-238142/21.
 XX Application of molecular marking technique in quick determination of true
 PT or false and purity of hybrid rice seed.
 XX Example 5; Page 10; 12pp; Chinese.
 XX This invention describes a novel molecular marking technique which allows
 CC the quick and accurate determination of authenticity and purity of rice
 CC hybridized combination and hybrid species. The method involves designing
 CC stable PCR primers from a PAPD marker and utilizing SCAR markers to make
 CC the determination of authenticity and purity of rice hybridized
 CC combination and hybrid species in 1-2 days. Accuracy is identical to that
 CC of planting determination, and is reliable. AA89110-289135 represent
 CC primers used in the method of the invention
 XX SQ Sequence 14 BP; 3 A; 6 C; 2 G; 3 T; 0 U; 0 Other;
 Query Match 0.8%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 232 GACTCAGACCTCTC 245
 DB 1 GACTCAGACCTCTC 14
 RESULT 344
 AAF19804/C
 ID AAF19804 standard; DNA; 14 BP.
 XX AAF19804;
 AC 14-MAR-2001 (first entry)
 DT Human substance P receptor polynucleotide fragment #1371.
 XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antihistatic; analgesic; hypotensive; cytostatic;
 KW surfactant hypoproduction; pulmonary obstruction; impeded respiration;
 KW respiratory distress syndrome; pain; cystic fibrosis; asthma; RDS;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX OS Homo sapiens.
 XX WO200062736-A2.
 XX 26-OCT-2000.
 XX 24-MAR-2000; 2000WO-US008020.
 XX 06-APR-1999; 99US-0127958P.
 XX (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.

XX NYCE JW;
 PI WPI; 2000-679539/66.
 DR Low adenosine (A) content antisense oligonucleotides which do not trigger
 PT adenosine receptors during metabolism, useful e.g. for treating cancers
 PT and respiratory obstructions.
 XX Claim 14; Page 245; 1592pp; English.
 PS The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (i) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (i) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antihistatic, hypotensive and cyostatic activities.
 CC The antisense oligonucleotides and (i) can be used to down-regulate the
 CC expression and/or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system peptide
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive proteins. The
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
 CC surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention
 XX SQ Sequence 14 BP; 0 A; 2 C; 4 G; 8 T; 0 U; 0 Other;
 Query Match 0.8%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 384 AGCCCAAAAAGAA 397
 DB 14 AGCCCAAAAAGAA 1
 RESULT 345
 AB272765
 ID AB272765 standard; RNA; 14 BP.
 XX AB272765;
 AC 09-APR-2003 (first entry)
 DT Rod opsin hairpin ribozyme target oligonucleotide SEQ ID NO:5.
 XX Hairpin ribozyme; hammerhead ribozyme; retinal disease; target;
 KW ophthalmological; gene therapy; eye; retinal dysfunction; AAV;
 KW diabetic retinopathy; macular degeneration; autosomal dominant retinitis;
 KW blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.
 XX OS Homo sapiens.
 XX WO200288320-A2.
 XX 07-NOV-2002.

XX	OS	Homo sapiens.
XX	PN	WO200285308-A2.
XX	PD	31-OCT-2002.
XX	PP	23-APR-2002; 2002WO-US013135.
XX	PR	24-APR-2001; 2001US-0286137P.
XX	PA	(EP1G-) EPIGENESIS PHARM INC.
XX	PI	Nyge JW, Li Y, Sandrasegura A, Katz E, Pabalan J, Aguilar D;
XX	PI	Miller S, Tang L, Shahabuddin S;
XX	DR	WPI; 2003-229219/22.
XX	PT	Pharmaceutical composition for treating ailments associated with impaired
XX	PT	respiration, has oligo(s) antisense to specific gene(s) or its
XX	PT	corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX	PT	ubiquinone.
XX	PS	Disclosure; SEQ ID NO 10740; 872pp; English.
XX	CC	The invention relates to a novel pharmaceutical composition, which has a
XX	CC	first active agent comprising an oligonucleotide antisense to the
XX	CC	initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX	CC	5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX	CC	junctions of genes encoding a polypeptide associated with lung and/or
XX	CC	nasal airway dysfunction and a second active agent comprising an
XX	CC	antiinflammatory steroid and ubiquinone. A composition of the invention
XX	CC	has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX	CC	immunosuppressive, and cytostatic activity. The composition may have a
XX	CC	use in antisense gene therapy. The composition is useful for treating or
XX	CC	preventing a respiratory, lung or malignant disease or condition, also
XX	CC	for enhancing the prophylactic or therapeutic respiratory effect of an
XX	CC	antiinflammatory steroid in a subject, for reducing or depleting levels
XX	CC	of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX	CC	receptor, producing bronchodilation, increasing levels of ubiquinone or
XX	CC	lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX	CC	lung inflammation, lung allergies, or a respiratory disease or condition.
XX	CC	Note: The sequence data for this patent is not represented in the printed
XX	CC	specification, but was obtained in electronic format directly from WIPO
XX	CC	at ftp.wipo.int/pub/published_pct_sequences
XX	XX	Sequence 14 BP; 0 A; 2 C; 4 G; 8 T; 0 U; 0 Other;
XX	XX	Query Match 0.84; Score 14; DB 1; Length 14;
XX	XX	Best Local Similarity 100.0%; Pred. No. 1.6e+02;
XX	XX	Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	QY	384 AGCCCAACAAAGAA 397
XX	Db	
XX		14 AGCCCAACAAAGAA 1
XX	RESULT 347	
XX	ABD19637/c	
XX	ID ABD19637 standard; DNA; 14 BP.	
XX	AC ABD19637;	
XX	DT 29-JUL-2004 (first entry)	
XX	DE Human substance P receptor DNA fragment 1362.	
XX	XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;	
XX	XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;	
XX	XX surfactant depletion; anti-allergic; antiinflammatory; antiasthmatic;	
XX	XX analgesic; hypotensive; immunosuppressive; cytosstatic; cystic fibrosis;	
XX	XX beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;	
XX	XX respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;	

KW	emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW	pulmonary transplantation rejection; ds.
XX	
XX	Homo sapiens.
XX	
XX	WO200285309-A2.
XX	
XX	31-OCT-2002.
XX	
XX	23-APR-2002; 2002WO-US013143.
XX	
XX	24-APR-2001; 2001US-0286036P.
XX	
XX	(EP1G-) EP1GENESIS PHARM INC.
XX	
XX	Nyze JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX	Miller S, Tang L, Shahbuddin S;
XX	
XX	WPI; 2003-093058/08.
XX	
XX	Pharmaceutical composition for treating asthma, has antisense
XX	oligonucleotide containing less percentage of adenosine, targeted to
XX	nucleic acids associated with lung airway or lung dysfunction, and
XX	bronchodilating agent.
XX	
XX	Claim 15; SEQ ID NO 10740; 7633P; English.
XX	
XX	This invention describes a novel composition (a) a first active agent,
XX	comprising oligonucleotides, effective for alleviating
XX	bronchoconstriction, respiratory tract inflammation, allergies and
XX	reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
XX	surfactant depletion or hyposecretion, when administered to a mammal. The
XX	oligonucleotides are derived from a gene encoding or regulating
XX	expression of a target polypeptide associated with lung airway or lung
XX	dysfunction or cancer and can be anti-sense to the corresponding mRNA.
XX	The invention also describes a kit, that comprises: (a) a delivery
XX	device, in separate containers, (b) the oligonucleotides, (c)
XX	instructions for adding a carrier and for use of the kit. The composition
XX	of the invention has anti-allergic, anti-inflammatory, antiasthmatic, is a
XX	analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
XX	beta-adrenergic agonist. The composition is useful for preventing or
XX	creating a respiratory, lung or malignant disease. The administered
XX	composition comprises oligo and is administered to reduce the production
XX	or availability, or to increase the degradation of the target mRNA or to
XX	reduce the amount of target polypeptide present in the lungs. The
XX	pulmonary obstruction, and/or surfactant hypoproduction and/or lung
XX	inflammation, allergies and/or bronchoconstriction are associated
XX	with a disease or condition such as pulmonary vasoconstriction,
XX	inflammation, allergies, asthma, impeded respiration, respiratory
XX	distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
XX	hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
XX	transplantation rejection, pulmonary infections, bronchitis or cancer.
XX	The reduced adenosine content of the anti-sense oligos corresponding to
XX	thymidines present in the target RNA serves to prevent the breakdown of
XX	the oligonucleotides into products that free adenosine into the system
XX	e.g., lung, brain, heart, kidney, etc. tissue environment and thereby, to
XX	prevent any unwanted effects due to it
XX	
SQ	Sequence 14 BP; 0 A; 2 C; 4 G; 8 T; 0 U; 0 Other;
	Query Match 0.8%; Score 14; DB 1; Length 14;
	Best Local Similarity 100.0%; Pred. No. 1.6e+02;
	Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	384 AGCCCAAAAAGAA 397
DB	14 AGCCCAAAAAGAA 1
RESULT 348	
ID	AAQ90578 standard; DNA; 15 BP.
XX	

AC	AAQ90578.	
XX		
DT	01-FEB-1996	(first entry)
DE	Encodes recombinant bile salt-activated lipase N-terminal sequence.	
XX		
KW	Bile salt activated lipase; BAL; C-terminal repeat; ss.	
XX		
OS	Synthetic.	
XX		
PN	JP0711891-A.	
XX		
PD	02-MAY-1995.	
XX		
PP	30-SEP-1993;	93JP-00245079.
XX		
PR	30-SEP-1993;	93JP-00245079.
XX		
PA	(MEIP) MEIJI MILK PROD CO LTD.	
XX		
DR	WPI; 1995-196318/26.	
DE	P-PSDB; AAR75106.	
XX		
PT	New recombinant bile salt-activating lipase(s), DNA encoding them and	
PT	vectors - useful for high level expression of the lipase(s) by fermenter-	
XX	culturing.	
PS		
XX	Claim 3; Page 10; 31p; Japanese.	
CC		
CC	New lipases are ones in which 1-15 repeats of any of the sequences	
CC	AAR75099-R75105 (encoded by AAQ90570-Q90576) are attached to the C-	
CC	terminus of the bile salt-activated lipase (BAL) of sequence AAR75098	
CC	(encoded by AAQ90569) and/or in which the amino acid sequence SWTGS	
CC	(encoded by AAQ90578) is attached to the N-terminus of the BAL. The	
CC	recombinant lipases can be produced by fermentation in transformed <i>E. coli</i>	
CC	pastoris GS 115 host cells	
XX		
SQ	Sequence 15 BP; 5 A; 3 C; 3 G; 4 T; 0 U; 0 Other;	
XX		
Query Match	0.8%; Score 14; DB 1; Length 15;	
Best Local Similarity	100.0%; Pred.No. 1.9e+02;	
Matches 14; Conservative	0; Mismatches 0; Indels	0
QY	1133 TCATGACGAGTTC 1146	
DB	1 TCATGACGAGTTC 14	
RESULT 349		
AAV93851		
ID	AAV93851 standard; RNA; 15 BP.	
XX		
AC	AAV93851;	
XX		
DT	18-FEB-1999	(first entry)
DE	Target sequence with sequence homology to C-raf and B-raf position 426.	
XX		
KW	Human; c-raf; A-raf; B-raf; hamsterhead ribozyme; hairpin ribozyme;	
KW	target; substrate; catalyst; modulation; expression; Raf gene; delivery;	
KW	screening; identification; synthesis; deprotection; purification; cancer;	
KW	inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;	
KW	restenosis; rheumatoid arthritis; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	W09850530-A2.	
XX		
PD	12-NOV-1998.	
XX		
PP	05-MAY-1998;	98MO-US009249.
XX		
PR	09-MAY-1997;	97US-0046059P.

PR 09-JUN-1997; 97US-0049002P.
PR 03-JUN-1997; 97US-0051718P.
PR 22-AUG-1997; 97US-0056808P.
PR 02-OCT-1997; 97US-0061321P.
PR 02-OCT-1997; 97US-0061324P.
PR 05-NOV-1997; 97US-0064866P.
PR 19-DEC-1997; 97US-0068212P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L,
PI Parry T, Beigelman L, Mcswigen JA, Karpelisy A, Burgin A;
PI Thompson J, Workman CT, Beaudry A, Sweedler D;
XX
XX WPI; 1999-009494/01.
XX
XX
XX Identifying new catalytic nucleic acid that modulates selected processes
PT - especially ribozymes that cleave Raf RNA for treating cancer,
PT restenosis, and also new ribozymes and modified nucleoside triphosphates
PT used as antiviral agents and synthons.
XX
XX
XX Claim 180; Page 177; 259pp; English.
XX
XX
XX A method has been developed for the identification of a nucleic acid
CC capable of modulating a process in a biological system. The method
CC comprises: (a) introducing into the system a random library of nucleic
CC acid catalyses (NAC) having a substrate binding domain (SBD), comprising
CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
CC in systems where modulation has occurred and/or determining the sequence
CC of at least part of the SBDs in such systems. Nucleic acid molecules with
CC endonuclease activity and catalytic activity, from the present invention,
CC are used to modulate gene expression in plant and mammalian cells and to
CC cleave target nucleic acid, particularly for treating systemic diseases
CC caused by infectious RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
CC acetosis and infection. They may also be used to detect genetic drift and
CC mutations in diseased cells and to determine c-rat RNA. Specifically NACs
CC with RNA-cleaving activity that modulate expression of the Raf gene, are
CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
CC generally any condition associated with the level of c-rat. Introduction
CC of sugar/phosphate modifications increases stability against nuclease and
CC activity. AAV90922 to AAV93877 represent NACs that can be used in the
CC method, specifically for modulating the expression of a Raf gene
XX
SQ Sequence 15 BP; 2 A; 6 C; 0 G; 0 T; 7 U; 0 Other;
Query Match 0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 57.1%; Pred. No. 1.9e+02;
Matches 8; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
Qy 1004 ACATCTTCTCCTC 1017
Db 1 ACAUCUUCUCCUC 14
RESULT 350
ABK63843/c
ID ABR63843 standard; DNA; 15 BP.
XX
AC ABR63843;
XX
DT 18-JUN-2002 (first entry)
XX
DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #7.
XX
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;
KW immune disorder; autoimmune disorder; cardiovascular disorder;
KW vascular disorder; airway disorder; neuropathic disorder; pain;
KW psychiatric disorder; central nervous system disorder; inflammation;
KW respiratory condition; ophthalmic condition; intestinal condition;
KW demyelinating disease; small cell lung cancer; depression;
KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
KW neuro-pathological disorder; stress; antisense; primer; ss.

XX
OS Homo sapiens.
XX
XX WO200213799-A2.
XX
XX 21-FEB-2002.
XX
XX 17-AUG-2001; 2001WO-IB001510.
XX
XX 18-AUG-2000; 2000US-0226086P.
XX
XX (UYMC-) UNIV MCGILL.
XX
PI Henry JL, Cahill CM, Yaehpal K;
XX
XX WPI; 2002-241835/29.
XX
XX
XX Treating pathological condition involving neurokinin receptor-1, e.g.
PT pain or inflammation, by administering oligonucleotide or a non-
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
PT pathway.
XX
XX
XX Claim 24; Page 65; 100pp; English.
XX
XX
XX The invention relates to a method of treating a pathological condition
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)
CC receptor, especially treating, attenuating or preventing pain or
CC inflammatory condition. The method comprises administering to a mammal, a
CC compound chosen from an oligonucleotide, its analogue, and a disruptor
CC which interferes with function or production of NK-1 receptors. The
CC method is useful for treating a pathological condition characterised by
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,
CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,
CC psychosocial and central nervous system disorders (e.g. anxiety,
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or
CC peripheral aspects of chronic or acute pain, and for treating,
CC attenuating or preventing pain or inflammation such as peripheral,
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or
CC pain relating to psychiatric disorders and central nervous system
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
CC in a mammal, in particular human. NK-1 receptor related disorders,
CC diseases, or pathological conditions treatable by this method include
CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and
CC Crohn's disease), cardiovascular conditions (stroke), chronic
CC gastrointestinal tract inflammation, and inflammatory diseases such as
CC cardiovascular pathologies including stroke, chronic inflammatory
CC diseases such as rheumatoid arthritis, demyelinating diseases such as
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
CC disorders such as allergies and poison ivy, vasospastic diseases such as
CC angina, addiction disorders such as alcoholism, neurodegenerative
CC disorders such as acquired immune deficiency syndrome (AIDS) related
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
CC disorders such as peripheral neuropathy, oedema, stress related and
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
CC effectively treat chronic conditions and other pathological states
CC without the co-administration of substance P, and reduce the number of
CC activated receptors while not reducing the number of quiescent NK-1
CC receptors. Receptors not chronically stimulated are less affected.
CC reducing side effects of treatment. ABR63834-ABK63906 represent NK-1
CC receptor coding sequences and oligonucleotides of the invention
XX
SQ Sequence 15 BP; 3 A; 3 C; 2 G; 7 T; 0 U; 0 Other;
Query Match 0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 209 AATGATTAACGTC 222
Db 14 AATGATTAACGTC 1

RESULT 351
 AAT94355
 ID AAT94355 standard; DNA; 16 BP.
 AC AAT94355;
 XX
 XX
 XX 04-MAR-1998 (first entry)
 DT
 DE Human DPC4 sequence tagged site sense primer D18s479.
 XX
 XX DPC4; pancreatic cancer; deleted; locus 4; diagnosis; human;
 KM tumour suppressor gene; proliferative disease; PCR primer;
 KM sequence tagged site; STS; ss.
 XX
 XX Synthetic.
 OS Homo sapiens.
 XX
 XX WO9726271-A1.
 PN
 XX 24-JUL-1997.
 PD
 XX 17-JAN-1997; 97WO-US000827.
 PF
 XX 19-JAN-1996; 96US-00588821.
 PR
 XX (UYUO) UNITV JOHNS HOPKINS SCHOOL MEDICINE.
 PA
 XX Kern SE, Hahn SA;
 PI
 XX WPI; 1997-385290/35.
 DR
 XX Deleted in Pancreatic Cancer locus 4 polypeptide - and related nucleic
 PT acids, used in diagnosis and treatment of proliferative diseases, e.g.
 PT cancer of pancreas or other organs.
 XX
 XX Example 2; Page 56; 104pp; English.
 PS
 XX The present sequence represents a sequence tagged site (STS) primer used
 CC in the isolation of cosmids from the DPC4 (deleted in pancreatic cancer,
 CC locus 4) region, and gene identification. DPC4 is a tumour suppressor
 CC gene. Detection of truncated DPC4 protein, or of homozygous deletions or
 CC intragenic mutations in nucleic acid encoding it, is used to diagnose (in
 CC vivo or in vitro) proliferative diseases, especially pancreatic
 CC carcinoma, bile duct, bladder or colorectal cancer, Crohn's disease,
 CC colitis-associated neoplasia or chronic ulcerative colitis. These
 CC conditions, where associated with a homozygous deletion, can be treated
 CC by administering an agent that: (a) modulates DPC4 expression,
 CC specifically a sense DPC4 sequence (particularly in the form of a vector,
 CC i.e. by gene therapy), but also an antisense sequence where DPC4 protein
 CC is over expressed or (b) mimics the activity of DPC4. DPC4 nucleic acid
 CC is also used as hybridisation probes for detecting presence/absence of
 CC human chromosome 18q21.1 fragments. When a homozygous deletion is
 CC detected in this region, an agent can be administered that accumulates
 CC within, or kills, only cells which contain such a deletion. This agent
 CC exploits the absence of an enzyme (or other protein) encoded by a
 CC neighbouring gene and lost by the deletion, i.e. it has a highly
 CC selective action
 CC
 XX
 XX Sequence 16 BP; 5 A; 4 C; 5 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 0.8%; Score 14; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. NO. 2.2e+02; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 730 ATGCCAGCAGAGT 743
 2 ATGCCAGCAGAGT 15
 RESULT 352
 AAV11865

ID AAV11865 standard; cDNA; 17 BP.
 XX
 XX AAV11865;
 AC
 XX 11-SEP-1998 (first entry)
 DT
 DE Mus musculus Tub Interactor gene PCR primer.
 XX
 XX
 XX PCR primer; tub interactor; treatment; obesity; cachexia;
 KM anorexia nervosa; diabetes; cell cycle progression; apoptosis;
 KM neurodegenerative disease; Alzheimer's disease; drug screening;
 KM Parkinson's disease; Huntington's chorea; detection; diagnosis;
 KM amyotrophic lateral sclerosis; spinocerebellar degeneration; ss.
 XX
 XX Synthetic.
 OS Mus musculus.
 XX
 XX WO9812302-A1.
 PN
 XX 26-MAR-1998.
 PD
 XX 05-SEP-1997; 97WO-US015627.
 PF
 XX 17-SEP-1996; 96US-00715032.
 PR
 XX 21-JUL-1997; 97US-00897340.
 PR
 XX (MILL-) MILLENNIUM PHARM INC.
 PA
 XX Gimeno CJ, Errada PR;
 PI
 XX WPI; 1998-217246/19.
 DR
 XX Tub interactor genes - used to develop products for the treatment of
 PT obesity, cachexia, anorexia nervosa or related disorders e.g. diabetes.
 PT
 XX Disclosure; Page 81; 120pp; English.
 PS
 XX The sequence is that of a PCR primer used in the identification of Tub
 CC Interactor (TI) gene mTI-3
 CC
 CC
 XX
 XX Sequence 17 BP; 5 A; 6 C; 3 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 0.8%; Score 14; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. NO. 2.6e+02; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 571 TACTGCATGACGCG 584
 3 TACTGCATGACGCG 16
 QY
 RESULT 353
 AAV93331
 ID AAV93331 standard; RNA; 17 BP.
 AC AAV93331;
 XX
 XX 18-FEB-1999 (first entry)
 DT
 DE Human B-raf substrate nucleotide position 425.
 XX
 XX Human; c-raf; A-raf; B-raf; hamsterhead ribozyme; hairpin ribozyme;
 KM target; substrate; catalyst; modulation; expression; Raf gene; delivery;
 KM screening; identification; synthesis; deprotection; purification; cancer;
 KM inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
 KM restenosis; rheumatoid arthritis; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO9850530-A2.
 PN
 XX 12-NOV-1998.
 PD
 XX

PF	05-MAY-1998;	98WO-US009249.
XX	09-MAY-1997;	97US-0046059P.
XX	09-JUN-1997;	97US-0049002P.
PR	03-JUL-1997;	97US-0051718P.
PR	22-AUG-1997;	97US-0056808P.
PR	02-OCT-1997;	97US-0061321P.
PR	02-OCT-1997;	97US-0061322P.
PR	05-NOV-1997;	97US-0064866P.
PR	19-DEC-1997;	97US-0068212P.
XX		
PA	(RIBO-) RIBOZYME PHARM INC.	
PI	Jarvie T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;	
PI	Parry T, Bergelman L, Mcswigen JA, Karpetsky A, Burgin A;	
PI	Thompson J, Workman CT, Beaudry A, Sweedler D;	
XX		
DR	WPI; 1999-009494/01.	
XX		
PT	Identifying new catalytic nucleic acid that modulates selected processes	
PT	- especially ribozymes that cleave Raf RNA for treating cancer,	
PT	restenosis, and also new ribozymes and modified nucleoside triphosphates	
PT	used as antiviral agents and synthons.	
XX		
PS	Claim 177; Page 166; 2592p; English.	
XX		
CC	A method has been developed for the identification of a nucleic acid	
CC	capable of modulating a process in a biological system. The method	
CC	comprises: (a) introducing into the system a random library of nucleic	
CC	acid catalysts (NAC) having a substrate binding domain (SBD), comprising	
CC	a random sequence, and a catalytic domain (CD); and (b) identifying NAC	
CC	in systems where modulation has occurred and/or determining the sequence	
CC	of at least part of the SBDs in such systems. Nucleic acid molecules with	
CC	endonuclease activity and catalytic activity, from the present invention,	
CC	are used to modulate gene expression in plant and mammalian cells and to	
CC	clavate target nucleic acid, particularly for treating systemic diseases	
CC	caused by specific RNA, e.g., cancer, inflammation, psoriasis, non-hepatic	
CC	ascites and infection. They may also be used to detect genetic drift and	
CC	mutations in diseased cells and to determine c-raf RNA. Specifically NACs	
CC	with RNA-cleaving activity that modulate expression of the Raf gene, are	
CC	used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or	
CC	generally any condition associated with the level of c-raf. Introduction	
CC	of sugar/phosphate modifications increases stability against nuclease and	
CC	activity. AAV90922 to AAV93877 represent NACs that can be used in the	
CC	method. AAV90922 for modulating the expression of a Raf gene	
XX		
SO	Sequence 17 BP; 2 A; 6 C; 0 G; 0 T; 9 U; 0 Other;	
XX		
Query Match	0.8%;	Score 14; DB 1; Length 17;
Best Local Similarity	57.1%;	Pred. No. 2.6e+02;
Matches	8; Conservative	6; Mismatches 0; Indels 0; Gaps 0.
QY	1004 ACATCTTCTTCCTC 1017	
	: : :	
Db	3 ACAUCUCUCUCUC 16	
RESULT 354		
AAA59530		
ID	AAA59530 standard; DNA; 17 BP.	
XX		
AC	AAA59530;	
XX		
DT	14-NOV-2000 (first entry)	
XX		
DE	PCR primer used to amplify DNA encoding beta-secretase enzyme.	
XX		
KW	Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;	
KW	amyloid plaque component; Alzheimer's disease; amyloidogenic disease;	
KW	inhibitor; PCR primer; ss.	
XX		
OS	Homo sapiens.	
XX		

PN	W020004761618-A2.
PD	17-AUG-2000.
PF	10-FEB-2000; 2000MO-US003819.
XX	
XX	10-FEB-1999; 99US-0119571P.
PR	15-JUN-1999; 99US-0139172P.
XX	
PA	(ELAN-) ELAN PHARM INC.
XX	
PI	Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M;
PI	Sinha S, Tatsuno G, Tung J, Wang S, Mcconlogue L;
DR	WPI; 2000-533011/48.
XX	
PT	Purified beta-secretase protein used in assays to discover inhibitors
PT	which can be used for the treatment of amyloidogenic diseases e.g.
PT	Alzheimer's disease.
XX	
XX	Example 3; Page 66; 121pp; English.
XX	
CC	The specification describes a beta-secretase enzyme. The enzyme cleaves
CC	beta-amyloid precursor protein to produce beta-amyloid peptide. This
CC	enzyme is therefore implicated in the production of amyloid plaque
CC	components which accumulate in the brains of individuals afflicted with
CC	Alzheimer's disease. Inhibitors of beta-secretase are administered to a
CC	mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease-
CC	like pathology to test if they maintain or improve cognitive ability or
CC	reduce the plaque burden. The compounds are used for the treatment of
CC	amyloidogenic diseases e.g. Alzheimer's disease. PCR primers AAA59530-49
XX	were used to amplify DNA encoding beta-secretase enzyme
XX	
SQ	Sequence 17 BP; 5 A; 2 C; 7 G; 0 T; 0 U; 3 Other;
Query Match	0.8%; Score 14; DB 1; Length 17;
Best Local Similarity	82.4%; Pred. No. 2.6e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	
QY	1306 GAGGAGGAGCCAGAGGA 1322
DB	1 GAYGARGAGCCGAGGA 17
RESULT 355	
ABK03568	
ID	ABK03568 standard; RNA; 17 BP.
XX	
AC	ABK03568;
XX	
DT	12-MAR-2002 (first entry)
XX	
DE	Human CD20 DNAzyme #22.
XX	
KM	Human; Bv; antiense therapy; cytosatic; antiinflammatory; haemostatic;
KM	cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
KM	muscular; CD20; neurite growth inhibitor gene; NOGO; hammetthead ribozyme;
KM	DNAzyme; inosyme; G-cleaver; amberzyme; zincyme; lymphoma; leukaemia;
KM	B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KM	human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KM	MCL; immunocytoxia; IMC; immune thrombocytopaenia; stroke; dementia;
KM	inflammatory arthropathy; central nervous system injury;
KM	cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KM	chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KM	Parkinson's disease; ataxia; Huntington's disease;
KM	Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
XX	W0200159103-A2.
PN	
PD	16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004273.
PF
XX 11-FEB-2000; 2000US-0181797P.
XX 28-FEB-2000; 2000US-0185516P.
PR 06-MAR-2000; 2000US-0187128P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT) BLATT L.
PA (MCSW/) MCSWIGGEN J.
PA (CHOW/) CHOWRIRA B M.
PI Blatt L, Mcswiggen J, Chowrira BM;
PI WPI; 2001-607195/69.
XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
XX constructs, which down regulate expression of a CD20 gene or neurite
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
PT central nervous system injury.
PS
XX Claim 30; Page 159; 200pp; English.
XX The invention relates to a nucleic acid molecule which down regulates
XX expression of a CD20 gene and a nucleic acid molecule which down
XX regulates expression of a neurite growth inhibitor gene (NGO). The
XX nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
XX DNAzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
XX possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
XX an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
XX with a XGY motif). The CD20-targeting nucleic acid is used to cleave RNA
XX of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
XX Furthermore, it may be contacted with a cell to reduce CD20 activity of
XX the cell and treat a patient having a condition associated with the level
XX of CD20. The treatment may further comprise the use of one or more
XX therapies. In particular, the CD20 targeting nucleic acid may be used to
XX treat lymphoma, leukemia, B-cell lymphoma, low-grade or follicular non-
XX Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
XX leukemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
XX lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
XX immune thrombocytopenia, and inflammatory arthropathy. The NGO-
XX targeting nucleic acid is used to cleave RNA of the NGO gene in the
XX presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
XX nucleic acid may be contacted with a cell to reduce NGO activity of the
XX cell and treat a patient having a condition associated with the level of
XX NGO. The treatment may further comprise the use of one or more
XX therapies. In particular, the NGO-targeting nucleic acid may be used to
XX treat central nervous system (CNS) injury and cerebrovascular accident
XX (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
XX chemothrapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
XX Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
XX disease, muscular dystrophy, and/or other neurodegenerative disease
XX states which respond to the modulation of NGO expression. The present
XX sequence is a DNAzyme molecule of the invention
XX
XX Sequence 17 BP; 1 A; 2 C; 7 G; 0 T; 7 U; 0 Other;
SQ
XX
XX Query Match 0.8%; Score 14; DB 1; Length 17;
XX Best Local Similarity 57.1%; Pred. No. 2.6e+02;
XX Matches 8; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 803 TCTGTGTCAGCTGCG 816
DB 1 UCUGUGUGACUGUG 14
ID RESULT 356
XX ADV07675/c
XX ADV07675 standard; RNA; 17 BP.
XX
XX ADV07675;
DT 10-FEB-2005 (first entry)

XX Human BACE amberzyme ribozyme substrate sequence #488.
DE
XX Enzymatic nucleic acid molecule; gene expression; down regulation;
XX protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;
XX MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
XX beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
XX c-erbB2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
XX hepatitis B virus; HBV; hammetthead; HH; hairpin; NCH; inozyme; G-cleaver;
XX amberzyme; zinzyme; DNAzyme; cancer; breast cancer; Alzheimer's disease;
XX diabetes; obesity; cardiac disease; heart disease; age-related disease;
XX hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
XX ss.
XX
XX Homo sapiens.
OS
XX
XX WO200116312-A2.
PN
XX
XX 08-MAR-2001.
PD
XX
XX 30-AUG-2000; 2000WO-US023998.
PF
XX
XX 31-AUG-1999; 99US-0151713P.
PR 27-SEP-1999; 99US-00406643.
PR 27-SEP-1999; 99US-0156236P.
PR 27-SEP-1999; 99US-0156467P.
PR 08-NOV-1999; 99US-00436430.
PR 06-DEC-1999; 99US-0169100P.
PR 29-DEC-1999; 99US-00474432.
PR 29-DEC-1999; 99US-0173512P.
PR 30-DEC-1999; 99US-00476387.
PR 04-FEB-2000; 2000US-00498824.
PR 10-MAR-2000; 2000US-00531025.
PR 14-APR-2000; 2000US-0197769P.
PR 23-MAY-2000; 2000US-00578223.
PR 09-AUG-2000; 2000US-00636385.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Mcswiggen J, Uman N, Blatt L, Beigelman L, Burgin A;
XX Karpelsky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
XX Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;
PI WPI; 2001-244406/25.
PI
XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules
XX are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
XX obesity and heart disease.
XX
XX Example 4; Page 403; 717pp; English.
XX
XX The present invention relates to the use of enzymatic nucleic acid
XX molecules (e.g. ribozymes) to modulate gene expression. The invention
XX also methods for their use to down regulate or inhibit the expression of
XX genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine
XX aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
XX alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
XX receptor-2 (HER2/c-erbB2/neu), and hepatitis B virus (HBV) proteins. The enzymatic
XX nucleic acid molecules used to inhibit the expression of the said genes
XX include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,
XX zinzyme, and/or DNAzyme motifs. The methods of the invention are useful
XX for treating cancer, in particular breast cancer, Alzheimer's disease,
XX diabetes, obesity, cardiac diseases e.g. heart disease, age-related
XX diseases, hepatitis B infections, and hepatitis and hepatocellular
XX carcinoma. The enzymatic nucleic acid molecules can also be used as
XX diagnostic tools to examine genetic drift and mutations within diseased
XX cells and to detect the presence of specific RNA in a cell. The present
XX sequence represents a substrate/target sequence for a ribozyme used in
XX the examples of the present invention. Note: Some SEQ ID Nos are repeated
XX more than once in the specification, but these have different sequences
XX associated with them.
XX

Sequence 17 BP; 3 A; 0 C; 8 G; 0 T; 6 U; 0 Other;
Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1277 CCACCATCTCCACA 1290
Db 16 CCACCATCTCCACA 3
RESULT 357
ADU86313
ID ADU86313 standard; DNA; 17 BP.
AC ADU86313;
XX 10-FEB-2005 (first entry)
XX Human TERT hammerhead ribozyme substrate sequence #344.
DE Enzymatic nucleic acid molecule; gene expression; down regulation;
XX protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;
XX MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
XX beta-secretase; BACE; human epidermal growth factor receptor-2; HBR2;
XX c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
XX hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
XX amberyzyme; zinzyme; DNazyme; cancer; breast cancer; Alzheimer's disease;
XX diabetes; obesity; cardiac disease; heart disease; age-related disease;
XX hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
XX de.
XX Homo sapiens.
OS WO200116312-A2.
XX 08-MAR-2001.
XX 30-AUG-2000; 2000MO-US023998.
XX 31-AUG-1999; 99US-0151713P.
XX 27-SEP-1999; 99US-00406643.
XX 27-SEP-1999; 99US-0156236P.
XX 27-SEP-1999; 99US-0156467P.
XX 08-NOV-1999; 99US-00436430.
XX 06-DEC-1999; 99US-0169100P.
XX 29-DEC-1999; 99US-00474432.
XX 29-DEC-1999; 99US-0173612P.
XX 30-DEC-1999; 99US-00476387.
XX 04-FEB-2000; 2000US-00498824.
XX 20-MAR-2000; 2000US-00531025.
XX 14-APR-2000; 2000US-0197769P.
XX 23-MAY-2000; 2000US-00578223.
XX 09-AUG-2000; 2000US-00636385.
XX (RIBO-) RIBOZYME PHARM INC.
XX McSwiggan J, Uzman N, Blatt L, Beigelman L, Burgin A;
XX Karpelsky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
XX Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;
XX WPI; 2001-244406/25.
XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules
XX are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
XX obesity and heart disease.
XX Example 1; Page 274; 717pp; English.
XX The present invention relates to the use of enzymatic nucleic acid
XX molecules (e.g. ribozymes) to modulate gene expression. The invention
XX also methods for their use to down regulate or inhibit the expression of
XX genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine

CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
CC nucleic acid molecules used to inhibit the expression of the said genes
CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberyzyme,
CC zinzyme, and/or DNazyme motifs. The methods of the invention are useful
CC for treating cancer, in particular breast cancer, Alzheimer's disease,
CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related
CC diseases, hepatitis B infections, and hepatitis and hepatocellular
CC carcinoma. The enzymatic nucleic acid molecules can also be used as
CC diagnostic tools to examine genetic drift and mutations within diseased
CC cells and to detect the presence of specific RNA in a cell. The present
CC sequence represents a substrate/target sequence for a ribozyme used in
CC the examples of the present invention. Note: Some SEQ ID Nos are repeated
CC more than once in the specification, but these have different sequences
CC associated with them.
XX
XX Sequence 17 BP; 3 A; 8 C; 1 G; 5 T; 0 U; 0 Other;
QY 1689 CCAGCTTTCTCTCA 1702
Db 1 CCAGCTTTCTCTCA 14
RESULT 358
ADU86312
ID ADU86312 standard; DNA; 17 BP.
AC ADU86312;
XX 10-FEB-2005 (first entry)
XX Human TERT hammerhead ribozyme substrate sequence #343.
DE Enzymatic nucleic acid molecule; gene expression; down regulation;
XX protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;
XX MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
XX beta-secretase; BACE; human epidermal growth factor receptor-2; HBR2;
XX c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
XX hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
XX amberyzyme; zinzyme; DNazyme; cancer; breast cancer; Alzheimer's disease;
XX diabetes; obesity; cardiac disease; heart disease; age-related disease;
XX hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
XX de.
XX Homo sapiens.
OS WO200116312-A2.
XX 08-MAR-2001.
XX 30-AUG-2000; 2000MO-US023998.
XX 31-AUG-1999; 99US-0151713P.
XX 27-SEP-1999; 99US-00406643.
XX 27-SEP-1999; 99US-0156236P.
XX 27-SEP-1999; 99US-0156467P.
XX 08-NOV-1999; 99US-00436430.
XX 06-DEC-1999; 99US-0169100P.
XX 29-DEC-1999; 99US-00474432.
XX 29-DEC-1999; 99US-0173612P.
XX 30-DEC-1999; 99US-00476387.
XX 04-FEB-2000; 2000US-00498824.
XX 20-MAR-2000; 2000US-00531025.
XX 14-APR-2000; 2000US-0197769P.
XX 23-MAY-2000; 2000US-00578223.
XX 09-AUG-2000; 2000US-00636385.

PA (RIBO-) RIBOZYME PHARM INC.

XX Maswiggen J, Uman N, Blatt L, Beigelman L, Burgin A,
PI Karpelsky A, Matulic-Adamic J, Swedler D, Draper K, Chowrira B,
PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS,
XX WPI; 2001-244406/25.

XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules
PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
PT obesity and heart disease.

PS Example 1; Page 274; 717pp; English.

XX The present invention relates to the use of enzymatic nucleic acid
CC molecules (e.g. ribozymes) to modulate gene expression. The invention
CC also methods for their use to down regulate or inhibit the expression of
CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine
CC aminopeptidase (MeAP-2), human telomerase (hTERT), protein kinase C
CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
CC nucleic acid molecules used to inhibit the expression of the said genes
CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberyzyme,
CC zincyme, and/or DNAzyme motifs. The methods of the invention are useful
CC for treating cancer, in particular breast cancer, Alzheimer's disease,
CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related
CC diseases, hepatitis B infections, and hepatitis and hepatocellular
CC carcinoma. The enzymatic nucleic acid molecules can also be used as
CC diagnostic tools to examine genetic drift and mutations within diseased
CC cells and to detect the presence of specific RNA in a cell. The present
CC sequence represents a substrate/target sequence for a ribozyme used in
CC the examples of the present invention. Note: Some SEQ ID Nos are repeated
CC more than once in the specification, but these have different sequences
CC associated with them.

XX Sequence 17 BP; 2 A; 8 C; 2 G; 5 T; 0 U; 0 Other;

XX Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1689 CCAGCTTTTCTCA 1702
|||
Db 2 CCAGCTTTTCTCA 15

RESULT 359

ABN06977
ID ABN06977 standard; DNA; 17 BP.

XX ABN06977;

DT 29-MAY-2002 (first entry)

DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:6969.

XX Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.

XX Homo sapiens.

XX WO200192524-A2.

XX 06-DEC-2001.

XX 25-MAY-2001; 2001WO-US016981.

XX 26-MAY-2000; 2000US-0207456P.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.

PA (AEOM-) AEOMICA INC.

XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
PI WPI; 2002-179446/23.

XX New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.

PS Disclosure; SEQ ID NO 6969; 214pp; English.

XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionization, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence

XX Sequence 17 BP; 7 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

XX Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 29 AGTGATCCAGAG 42
|||
Db 1 AGTGATCCAGAG 14

RESULT 360

ABN06973
ID ABN06973 standard; DNA; 17 BP.

XX ABN06973;

DT 29-MAY-2002 (first entry)

DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:6965.

XX Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.

XX Homo sapiens.

XX WO200192524-A2.
PN
XX
XX 06-DEC-2001.
PD
XX
XX 25-MAY-2001; 2001WO-US016981.
PF
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 05-FEB-2001; 2001US-0266860P.
PR
XX
XX (ABOM-) AEWOMICA INC.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
PI
XX WPI; 2002-179446/23.
XX
XX
XX New polypeptide, for raising antibodies that recognise hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
XX Disclousure; SEQ ID NO 6965; 214pp; English.
XX
XX
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and vaccine production. The hGDMLP-1
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acid can be used as probes to detect, characterise and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ffp.wipo.int/pub/published_pcc_sequence
XX
XX
SQ Sequence 17 BP; 6 A; 5 C; 4 G; 2 T; 0 U; 0 Other;
XX
XX
XX Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 28 CAGTCATCCAGAA 41
Db 4 CAGTCATCCAGAA 17
XX
XX
XX RESULT 361
ADM54123
ID ADM54123 standard; mRNA; 17 BP.
XX

AC ADM54123;
XX
XX 03-JUN-2004 (first entry)
DT
XX
XX
XX Human GRID mRNA substrate sequence #398.
DE
XX
XX
XX Human; seq, GRID; Grb2-related with insert domain; hammerhead ribozyme;
KW NCH ribozyme; G-cleaver ribozyme; Zinzyne; DNAzyme; Inozyme;
KW hairpin ribozyme; tissue rejection; graft rejection; leukaemia.
OS
XX Homo sapiens.
XX
XX US2003134806-A1.
XX
XX 17-JUL-2003.
XX
XX 23-FEB-2001; 2001US-00792818.
XX
XX 10-FEB-2000; 2000US-0181594P.
XX
XX (JARYV) JARVIS T.
XX (CARL) CARLOWITZ I V.
XX (MCSW) MCSWIGEN J.
XX (HAMB) HAMBELIN P A.
XX (ELLI) ELLIS J H.
XX
XX Jarvis T, Carlowitz IV, Mcswigen J, Hamblin PA, Ellis JH;
PI
XX WPI; 2003-829646/77.
XX
XX
XX New nucleic acid molecule that down-regulates expression of Grb2-related
PT with insert domain (GRID) gene, useful for treating a condition and
PT associated with the level of GRID, e.g. tissue/graft rejection and
PT leukemia.
XX
XX
XX Claim 4; SEQ ID NO 398; 74pp; English.
XX
XX
XX The invention relates to a nucleic acid molecule that down-regulates
CC expression of Grb2-related with insert domain (GRID) gene, e.g. a
CC hammerhead ribozyme, NCH ribozyme, G-cleaver ribozyme, Zinzyne, DNAzyme,
CC amberyne, inozyme or hairpin ribozyme. Also include are a mammalian cell
CC including the novel nucleic acid molecule, reducing GRID activity in a
CC cell by contacting the cell with the novel nucleic acid molecule,
CC treating a patient having a condition associated with the level of GRID
CC (e.g. tissue/graft rejection or leukaemia) by contacting the cell with
CC the novel nucleic acid molecule, cleaving RNA of a GRID gene by
CC contacting the cell with the novel nucleic acid molecule, an expression
CC vector comprising a nucleic acid sequences (encoding at least the novel
CC nucleic acid molecule in a manner that allows its expression), a
CC mammalian cell including the expression vector and an enzymatic nucleic
CC acid molecule that cleaves RNA derived from a GRID gene. The nucleic acid
CC molecule is useful for treating a condition associated with the level of
CC GRID, e.g. tissue/graft rejection and leukaemia. The present sequence is
CC a target region for the enzymatic nucleic acids of the invention.
XX
XX
SQ Sequence 17 BP; 5 A; 9 C; 1 G; 0 T; 2 U; 0 Other;
XX
XX
XX Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1276 ACCACCATCTCCAC 1289
Db 4 ACCACCATCTCCAC 17
XX
XX
XX RESULT 362
ADL82294
ID ADL82294 standard; DNA; 17 BP.
XX
XX ADL82294;
XX
XX 20-MAY-2004 (first entry)
DT

```

XX DE Human ER+ breast cancer differentially expressed sequence #264.
XX KW gene therapy; de; breast cancer; human; ER+ breast cancer.
XX OS Homo sapiens.
XX PN US2003166026-A1.
XX PD 04-SEP-2003.
XX PF 08-JAN-2003; 2003US-00339782.
XX PR 09-JAN-2002; 2002US-0348053P.
XX PA (LYNX-) LYNX THERAPEUTICS INC.
XX PI Goodman LJ, Bowen BA;
XX DR WPI; 2004-069003/07.
XX PT Vector containing nucleic acid associated with breast cancer, useful for
XX PT treating, diagnosing and characterizing breast cancer, also related
XX PT polypeptides and antibodies.
XX PS Claim 1, SEQ ID NO 265; 61pp; English.
XX CC The invention relates to a composition which contains at least one vector
XX CC (B) containing a nucleic acid (I) associated with breast cancer. The
XX CC vector (B), also polypeptides (II) encoded by (I), are used for treatment
XX CC of breast cancer. Arrays based on (I), (II), or their fragments, and (II)
XX CC -specific antibodies (Ab) are used to predict characteristics (e.g.
XX CC invasiveness or stage) of breast cancer, and (I), or its fragments, are
XX CC used to modulate characteristics of such cells; to identify breast cancer
XX CC genes and to detect breast cancer (by detecting polymorphic nucleic acid
XX CC or its products). The present sequence represents a human ER+ breast
XX CC cancer differentially expressed sequence.
XX SQ Sequence 17 BP; 2 A; 10 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 617 ATCCCTCCAGCCC 630
Db 2 ATCCCTCCAGCCC 15

RESULT 363
ADNR31412/C
ID ADR31412 standard; DNA; 17 BP.
XX AC ADR31412;
XX AC 04-NOV-2004 (first entry)
XX DT 04-NOV-2004 (first entry)
XX DE Bovine RORCGH DNA specific PCR primer, RORCGHD3.
XX KW Marbling; RORC; retinoid related orphan receptor C (gamma);
XX KW RAR-related orphan receptor gamma; nuclear receptor ROR-gamma;
XX KW retinoic acid-binding receptor gamma; fat deposit; bovine; RORCGH; PCR;
XX KW primer; ss.
XX OS Bos sp.
XX PN WO2004070055-A1.
XX PD 19-AUG-2004.
XX PF 04-FEB-2004; 2004WO-AU000127.
XX PR 04-FEB-2003; 2003AU-00900454.

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XX PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX PA (OUE-) STATE QUEENSLAND DEPT PRIMARY IND.
XX PA (OUE-) UNIV NEW ENGLAND.
XX PA (NEWS-) NEW SOUTH WALES DEPT AGRIC.
XX PA (MEAT-) MEAT & LIVESTOCK AUSTRALIA LTD.
XX PI Barendse W;
XX DR WPI; 2004-604466/58.
XX PT Assessing propensity for marbling in animal meat useful for selecting
XX PT animal to improve marbling in herd, involves detecting alleles of
XX PT retinoid related orphan receptor C gamma gene associated with increased
XX PT fat deposition in muscle.
XX PS Disclosure; SEQ ID NO 10; 53pp; English.
XX CC The present invention relates to a method for assessing the propensity
XX CC for marbling in meat derived from an animal. The method involves testing
XX CC the animal for the presence or absence of one or more alleles of the gene
XX CC encoding the retinoid related orphan receptor C (gamma) (RORC) also known
XX CC as RAR-related orphan receptor gamma, nuclear receptor ROR-gamma and
XX CC retinoic acid-binding receptor gamma, associated with increased fat
XX CC deposition in muscle tissue and genetic variation located external to the
XX CC RORC gene which shows allelic association with it. The invention is
XX CC useful for selection and breeding of animal with improved fat deposition
XX CC characteristics, particularly high marbling scores. The present sequence
XX CC is bovine RORC allelic variant, RORCGH DNA specific PCR primer.
XX SQ Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1235 TCCGAGCCCGGGC 1248
Db 16 TCCGAGCCCGGGC 3

RESULT 364
ACN70067
ID ACN70067 standard; DNA; 17 BP.
XX AC ACN70067;
XX DT 02-DEC-2004 (first entry)
XX DE Human GDMLP-1 probe SEQ ID NO:6969.
XX KW Human; ss; probe; myosin-like protein-1; hGDMLP-1;
XX KW hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
XX KW skeletal muscle function.
XX OS Homo sapiens.
XX PN US2004137589-A1.
XX PD 15-JUL-2004.
XX PF 26-NOV-2003; 2003US-00723361.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PR 30-JAN-2001; 2001WO-US000661.
XX PR 30-JAN-2001; 2001WO-US000662.
XX PR 30-JAN-2001; 2001WO-US000663.
XX PR 30-JAN-2001; 2001WO-US000664.
XX PR 30-JAN-2001; 2001WO-US000665.
XX PR 30-JAN-2001; 2001WO-US000666.

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PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
PR 25-MAY-2001; 2001US-00866108.
XX
PA (GUY/) GU Y.
PA (JIY/) JI Y.
PA (PENN/) PENN S G.
PA (HANZ/) HANZEL D K.
PA (RANK/) RANK D.
PA (CHEN/) CHEN W.
PA (SHAN/) SHANNON M E.
PI Gu Y, JI Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
DR WPI; 2004-533378/51.
XX
PT Novel myosin-like protein-1, useful for treating or preventing disorder
PT associated with decreased expression or activity of human genome-derived
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT function.
XX
PS Disclosure; SEQ ID NO 6969; Opp; English.
XX
XX The invention relates to a novel polypeptide (I) comprising a sequence
CC (S1) of myosin-like protein-1 (hGDMPL-1) having 2568 amino acids fully
CC defined in the specification, a fragment of at least 8 amino acids of
CC (S1), 95% deviation from (S1) which are conservative substitutions, and
CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
CC antagonist of hGDMPL-1, or as an inhibitor of hGDMPL-1 activity. A
CC pharmaceutical composition of the invention is useful for treating or
CC preventing a disorder associated with decreased expression or activity of
CC hGDMPL-1, such as a disorder of heart and/or skeletal muscle function.
CC The present sequence represents a 17-mer nucleotide, used in the
CC invention for scanning the sequence represented in ACN63103
XX
SQ Sequence 17 BP; 7 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 29 AGTGCATCCAGAG 42
DB 1 AGTGCATCCAGAG 14
ACNT7063
RESULT 365
ID ACN70063 standard; DNA; 17 BP.
XX
XX ACN70063;
XX
XX 02-DEC-2004 (first entry)
XX
XX Human GDMPL-1 probe SEQ ID NO:6965.
XX
XX Human; ss; probe: myosin-like protein-1; hGDMPL-1;
KM hGDMPL-1 agonist hGDMPL-1 antagonist; hGDMPL inhibitor; heart disorder;
KM skeletal muscle function.
XX
OS Homo sapiens.
XX
XX US2004137589-A1.
XX
XX 15-JUL-2004.
XX
XX 26-NOV-2003; 2003US-00723361.
XX
XX 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
PR 25-MAY-2001; 2001US-00866108.
XX
XX (GUY/) GU Y.
XX (JIY/) JI Y.
XX (PENN/) PENN S G.
XX (HANZ/) HANZEL D K.
XX (RANK/) RANK D.
XX (CHEN/) CHEN W.
XX (SHAN/) SHANNON M E.
PI Gu Y, JI Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
DR WPI; 2004-533378/51.
XX
XX Novel myosin-like protein-1, useful for treating or preventing disorder
PT associated with decreased expression or activity of human genome-derived
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT function.
XX
PS Disclosure; SEQ ID NO 6965; Opp; English.
XX
XX The invention relates to a novel polypeptide (I) comprising a sequence
CC (S1) of myosin-like protein-1 (hGDMPL-1) having 2568 amino acids fully
CC defined in the specification, a fragment of at least 8 amino acids of
CC (S1), 95% deviation from (S1) which are conservative substitutions, and
CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
CC antagonist of hGDMPL-1, or as an inhibitor of hGDMPL-1 activity. A
CC pharmaceutical composition of the invention is useful for treating or
CC preventing a disorder associated with decreased expression or activity of
CC hGDMPL-1, such as a disorder of heart and/or skeletal muscle function.
CC The present sequence represents a 17-mer nucleotide, used in the
CC invention for scanning the sequence represented in ACN63103
XX
SQ Sequence 17 BP; 6 A; 5 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 28 CAGTGCATCCAGAA 41
DB 4 CAGTGCATCCAGAA 17
ADSA1403/c
RESULT 366
ID ADSA1403 standard; DNA; 17 BP.
XX
XX ADSA1403;
XX
XX 16-DEC-2004 (first entry)
XX
XX Human autoimmune disease-related PCR primer - SEQ ID 6617.
XX
XX single nucleotide polymorphism detection; SNP detection;
KM rheumatoid arthritis; type 1 diabetes; multiple sclerosis;
KM systemic lupus erythematosus; inflammatory bowel disease; psoriasis;
KM thyroiditis; celiac disease; pernicious anaemia; asthma; vitiligo;
KM glomerulonephritis; Grave's disease; myocarditis; Sjogren's disease;
KM primary systemic vasculitis; PCR; primer; ss.

XX Homo sapiens.
XX OS
XX PN WO2004083403-A2.
XX PD
XX 30-SEP-2004.
XX PF 18-MAR-2004; 2004WO-US008461.
XX PR 18-MAR-2003; 2003US-0455444P.
XX PR 25-APR-2003; 2003US-0465241P.
XX PA (APPL-) APPLERA CORP.
XX PI Cargill M, Begovich AB, Alexander HC;
XX WPI, 2004-728480/71.
XX DR
XX New isolated nucleic acid molecule comprises at least 8 contiguous
PT nucleotides where one of the nucleotides is a single nucleotide
PT polymorphism (SNP), useful for diagnosing or treating autoimmune
PT diseases, e.g. rheumatoid arthritis.
XX
XX Claim 21; SEQ ID NO 6617; 123pp; English.
XX
XX The invention comprises amino acid and coding sequences containing
CC genetic polymorphisms associated with an altered risk of developing an
CC autoimmune disease (e.g. rheumatoid arthritis). The invention further
CC comprises a method of identifying an individual that has an altered risk
CC of developing an autoimmune disease, comprising detecting a single
CC nucleotide polymorphism (SNP) in a nucleic acid of the invention. The DNA
CC and protein sequences of the invention are useful for diagnosing and
CC treating autoimmune diseases, such as: rheumatoid arthritis, type 1
CC diabetes, multiple sclerosis, systemic lupus erythematosus, inflammatory
CC bowel diseases, psoriasis, thyroiditis, celiac disease, pernicious
CC anaemia, asthma, vitiligo, glomerulonephritis, Grave's disease,
CC myocarditis, Sjogren's disease, or primary systemic vasculitis. The
CC present DNA sequence represents a human autoimmune disease-related PCR
CC primer of the invention. NOTE: The present sequence is not shown in the
CC specification, but has been retrieved from the WIPO website.
XX
XX Sequence 17 BP; 5 A; 3 C; 8 G; 1 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.6e+02; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0;
QY 677 TCCGCGCTCTCCG 690
DB 14 TCTGCGCTCTCTG 1
RESULT 367
AAQ30775
ID AAQ30775 standard; DNA; 17 BP.
XX
XX AAQ30775;
AC
XX 25-MAR-2003 (revised)
DT 22-MAR-1993 (first entry)
XX
XX PCR primer rspr284h to amplify human NKIR sF core region.
DE Neurokinin-1 receptor short form; arthritis; Substance P;
XX polymerase chain reaction; rat NKIR; ss.
XX
XX Synthetic.
OS
XX EP514207-A2.
PN
XX 19-NOV-1992.
PD
XX 15-MAY-1992; 92EP-00304432.
PF

XX 17-MAY-1991; 91US-00701930.
XX PR 17-MAY-1991; 91US-00701935.
XX PR 17-MAY-1991; 91US-00701937.
XX
XX (MERI) MERCK & CO INC.
XX
XX Strader CD, Fong TM;
XX WPI, 1992-384034/47.
XX
XX New human neurokinin-1 receptor short form protein - useful for
PT identifying and determining substance P antagonists in arthritic
PT patients.
XX
XX Example 1; Page 8; 36pp; English.
XX
XX Human mRNA was prepared from 3 glioblastoma cell lines T98G, CCF-SSTG1
CC and U87MG. First strand cDNA was synthesised and used as template with
CC rat primers rspr284, rspr284h and rspr7a2 (AAQ30774-6) in first round PCR
CC amplification. Secondary PCR was performed on the amplified product using
CC the same 3 primers prior to a third round of amplification, this time
CC using the primers rspr284, rspr284h, rspr7a1 (AAQ30777) and rspr7a1h
CC (AAQ30778). The tertiary PCR product was sequenced and was found to have
CC 90% identity at the nucleotide level with the central core region of the
CC rat NKIR from amino acid 91 to 280. Primer rspr284h is a sense primer
CC based on the rat NKIR sequence 238-255 (numbering as in J.Biol.Chem. 264:
CC 17649-17652, 1989), but designed to incorporate the human codon bias.
XX (updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 17 BP; 3 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.8e+02; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 2;
QY 448 TCCATGCGTCGATTCAA 464
DB 1 TGCATGCGTCCTTCAA 17
RESULT 368
AAQ47255/C
ID AAQ47255 standard; DNA; 17 BP.
XX
XX AAQ47255;
AC
XX 25-MAR-2003 (revised)
DT 25-JAN-1994 (first entry)
XX
XX PCR primer for amplifying tachykinin receptor specific mRNA from human
DE leukocytes.
XX
XX Polynucleotide; synthesis; solid support; ss.
XX
XX Synthetic.
OS
XX WO9315228-A1.
PN
XX 05-AUG-1993.
PD
XX 29-JAN-1993; 93WO-US001040.
XX PF 29-JAN-1992; 92US-00827975.
XX PR 29-JAN-1992; 92US-00827975.
XX
XX (HITB) HITACHI CHEM CO LTD.
XX (HITB) HITACHI CHEM RES CENT INC.
XX
XX Keller C, Misuhashi M, Akitaya T;
XX WPI, 1993-258700/32.
XX
XX Prodn. of double stranded cDNA immobilised support - by binding
PT

PT polynucleotide with sequence complementary to poly-adenylic acid tail of
PT mRNA to insol. support.
XX
XX Example 3; Page 26; 54pp; English.
XX
CC A polynucleotide is immobilised on an insoluble solid support and used to
CC synthesize ds-cDNA, ss-cDNA and both sense and antisense mRNA. The
CC advantage of this system is that RNA bound to the solid support need not
CC be precipitated when changing solutions. Two primers were used to amplify
CC tachykinin receptor specific mRNA after its synthesis using the above
CC method (AA047254, AA047255). (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 17 BP; 4 A; 4 C; 8 G; 1 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 983 CCATCTGCTGCTGCC 999
DB 17 CCATCTGCTGCTGCC 1
RESULT 369
AAx71369/c
ID AAx71369 standard; RNA; 17 BP.
XX
AC AAx71369;
XX
DT 28-JUL-1999 (first entry)
XX
DE Human KDR VEGF receptor hammerhead ribozyme substrate #381.
XX
KM Vascular endothelial growth factor receptor; VEGF receptor; flk-1; flk-1;
KM KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KM tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KM fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KM foetal liver kinase 1; ss.
XX
XX Homo sapiens.
XX
PN WO9715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US017480.
XX
PR 26-OCT-1995; 95US-0005974P.
PR 11-JAN-1996; 96US-00584040.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (CHIR) CHIRON CORP.
XX
PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX
DR WPI; 1997-259017/23.
XX
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
XX Claim 4; Page 108; 218pp; English.
XX
XX The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAx67275 to AAx75752 represent specific examples

CC of nucleic acid molecules from the present invention
XX
SQ Sequence 17 BP; 6 A; 3 C; 4 G; 0 T; 4 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1505 TTCACTCGAACCATCA 1521
DB 17 TTCACTCGAATCCATGA 1
RESULT 370
AAx72795/c
ID AAx72795 standard; RNA; 17 BP.
XX
AC AAx72795;
XX
DT 28-JUL-1999 (first entry)
XX
DE Mouse flk-1 VEGF receptor hammerhead ribozyme substrate #228.
XX
KM Vascular endothelial growth factor receptor; VEGF receptor; flk-1; flk-1;
KM KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KM tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KM fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KM foetal liver kinase 1; ss.
XX
XX Mus sp.
XX
PN WO9715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US017480.
XX
PR 26-OCT-1995; 95US-0005974P.
PR 11-JAN-1996; 96US-00584040.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (CHIR) CHIRON CORP.
XX
PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX
DR WPI; 1997-259017/23.
XX
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
XX Claim 4; Page 129; 218pp; English.
XX
XX The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAx67275 to AAx75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
SQ Sequence 17 BP; 0 A; 3 C; 6 G; 0 T; 8 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 714 CTCACCCAGAGACCA 730
DB 17 CACACCCAGAGACCA 1

RESULT 371
AAK72944/c
ID AAK72944 standard; RNA; 17 BP.
XX
AC AAK72944;
XX
DT 28-JUL-1999 (first entry)
XX
DE Mouse flk-1 VEGF receptor hammerhead ribozyme substrate #377.
XX
KM Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KM KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KM tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KM fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KM foetal liver kinase 1; ss.
XX
OS Mus sp.
XX
PN MO9715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US017480.
XX
PR 26-OCT-1995; 95US-0005974P.
XX
PR 11-JAN-1996; 96US-00584040.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (CHIR) CHIRON CORP.
XX
PI Pavco P, Mcswigen J, Stinchcomb D, Escobedo J;
XX
PI WPI; 1997-259017/23.
XX
DR Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
XX PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
XX PT rheumatoid arthritis, etc., in a human patient.
XX
PS Claim 4; Page 134; 218pp; English.
XX
XX The present invention describes nucleic acid molecules which modulate the
XX synthesis, expression and/or stability of a mRNA encoding 1 or more
XX receptors of vascular endothelial growth factor (VEGF). A patient
XX (preferably human) having a condition associated with the level of the
XX fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
XX receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
XX angiogenesis, ocular disease, psoriasis and rheumatoid arthritis) can be
XX treated by administering the nucleic acid molecule or the expression
XX vector to the patient. AAK67275 to AAK75752 represent specific examples
XX of nucleic acid molecules from the present invention
XX
SQ Sequence 17 BP; 6 A; 3 C; 4 G; 0 T; 4 U; 0 Other;
XX
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1505 TTCATCTGGACCATCA 1521
DB 17 TTCATCTGGACCATCA 1
XX
RESULT 372
AAK71197/c
ID AAK71197 standard; RNA; 17 BP.
XX
AC AAK71197;
XX
DT 28-JUL-1999 (first entry)
XX
DE Human KDR VEGF receptor hammerhead ribozyme substrate #209.
XX

XX
KM Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KM KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KM tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KM fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KM foetal liver kinase 1; ss.
XX
OS Homo sapiens.
XX
PN MO9715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US017480.
XX
PR 26-OCT-1995; 95US-0005974P.
XX
PR 11-JAN-1996; 96US-00584040.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (CHIR) CHIRON CORP.
XX
PI Pavco P, Mcswigen J, Stinchcomb D, Escobedo J;
XX
PI WPI; 1997-259017/23.
XX
DR Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
XX PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
XX PT rheumatoid arthritis, etc., in a human patient.
XX
PS Claim 4; Page 103; 218pp; English.
XX
XX The present invention describes nucleic acid molecules which modulate the
XX synthesis, expression and/or stability of a mRNA encoding 1 or more
XX receptors of vascular endothelial growth factor (VEGF). A patient
XX (preferably human) having a condition associated with the level of the
XX fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
XX receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
XX angiogenesis, ocular disease, psoriasis and rheumatoid arthritis) can be
XX treated by administering the nucleic acid molecule or the expression
XX vector to the patient. AAK67275 to AAK75752 represent specific examples
XX of nucleic acid molecules from the present invention
XX
SQ Sequence 17 BP; 0 A; 3 C; 6 G; 0 T; 8 U; 0 Other;
XX
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 714 CTCACACACAGAGACCA 730
DB 17 CACACACAGAGACCA 1
XX
RESULT 373
AAK62890/c
ID AAK62890 standard; RNA; 17 BP.
XX
AC AAK62890;
XX
DT 16-JUL-1999 (first entry)
XX
DE Delta-9 desaturase hammerhead ribozyme target SEQ ID NO:765.
XX
KM Maize; corn; Zea mays; delta-9 desaturase; GBSs; target; substrate;
KM granule bound starch synthase; hammerhead ribozyme; hairpin ribozyme;
KM modulation; gene expression; transgenic plant; cleavage; canola plant;
KM caffeine synthesis; coffee plant; nicotine production; tobacco;
KM fruit ripening; flower pigmentation; lignin production; ss.
XX
OS Zea mays.
XX
PN MO9710328-A2.
XX

PD 20-MAR-1997.
XX
XX 12-JUL-1996; 96WO-US011689.
XX
XX 13-JUL-1995; 95US-0001135P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (DMC) DOWELANCO.
XX
XX Zwick MG, Edington BE, Mcswigen JA, Merlo PAO, Guo L, Skokut TA,
PI Young SA, Folkerts O, Merlo DJ;
XX
XX WPI; 1997-202224/18.
XX
XX Ribozyyme which modulates plant gene expression - preferably modulates
PT expression of DELTA-9 desaturase or granule bound starch synthase in
PT maize or canola.
XX
XX
XX Claim 38; Page 86; 155pp; English.
XX
XX The present invention describes an enzymatic nucleic acid molecule (I)
CC with RNA cleaving activity, which modulates the expression of a plant
CC gene. Also described is a gene comprising a cDNA sequence encoding maize
CC Delta-9 desaturase. (I) can be used to modulate expression of a gene,
CC preferably Delta-9 desaturase or a granule bound starch synthase (GBSS)
CC gene, in a plant (preferably a maize or canola plant). (I) can be used to
CC modulate caffeine synthesis in a coffee plant, nicotine production in a
CC tobacco plant, fruit ripening processes in an apple, tomato, pear, plum
CC or peach plant, flower pigmentation in a rose, petunia, chrysanthemum or
CC marigold plant or lignin production in a tobacco, aspen, poplar or pine
CC plant
XX
XX
SQ Sequence 17 BP; 1 A; 5 C; 6 G; 0 T; 5 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 636 GTCAGCCACGACCCCA 652
DB 17 GTCAGCCACGACCCCA 1
RESULT 374
AAV97463/C
ID AAV97463 standard; RNA; 17 BP.
XX
XX AAV97463;
AC
XX
XX 17-MAR-1999 (first entry)
DT
XX
XX Human EGF-R target sequence nucleotide position 2148.
DE
XX
XX Human; epidermal growth factor receptor; EGFR; EGF-R; target sequence;
KM hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;
KM cancer; genetic drift; detection; mutation; ss.
XX
XX Homo sapiens.
OS
XX
XX WO9833893-A2.
PN
XX
XX 06-AUG-1998.
PD
XX
XX 14-JAN-1998; 98WO-US000730.
PF
XX
XX 31-JAN-1997; 97US-0036476P.
PR
XX 04-DEC-1997; 97US-00985162.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX (UTAS-) UNITV ASTON.
PA
XX
XX Akhtar S, Fell P, Mcswigen JA;
PI

DR WPI; 1998-437449/37.
XX
XX Enzymatic nucleic acids - which cleave RNA derived from an epidermal
PT growth factor receptor, useful for inhibiting cell proliferation and for
PT treating cancers.
XX
XX
XX Claim 5; Page 73; 109pp; English.
XX
XX The present invention describes enzymatic nucleic acid molecules (NMs)
CC which specifically cleave RNA derived from an epidermal growth factor
CC receptor (EGF-R) gene. AAV97221 to AAV98043 and AAV98979 to AAV99090
CC represent specifically claimed target sequence from human EGF-R. AAV98044
CC to AAV98866 and AAV98867 to V9878 represent hammerhead ribozymes and
CC hairpin ribozymes respectively for human EGF-R. The NMs are useful for
CC cleaving EGF-R RNA in the treatment of a condition associated with EGFR
CC expression levels e.g. to inhibit cell proliferation in the prevention or
CC treatment of cancers. The NMs can also be used as diagnostic tools to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of EGF-R RNA in a cell
XX
XX
SQ Sequence 17 BP; 0 A; 7 C; 5 G; 0 T; 5 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1313 AGCCAGAGAGCGGCC 1329
DB 17 AGCCAGAGAGCGGCC 1
RESULT 375
AAA20669/C
ID AAA20669 standard; RNA; 17 BP.
XX
XX AAA20669;
AC
XX
XX 19-JUN-2000 (first entry)
DT
XX
XX Integrin alpha 6 subunit substrate sequence SEQ ID NO:3895.
DE
XX
XX Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KM integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KM hammerhead ribozyme; angiogenic factor; cytoskeletal; antidiabetic;
KM opthalmologic; antiinflammatory; antiarthritic; antidiabetic; AMD;
KM dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KM age related macular degeneration; inflammation; neovascular glaucoma;
KM myopic degeneration; psoriasis; verruca vulgaris; angiodiroma;
KM tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
KM Kippel-Trenunay-Weber syndrome; Obler-Weber-Rendu syndrome; ss.
XX
XX Homo sapiens.
OS
XX
XX WO9950403-A2.
PN
XX
XX 07-OCT-1999.
PD
XX
XX 24-MAR-1999; 99WO-US006507.
PF
XX
XX 27-MAR-1998; 98US-0079678P.
PR
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswigen JA;
PI WPI; 1999-591315/50.
XX
XX
XX Novel ribozymes for modulating the synthesis, expression and/or stability
PT of an mRNA encoding an angiogenic factors.
XX
XX Claim 55; Page 160; 305pp; English.
XX
XX The present invention describes enzymatic nucleic acid molecules with RNA
CC

cleaving activity, which specifically cleave RNA encoded by an aryl hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT, CC AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to CC AAA19154 represent ribozyme sequences for Tie-2, and AAA19386 to AAA19086 CC and AAA19155 to AAA19222 represent their corresponding target sequences; CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and CC AAA21596 to AAA21688 represent their corresponding target sequences; CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme CC sequences for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to CC AAA23422 represent their corresponding target sequences. The ribozymes of CC the invention are used for modulating the synthesis, expression and/or CC stability of an mRNA encoding angiogenic factor, especially ARNT, CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are CC especially used to treat cancer, diabetic retinopathy, age related CC macular degeneration (ARMD), inflammation, and arthritis, as well as CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris, CC angiodiroma of tuberous sclerosis, pot-wine stains, Sturge Weber CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome, CC and other syndromes and diseases related to the levels of ARNT, Tie-2, CC integrin subunit alpha-6, or integrin subunit beta-3

Sequence 17 BP; 6 A; 4 C; 2 G; 0 T; 5 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1720 ATTTCGAGAGTACTT 1736
17 ACTTCTGAGAGTCAATT 1

RESULT 376
AAH94825/c
ID AAH94825 standard; RNA; 17 BP.

AC AAH94825;
XX
XX 09-OCT-2001 (first entry)
DT
XX
XX Human Chk1 ribozyme substrate SEQ ID NO: 250.
DE

XX Human; checkpoint kinase-1; Chk1; antisense; ribozyme; gene therapy;
KW RNA cleavage; cancer; ss.
XX

OS Homo sapiens.
XX
XX WO200157206-A2.
FN

XX 09-AUG-2001.
PD

XX 02-FEB-2001; 2001WO-US003504.
PP

XX 03-FEB-2000; 2000US-0179983P.
PR

XX (RIBO-) RIBOZYME PHARM INC.
PA (PATT/) PATTALEY A R.

XX Patlaey AR, Jarvis T, Mcswiggen J, Booher RN, Holman PS;
PI

XX WPI; 2001-496922/54.
DR

XX Novel nucleic acid molecule e.g., ribozymes or antisense nucleic acid
PT molecules, which downregulate expression of a checkpoint kinase-1 gene,
PT useful for treating colorectal, lung, breast or prostate cancers.
PI

XX Claim 4, Page 57, 115pp; English.
XX

XX The present invention provides nucleic acid molecules capable of
CC

CC downregulating the expression of the human checkpoint kinase-1 (Chk1)
CC gene. These may be antisense or ribozyme sequences, and are useful in the
CC treatment of diseases associated with conditions affected by Chk1 levels,
CC including cancer. The present sequence is an oligonucleotide described in
CC the exemplification of the invention

Sequence 17 BP; 6 A; 4 C; 4 G; 0 T; 3 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1369 TCTTCACGAGTCTC 1385
17 TCTTCACGAGTCTC 1

RESULT 377
ABK01580
ID ABK01580 standard; RNA; 17 BP.

AC ABK01580;
XX

XX 12-MAR-2002 (first entry)
DT

XX Human NOGO G-Cleaver #36.
DE

XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW cerebroprotective; neuroprotective; antiparkinsonian;
KW musclicular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KW DNAAzyme; inozyme; G-cleaver; amberszyme; zinzyme; lymphoma; leukaemia;
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
KW inflammatory arthropathy; central nervous system injury;
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW chemotherapeutic-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW Parkinson's disease; ataxia; Huntington's disease;
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX Homo sapiens.
OS Synthetic.
OS

XX WO200159103-A2.
FN

XX 16-AUG-2001.
PD

XX 09-FEB-2001; 2001WO-US004273.
PP

XX 11-FEB-2000; 2000US-0181797P.
PR

XX 28-FEB-2000; 2000US-0185516P.
PR

XX 06-MAR-2000; 2000US-0187128P.
PR

XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.

XX (MCSW/) MCSWIGGEN J.
PA (CHOW/) CHOWRIRA B M.

XX Blatt L, Mcswiggen J, Chowrira BM;
PI

XX WPI; 2001-607195/69.
DR

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
PT constructs, which down regulate expression of a CD20 gene or neurite
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
PT central nervous system injury.
PI

XX Claim 88; Page 92; 200pp; English.
XX

XX The invention relates to a nucleic acid molecule which down regulates
CC expression of a CD20 gene and a nucleic acid molecule which down
CC regulates expression of a neurite growth inhibitor gene (NOGO). The
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a

CC DNazyme) an Inozyme (an endolytic nucleic acid cleaving a an RNA molecule
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr
CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
CC of CD20 in the presence of a divalent cation that is preferably Mg^{2+} .
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
CC the cell and treat a patient having a condition associated with the level
CC of CD20. The treatment may further comprise the use of one or more
CC therapies. In particular, the CD20 targeting nucleic acid may be used to
CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-
CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
CC presence of a divalent cation that is preferably Mg^{2+} . Furthermore, the
CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
CC cell and treat a patient having a condition associated with the level of
CC NOGO. The treatment may further comprise the use of one or more
CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
CC treat central nervous system (CNS) injury and cerebrovascular accident
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NOGO expression. The present
CC sequence is a G-cleaver molecule of the invention
XX
SQ Sequence 17 BP; 1 A; 9 C; 3 G; 0 T; 4 U; 0 Other;
XX
Query Match 0.8*; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 2.8e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
XX
QY 545 CCAATCGCCGCTGCTTC 561
1 CCAATCCCGCGCTGCTTC 17
Db
RESULT 378
ABK02357/c
ID ABK02357 standard; RNA; 17 BP.
XX
AC ABK02357;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human NOGO Amberzyme #29.
XX
KW Human; ss; antisense therapy; cytosstatic; antiinflammatory; haemostatic;
KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
KW inflammatory arthropathy; central nervous system injury;
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW Parkinson's disease; ataxia; Huntington's disease;
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200159103-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001, 2001WO-US004273.
XX
PR 11-FEB-2000, 2000US-0181797P.
PR 28-FEB-2000, 2000US-0185516P.

PR 06-MAR-2000; 2000US-0187128P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGEN J.
PA (CHOW/) CHOWRIRA B M.
PI Blatt L, Mcswigen J, Chowrira BM;
XX
XX WPI; 2001-607195/69.
DR
XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
PT constructs, which down regulate expression of a CD20 gene or neurite
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
PT central nervous system injury.
XX
PS Claim 88; Page 131; 200pp; English.
XX
CC The invention relates to a nucleic acid molecule which down regulates
CC expression of a CD20 gene and a nucleic acid molecule which down
CC regulates expression of a neurite growth inhibitor gene (NOGO). The
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
CC DNazyme) an Inozyme (an endolytic nucleic acid cleaving a an RNA molecule
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr
CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
CC of CD20 in the presence of a divalent cation that is preferably Mg^{2+} .
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
CC the cell and treat a patient having a condition associated with the level
CC of CD20. The treatment may further comprise the use of one or more
CC therapies. In particular, the CD20 targeting nucleic acid may be used to
CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-
CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
CC presence of a divalent cation that is preferably Mg^{2+} . Furthermore, the
CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
CC cell and treat a patient having a condition associated with the level of
CC NOGO. The treatment may further comprise the use of one or more
CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
CC treat central nervous system (CNS) injury and cerebrovascular accident
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NOGO expression. The present
CC sequence is an amberzyme molecule of the invention
XX
SQ Sequence 17 BP; 8 A; 0 C; 9 G; 0 T; 0 U; 0 Other;
XX
Query Match 0.8*; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1003 CACATCTTCTTCTCTCT 1019
17 CTCCTCTTCTTCTCTCT 1
Db
RESULT 379
ABK02363
ID ABK02363 standard; RNA; 17 BP.
XX
AC ABK02363;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human NOGO Amberzyme #35.
XX
KW Human; ss; antisense therapy; cytosstatic; antiinflammatory; haemostatic;
KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;

muscular; CD20; neurite growth inhibitor gene; NODG; hammerhead ribozyme;
DNAzyme; inozyme; G-cleaver; amberyze; zinzyme; lymphoma; leukemia;
B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukemia;
human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
inflammatory arthropathy; central nervous system injury;
cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
Parkinson's disease; ataxia; Huntington's disease;
Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

Homo sapiens.
Synthetic.
WO200159103-A2.
16-AUG-2001.
09-FEB-2001; 2001WO-US004273.
11-FEB-2000; 2000US-0181797P.
28-FEB-2000; 2000US-018516P.
06-MAR-2000; 2000US-0187128P.
(RIBO-) RIBOZYME PHARM INC.
(BLAT/) BLATT L.
(MCSW/) MCSWIGEN J.
(CHOW/) CHOWRIRA B M.
Blatt L, Mcswigen J, Chowrira BM;
WPI; 2001-607195/69.
Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
constructs, which down regulate expression of a CD20 gene or neurite
growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
central nervous system injury.

Claim 88; Page 131; 200P; English.

The invention relates to a nucleic acid molecule which down regulates
expression of a CD20 gene and a nucleic acid molecule which down
regulates expression of a neurite growth inhibitor gene (NODG). The
nucleic acid may be enzymatic nucleic acids (e.g. a ribozyme or a
DNAzyme) and inozyme (an endolytic nucleic acid cleaving an RNA molecule
possessing an NCH motif), a G-cleaver (cleaving RNA with a NTR motif) or
an amberyze (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
with a VGY motif). The CD20-targeting nucleic acid is used to cleave RNA
of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
Furthermore, it may be contacted with a condition associated with the level
of CD20. The treatment may further comprise the use of one or more
therapies. In particular, the CD20 targeting nucleic acid may be used to
treat lymphoma, leukemia, B-cell lymphoma, low-grade or follicular NHL, lymphocytic
Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, mantle-cell
leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
immune thrombocytopenia, and inflammatory arthropathy. The NODG-
targeting nucleic acid is used to cleave RNA of the NODG gene in the
presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
nucleic acid may be contacted with a cell to reduce NODG activity of the
cell and treat a patient having a condition associated with the level of
NODG. The treatment may further comprise the use of one or more
therapies. In particular, the NODG-targeting nucleic acid may be used to
treat central nervous system (CNS) injury and cerebrovascular accident
(CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
disease, muscular dystrophy, and/or other neurodegenerative disease
states which respond to the modulation of NODG expression. The present
sequence is an amberyze molecule of the invention

Sequence 17 BP; 7 A; 0 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1306 GAGGAGGAGCCAGAGGA 1322
DB 1 GAGGAGGAGGAGGAGGA 17
|||||
RESULT 380
ADU93087
ID ADU93087 standard; DNA; 17 BP.
XX
AC ADU93087;
XX
DT 10-FEB-2005 (first entry)
XX
DE Human TERT NCH ribozyme substrate sequence #380.
XX
KW Enzymatic nucleic acid molecule; gene expression; down regulation;
XX protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;
KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
KW C-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
KW amberyze; zinzyme; DNAzyme; cancer; breast cancer; Alzheimer's disease;
KW diabetes; obesity; cardiac disease; heart disease; age-related disease;
KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
KW ds.
XX
OS Homo sapiens.
XX
XX WO200116312-A2.
XX
XX 08-MAR-2001.
XX
XX 30-AUG-2000; 2000WO-US023998.
XX
XX 31-AUG-1999; 99US-0151713P.
XX 27-SEP-1999; 99US-00406643.
XX 27-SEP-1999; 99US-0156236P.
XX 27-SEP-1999; 99US-0156467P.
XX 08-NOV-1999; 99US-00436430.
XX 06-DEC-1999; 99US-0169100P.
XX 29-DEC-1999; 99US-00474432.
XX 29-DEC-1999; 99US-0173612P.
XX 30-DEC-1999; 99US-00476387.
XX 04-FEB-2000; 2000US-00498824.
XX 20-MAR-2000; 2000US-00531025.
XX 14-APR-2000; 2000US-0197769P.
XX 23-MAY-2000; 2000US-00578223.
XX 09-AUG-2000; 2000US-00636385.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
XX Mcswigen J, Usman N, Blatt L, Beigelman L, Burgin A;
XX Karpelsky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
XX Stinchcomb D, Beaudry A, Zinnen S, Lugwig J, Sproat BS;
XX
XX WPI; 2001-244406/25.
XX
XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules
XX are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
XX obesity and heart disease.
XX
XX Example 1; Page 284; 717P; English.

The present invention relates to the use of enzymatic nucleic acid
molecules (e.g. ribozymes) to modulate gene expression. The invention of
also methods for their use to down regulate or inhibit the expression of
genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine
aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C

CC	alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
CC	receptor-2 (HER2/c-erbB2/neu), phospholamban (PLN), presenilin-1 (ps-1),
CC	presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
CC	nucleic acid molecules used to inhibit the expression of the said genes
CC	include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,
CC	zincyme, and/or DNAzyme motifs. The methods of the invention are useful
CC	for treating cancer, in particular breast cancer, Alzheimer's disease,
CC	diabetes, obesity, cardiac diseases e.g. heart disease, age-related
CC	diseases, hepatitis B infections, and hepatitis and hepatocellular
CC	carcinoma. The enzymatic nucleic acid molecules can also be used as
CC	diagnostic tools to examine genetic drift and mutations within diseased
CC	cells and to detect the presence of specific RNA in a cell. The present
CC	sequence represents a substrate/target sequence for a ribozyme used in
CC	the examples of the present invention. Note: Some SEQ ID Nos are repeated
CC	more than once in the specification, but these have different sequences
CC	associated with them.
SQ	Sequence 17 BP; 2 A; 6 C; 8 G; 1 T; 0 U; 0 Other;
Query Match	0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity	88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
Gy	1295 TGGGCGCCACGAGGAG 1311 Db 1 TGGCGCGCCCCGAGGAG 17
RESULT 381	
ID ADU93088	standard; DNA; 17 BP.
AC ADU93088;	
XX 10-FEB-2005	(first entry)
DT Human TERT NCH ribozyme substrate sequence #381.	
DE	
XX Enzymatic nucleic acid molecule; gene expression; down regulation; KW protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase; KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha; KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2; KW c-erbB2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2; KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver; KW amberzyme; zincyme; DNzyme; cancer; breast cancer; Alzheimer's disease; KW diabetes; obesity; cardiac disease; heart disease; age-related disease; KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human; KW da. KM Homo sapiens. OS XX XX WO200116312-A2. PN PD 08-MAR-2001. DD PF 30-AUG-2000; 200OWO-US023998. XX XX 31-AUG-1999; 99US-0151713P. PR 27-SEP-1999; 99US-00406643. PR 27-SEP-1999; 99US-0156236P. PR 27-SEP-1999; 99US-0156467P. PR 08-NOV-1999; 99US-00436430. PR 06-DEC-1999; 99US-0169100P. PR 29-DEC-1999; 99US-00474432. PR 29-DEC-1999; 99US-0173612P. PR 30-DEC-1999; 99US-00476367. PR 04-FEB-2000; 2000US-00498824. PR 20-MAR-2000; 2000US-0053102S. PR 14-APR-2000; 2000US-0197769P. PR 23-MAY-2000; 2000US-00578223. PR 09-AUG-2000; 2000US-00636385. XX PA (RIBO-) RIBOZYME PHARM INC.	

```

XX PI McSwiggen J, Usman N, Blatt L, Beigelman L, Burgin A;
PI Karpelisky A, Matulic-Adamic J, Swiedler D, Draper K, Chowrira B;
PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;
XX WPI, 2001-244406/25.
XX
XX PS Example 1; Page 284; 717pp; English.
XX
XX CC The present invention relates to the use of enzymatic nucleic acid
XX CC molecules (e.g. ribozymes) to modulate gene expression. The invention
XX CC also methods for their use to down regulate or inhibit the expression of
XX CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine
XX CC aminopeptidase (MeCAP-2), human telomerase (hTERT), protein kinase C
XX CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
XX CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
XX CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
XX CC nucleic acid molecules used to inhibit the expression of the said genes
XX CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,
XX CC zinczyme, and/or DNzyme motifs. The methods of the invention are useful
XX CC for treating cancer, in particular breast cancer, Alzheimer's disease,
XX CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related
XX CC diseases, hepatitis B infections, and hepatitis and hepatocellular
XX CC carcinoma. The enzymatic nucleic acid molecules can also be used as
XX CC diagnostic tools to examine genetic drift and mutations within diseased
XX CC cells and to detect the presence of specific RNA in a cell. The present
XX CC sequence represents a substrate/target sequence for a ribozyme used in
XX CC the examples of the present invention. Note: Some SEQ ID Nos are repeated
XX CC more than once in the specification, but these have different sequences
XX CC associated with them.
XX
XX SQ Sequence 17 BP; 2 A; 6 C; 9 G; 0 T; 0 U; 0 Other;
XX
XX QY 1296 GGGGGCCCGCAGGAGG 1312
XX |||||||
XX 1 GGGGGCCCGCAGGAGG 17
XX
XX DB
XX
XX RESULT 382
XX ADU86314
XX ID ADU86314 standard; DNA; 17 BP.
XX
XX AC ADU86314;
XX
XX DT 10-FEB-2005 (first entry)
XX
XX DE Human TERT hammerhead ribozyme substrate sequence #345.
XX
XX KW Enzymatic nucleic acid molecule; gene expression; down regulation;
XX KW protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase;
XX KW MeCAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
XX KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
XX KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
XX KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
XX KW amberzyme; zinczyme; DNzyme; cancer; breast cancer; Alzheimer's disease;
XX KW diabetes; obesity; cardiac disease; heart disease; age-related disease;
XX KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
XX KW ds.
XX
XX OS Homo sapiens.
XX
XX FN WO200116312-A2.
XX
XX PD 08-MAR-2001.
XX

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30-AUG-2000; 2000MO-US023998.
 31-AUG-1999; 99US-0151713P.
 27-SEP-1999; 99US-00406643.
 27-SEP-1999; 99US-0156236P.
 27-SEP-1999; 99US-0156467P.
 08-NOV-1999; 99US-00436430.
 06-DEC-1999; 99US-0169100P.
 29-DEC-1999; 99US-00474432.
 29-DEC-1999; 99US-0173612P.
 30-DEC-1999; 99US-00476387.
 04-FEB-2000; 2000US-00498824.
 20-MAR-2000; 2000US-00531025.
 14-APR-2000; 2000US-0197769P.
 23-MAY-2000; 2000US-00578223.
 09-AUG-2000; 2000US-00636385.
 (RIBO-) RIBOZYME PHARM INC.
 Mcswiggen J, Usman N, Blatt L, Beigelman L, Burgin A, Chowrira B, Karpelsky A, Matulich-Adamic J, Sweedler D, Draper K, Sproat BS, Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;
 WPI; 2001-244406/25.
 Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes, obesity and heart disease.
 Example 1; Page 274; 717P; English.
 The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention of also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine C aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C receptor-2 (PKC alpha), beta-secretase (BACE), human epidermal growth factor receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1), and hepatitis B virus (HBV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, zinczyme, and/or DNAzyme motifs. The methods of the invention are useful for treating cancer, in particular breast cancer, Alzheimer's disease, diabetes, obesity, cardiac diseases e.g. heart disease, age-related diseases, hepatitis B infections, and hepatitis and hepatocellular carcinoma. The enzymatic nucleic acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased cells and to detect the presence of specific RNA in a cell. The present invention represents a substrate/target sequence for a ribozyme used in the examples of the present invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have different sequences associated with them.
 Sequence 17 BP; 3 A; 7 C; 2 G; 5 T; 0 U; 0 Other;
 Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No.2.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1690 CAGCTTTCTCAAG 1706
 DB 1 CAGCTTTCTCAAG 17
 RESULT 383
 ADU92547/c
 ID ADU92547 standard; DNA; 17 BP.
 AC ADU92547;
 XX 10-FEB-2005 (first entry)
 XX Human TERT NCH ribozyme substrate sequence #122.
 DE

Enzymatic nucleic acid molecule; gene expression; down regulation;
 protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;
 MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
 beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
 c-erbB; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
 hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
 amberzyme; zinczyme; DNAzyme; cancer; breast cancer; Alzheimer's disease;
 diabetes; obesity; cardiac disease; heart disease; age-related disease;
 hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
 ds.
 Homo sapiens.
 WO200116312-A2.
 08-MAR-2001.
 30-AUG-2000; 2000MO-US023998.
 31-AUG-1999; 99US-0151713P.
 27-SEP-1999; 99US-00406643.
 27-SEP-1999; 99US-0156236P.
 27-SEP-1999; 99US-0156467P.
 08-NOV-1999; 99US-00436430.
 06-DEC-1999; 99US-0169100P.
 29-DEC-1999; 99US-00474432.
 29-DEC-1999; 99US-0173612P.
 30-DEC-1999; 99US-00476387.
 04-FEB-2000; 2000US-00498824.
 20-MAR-2000; 2000US-00531025.
 14-APR-2000; 2000US-0197769P.
 23-MAY-2000; 2000US-00578223.
 09-AUG-2000; 2000US-00636385.
 (RIBO-) RIBOZYME PHARM INC.
 Mcswiggen J, Usman N, Blatt L, Beigelman L, Burgin A, Chowrira B, Karpelsky A, Matulich-Adamic J, Sweedler D, Draper K, Chowrira B, Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;
 WPI; 2001-244406/25.
 Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes, obesity and heart disease.
 Example 1; Page 278; 717P; English.
 The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention of also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine C aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor receptor-2 (PKC alpha), beta-secretase (BACE), human epidermal growth factor receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1), and hepatitis B virus (HBV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, zinczyme, and/or DNAzyme motifs. The methods of the invention are useful for treating cancer, in particular breast cancer, Alzheimer's disease, diabetes, obesity, cardiac diseases e.g. heart disease, age-related diseases, hepatitis B infections, and hepatitis and hepatocellular carcinoma. The enzymatic nucleic acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased cells and to detect the presence of specific RNA in a cell. The present invention represents a substrate/target sequence for a ribozyme used in the examples of the present invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have different sequences associated with them.
 Sequence 17 BP; 0 A; 4 C; 9 G; 4 T; 0 U; 0 Other;
 SQ

Query Match 0.8*; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
1450 GCAGGTGCGCCGCCAC 1466
17 GCAGCAGCAGCCGCCAC 1
Db

RESULT 384
ADU93086
ID ADU93086 standard; DNA; 17 BP.
XX
AC ADU93086;
XX
DT 10-FEB-2005 (first entry)
XX
DE Human TERT NCH ribozyme substrate sequence #379.
XX
KM Enzymatic nucleic acid molecule; gene expression; down regulation;
KM protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;
KM MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
KM beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
KM c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
KM hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
KM amberyyme; zinzyme; DNAzyme; cancer; breast cancer; Alzheimer's disease;
KM diabetes; obesity; cardiac disease; heart disease; age-related disease;
KM hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
KM de.
XX
OS Homo sapiens.
XX
PN WO200116312-A2.
XX
PD 08-MAR-2001.
XX
PF 30-AUG-2000; 2000WO-US023998.
XX
PR 31-AUG-1999; 99US-0151713P.
PR 27-SEP-1999; 99US-00406643.
PR 27-SEP-1999; 99US-0156236P.
PR 27-SEP-1999; 99US-0156467P.
PR 08-NOV-1999; 99US-00436430.
PR 06-DEC-1999; 99US-0169100P.
PR 29-DEC-1999; 99US-00474432.
PR 29-DEC-1999; 99US-0173612P.
PR 30-DEC-1999; 99US-00476387.
PR 04-FEB-2000; 2000US-00498824.
PR 20-MAR-2000; 2000US-00531025.
PR 14-APR-2000; 2000US-0197769P.
PR 23-MAY-2000; 2000US-00578223.
PR 09-AUG-2000; 2000US-00636385.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Ueman N, Blatt L, Beigelman L, Burgin A;
PI Karpelesky A, Matulic-Adamic J, Sweedler D, Draper K, Chowwira B;
PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sprout BS;
XX
XX WPI; 2001-244406/25.
XX
PT Enzymatic nucleic acid molecules able to cleave separate RNA molecules
PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
PT obesity and heart disease.
XX
XX Example 1; Page 284; 717pp; English.
XX
XX The present invention relates to the use of enzymatic nucleic acid
XX molecules (e.g. ribozymes) to modulate gene expression. The invention
XX also methods for their use to down regulate or inhibit the expression of
XX genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine
XX aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
XX alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor

CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
CC nucleic acid molecules used to inhibit the expression of the said genes
CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberyyme,
CC zinzyme, and/or DNAzyme motifs. The methods of the invention are useful
CC for treating cancer, in particular breast cancer, Alzheimer's disease,
CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related
CC diseases, hepatitis B infections, and hepatitis and hepatocellular
CC carcinoma. The enzymatic nucleic acid molecules can also be used as
CC diagnostic tools to examine genetic drift and mutations within diseased
CC cells and to detect the presence of specific RNA in a cell. The present
CC sequence represents a substrate/target sequence for a ribozyme used in
CC the examples of the present invention. Note: Some SEQ ID Nos are repeated
CC more than once in the specification, but these have different sequences
CC associated with them.
XX
XX SQ Sequence 17 BP; 2 A; 6 C; 8 G; 1 T; 0 U; 0 Other;
XX

Query Match 0.8*; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
1294 GTGGGCGCCCGCAGCA 1310
1 GTGGCGCCCGCCGAGCA 17
Db

RESULT 385
ADV62161
ID ADV62161 standard; RNA; 17 BP.
XX
AC ADV62161;
XX
DT 10-FEB-2005 (first entry)
XX
DE HBV amberyyme ribozyme substrate sequence #528.
XX
KM Enzymatic nucleic acid molecule; gene expression; down regulation;
KM protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;
KM MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
KM beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
KM c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
KM hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
KM amberyyme; zinzyme; DNAzyme; cancer; breast cancer; Alzheimer's disease;
KM diabetes; obesity; cardiac disease; heart disease; age-related disease;
KM hepatitis B infection; hepatocellular carcinoma; genetic drift; ss.
XX
XX Hepatitis B virus.
XX
PN WO200116312-A2.
XX
PD 08-MAR-2001.
XX
PF 30-AUG-2000; 2000WO-US023998.
XX
PR 31-AUG-1999; 99US-0151713P.
PR 27-SEP-1999; 99US-00406643.
PR 27-SEP-1999; 99US-0156236P.
PR 27-SEP-1999; 99US-0156467P.
PR 08-NOV-1999; 99US-00436430.
PR 06-DEC-1999; 99US-0169100P.
PR 29-DEC-1999; 99US-00474432.
PR 29-DEC-1999; 99US-0173612P.
PR 30-DEC-1999; 99US-00476387.
PR 04-FEB-2000; 2000US-00498824.
PR 20-MAR-2000; 2000US-00531025.
PR 14-APR-2000; 2000US-0197769P.
PR 23-MAY-2000; 2000US-00578223.
PR 09-AUG-2000; 2000US-00636385.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Ueman N, Blatt L, Beigelman L, Burgin A;

PI Karpelsky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;
XX WPI; 2001-244406/25.
XX
XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules
PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
PT obesity and heart disease.
XX
XX Example 6; Page 578; 717pp; English.
XX
XX The present invention relates to the use of enzymatic nucleic acid
XX molecules (e.g. ribozymes) to modulate gene expression. The invention
XX also methods for their use to down regulate or inhibit the expression of
XX genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine
XX aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
XX alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
XX receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presentin-1 (ps-1),
XX presentin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
XX nucleic acid molecules used to inhibit the expression of the said genes
XX include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,
XX zincyme, and/or DNAzyme motifs. The methods of the invention are useful
XX for treating cancer, in particular breast cancer, Alzheimer's disease,
XX diabetes, obesity, cardiac diseases e.g. heart disease, age-related
XX diseases, hepatitis B infections, and hepatitis and hepatocellular
XX carcinoma. The enzymatic nucleic acid molecules can also be used as
XX diagnostic tools to examine genetic drift and mutations within diseased
XX cells and to detect the presence of specific RNA in a cell. The present
XX sequence represents a substrate for a ribozyme used in the examples of
XX the present invention. Note: Some SEQ ID Nos are repeated more than once
XX in the specification, but these have different sequences associated with
XX them.
XX
XX SEQ Sequence 17 BP; 4 A; 6 C; 5 G; 0 T; 2 U; 0 Other;
XX
XX Query Match 0.8%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 76.5%; Pred. No. 2.8e+02;
XX Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1267 CGCGCTGAGACGCCAT 1283
XX 1 CGCAUGGAGACCAACCGU 17
XX
XX RESULT 386
XX ID ADV62160 standard; RNA; 17 BP.
XX AC ADV62160;
XX
XX DT 10-FEB-2005 (first entry)
XX
XX DE HBV amberzyme ribozyme substrate sequence #527.
XX
XX Enzymatic nucleic acid molecule; gene expression; down regulation;
XX protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase;
XX MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
XX beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
XX c-erb2; neu; phospholamban; PLN; presentin-1; ps-1; presentin-2; ps-2;
XX hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
XX amberzyme; zincyme; DNAzyme; cancer; breast cancer; Alzheimer's disease;
XX diabetes; obesity; cardiac disease; heart disease; age-related disease;
XX hepatitis B infection; hepatocellular carcinoma; genetic drift; ss.
XX
XX KW Hepatitis B virus.
XX OS
XX AC
XX PN WO200116312-A2.
XX
XX PD 08-MAR-2001.
XX
XX PF 30-AUG-2000; 2000WO-US023998.
XX
XX PR 31-AUG-1999; 99US-0151713P.
XX

PR 27-SEP-1999; 99US-00406643.
PR 27-SEP-1999; 99US-016236P.
PR 27-SEP-1999; 99US-016467P.
PR 08-NOV-1999; 99US-00436430.
PR 06-DEC-1999; 99US-0169100P.
PR 29-DEC-1999; 99US-00474432.
PR 29-DEC-1999; 99US-0173612P.
PR 30-DEC-1999; 99US-00476387.
PR 04-FEB-2000; 2000US-00498824.
PR 20-MAR-2000; 2000US-00531025.
PR 14-APR-2000; 2000US-0197769P.
PR 23-MAY-2000; 2000US-00578223.
PR 09-AUG-2000; 2000US-00636385.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX PA
XX PI Meswigen J, Usman N, Blatt L, Beigelman L, Burgin A;
XX Karpelsky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
XX Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;
XX WPI; 2001-244406/25.
XX
XX DR
XX XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules
XX are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
XX obesity and heart disease.
XX
XX XX Example 6; Page 578; 717pp; English.
XX
XX PS The present invention relates to the use of enzymatic nucleic acid
XX molecules (e.g. ribozymes) to modulate gene expression. The invention
XX also methods for their use to down regulate or inhibit the expression of
XX genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine
XX aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
XX alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
XX receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presentin-1 (ps-1),
XX presentin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
XX nucleic acid molecules used to inhibit the expression of the said genes
XX include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,
XX zincyme, and/or DNAzyme motifs. The methods of the invention are useful
XX for treating cancer, in particular breast cancer, Alzheimer's disease,
XX diabetes, obesity, cardiac diseases e.g. heart disease, age-related
XX diseases, hepatitis B infections, and hepatitis and hepatocellular
XX carcinoma. The enzymatic nucleic acid molecules can also be used as
XX diagnostic tools to examine genetic drift and mutations within diseased
XX cells and to detect the presence of specific RNA in a cell. The present
XX sequence represents a substrate for a ribozyme used in the examples of
XX the present invention. Note: Some SEQ ID Nos are repeated more than once
XX in the specification, but these have different sequences associated with
XX them.
XX
XX SQ Sequence 17 BP; 4 A; 6 C; 5 G; 0 T; 2 U; 0 Other;
XX
XX Query Match 0.8%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 82.4%; Pred. No. 2.8e+02;
XX Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1265 GCGCGCTGAGACGCC 1281
XX 1 GUGCGAUGGAGACCAACC 17
XX
XX RESULT 387
XX ID ADV03744 standard; RNA; 17 BP.
XX AC ADV03744;
XX
XX DT 10-FEB-2005 (first entry)
XX
XX DE Human BACE NCH ribozyme substrate sequence #555.
XX
XX KW Enzymatic nucleic acid molecule; gene expression; down regulation;
XX protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase;
XX

KM MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
KM beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
KM c-erbB2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
KM hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
KM amberzyme; zinzyme; DNazyme; cancer; breast cancer; Alzheimer's disease;
KM diabetes; obesity; cardiac disease; heart disease; age-related disease;
KM hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
KM sr.
XX Homo sapiens.
XX
XX WO200116312-A2.
XX
XX 08-MAR-2001.
XX
XX 30-AUG-2000; 2000WO-US023998.
XX
XX 31-AUG-1999; 99US-0151713P.
XX 27-SEP-1999; 99US-00406643.
XX 27-SEP-1999; 99US-0156236P.
XX 27-SEP-1999; 99US-0156467P.
XX 08-NOV-1999; 99US-00436430.
XX 06-DEC-1999; 99US-0169100P.
XX 29-DEC-1999; 99US-00474432.
XX 29-DEC-1999; 99US-0173612P.
XX 30-DEC-1999; 99US-00476387.
XX 04-FEB-2000; 2000US-00498824.
XX 20-MAR-2000; 2000US-00531025.
XX 14-APR-2000; 2000US-0197769P.
XX 23-MAY-2000; 2000US-00578223.
XX 09-AUG-2000; 2000US-00636385.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX McSwiggen J, Uzman N, Blatt L, Beigelman L, Burgin A;
XX Karpelsky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
XX Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;
XX WPI; 2001-244406/25.
XX
XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules
XX are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
XX obesity and heart disease.
XX
XX Example 4; Page 360; 717pp; English.
XX
XX The present invention relates to the use of enzymatic nucleic acid
XX molecules (e.g. ribozymes) to modulate gene expression. The invention
XX also methods for their use to down regulate or inhibit the expression of
XX genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine
XX aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
XX alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
XX receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
XX presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
XX nucleic acid molecules used to inhibit the expression of the said genes
XX include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,
XX zinzyme, and/or DNazyme motifs. The method of the invention are useful
XX for treating cancer, in particular breast cancer, Alzheimer's disease,
XX diabetes, obesity, cardiac diseases e.g. heart disease, age-related
XX diseases, hepatitis B infections, and hepatitis and hepatocellular
XX carcinoma. The enzymatic nucleic acid molecules can also be used as
XX diagnostic tools to examine genetic drift and mutations within diseased
XX cells and to detect the presence of specific RNA in a cell. The present
XX sequence represents a substrate/target sequence for a ribozyme used in
XX the examples of the present invention. Note: Some SEQ ID Nos are repeated
XX more than once in the specification, but these have different sequences
XX associated with them.
XX
XX Sequence 17 BP; 3 A; 10 C; 2 G; 0 T; 2 U; 0 Other;
XX
XX Query Match 0.84; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 76.5%; Pred. No. 2.8e+02;
XX Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1346 CCTGACCTGACCTCC 1362
Db 1 CCCUGACACACACUCC 17
RESURF 388
ADU93089
ID ADU93089 standard; DNA; 17 BP.
XX
XX AC ADU93089;
XX
XX 10-FEB-2005 (first entry)
XX
XX DE Human TERT NCH ribozyme substrate sequence #382.
XX
XX Enzymatic nucleic acid molecule; gene expression; down regulation;
KM protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase;
KM MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
KM beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
KM c-erbB2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
KM hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
KM amberzyme; zinzyme; DNazyme; cancer; breast cancer; Alzheimer's disease;
KM diabetes; obesity; cardiac disease; heart disease; age-related disease;
KM hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
KM sr.
XX
XX Homo sapiens.
XX
XX WO200116312-A2.
XX
XX 08-MAR-2001.
XX
XX 30-AUG-2000; 2000WO-US023998.
XX
XX 31-AUG-1999; 99US-0151713P.
XX 27-SEP-1999; 99US-00406643.
XX 27-SEP-1999; 99US-0156236P.
XX 27-SEP-1999; 99US-0156467P.
XX 08-NOV-1999; 99US-00436430.
XX 06-DEC-1999; 99US-0169100P.
XX 29-DEC-1999; 99US-00474432.
XX 29-DEC-1999; 99US-0173612P.
XX 30-DEC-1999; 99US-00476387.
XX 04-FEB-2000; 2000US-00498824.
XX 20-MAR-2000; 2000US-00531025.
XX 14-APR-2000; 2000US-0197769P.
XX 23-MAY-2000; 2000US-00578223.
XX 09-AUG-2000; 2000US-00636385.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX McSwiggen J, Uzman N, Blatt L, Beigelman L, Burgin A;
XX Karpelsky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
XX Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;
XX WPI; 2001-244406/25.
XX
XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules
XX are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
XX obesity and heart disease.
XX
XX Example 1; Page 284; 717pp; English.
XX
XX The present invention relates to the use of enzymatic nucleic acid
XX molecules (e.g. ribozymes) to modulate gene expression. The invention
XX also methods for their use to down regulate or inhibit the expression of
XX genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine
XX aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
XX alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
XX receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
XX presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
XX nucleic acid molecules used to inhibit the expression of the said genes

PA (AEOM-) AEOMICA INC.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
XX Disclosure; SEQ ID NO 2756; 214bp; English.
XX
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates; to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
XX Sequence 17 BP; 4 A; 2 C; 8 G; 3 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1196 GCGACTATGAGGCGCTG 1212
Db 1 GCGAGTATGAGAGCTG 17
RESULT 391
AB063570
ID AB063570 standard; DNA; 17 BP.
XX
XX AB063570;
AC
XX 20-AUG-2002 (first entry)
XX
XX
DE Human KTOM1a portion (AB063232) probe # 283.
XX
XX Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytoskeletal;
XX gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
XX kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.
OS
XX Homo sapiens.
XX
XX WO200224750-A2.
XX
XX 28-MAR-2002.
PD
XX 21-SEP-2001; 2001WO-US029656.
PF
XX 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.

PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 28-AUG-2001; 2001US-0315676P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Zhang J;
XX WPI; 2002-479509/51.
XX
XX New human kidney tumor overexpressed membrane (KTOM1) protein and nucleic
PT acids encoding the protein, useful for treating subjects having defects
PT in KTOM1 which can manifest as cancer of the kidney, or as a disorder of
PT e.g., liver or bone.
XX
XX Example 2; Page 194; 418bp; English.
XX
XX The invention relates to a novel isolated nucleic acid encoding human
CC KTOM1 (kidney tumour overexpressed membrane) protein. The protein of the
CC invention has cytostatic activity. The nucleotide may have a use in gene
CC therapy. The KTOM1 nucleic acids may be used to diagnose, treat or
CC monitor a disease caused by altered expression of human KTOM1.
CC Compositions comprising the nucleic acids, proteins or antibodies may be
CC used to treat subjects having defects in KTOM1 which can manifest as
CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,
CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
CC function. The sequence represents a probe used in the invention to scan
CC the nt 1-1001 portion of human KTOM1a (AB063232)
XX
XX Sequence 17 BP; 2 A; 5 C; 2 G; 8 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1402 AGCTTCAGTTCTTCCTC 1418
Db 1 AGCTTCAGTTCTTCCTC 17
RESULT 392
ABV83022/C
ID ABV83022 standard; DNA; 17 BP.
XX
XX ABV83022;
AC
XX 03-JAN-2003 (first entry)
XX
XX
DE Human HTP1 scanning oligonucleotide SEQ ID 4268.
XX
XX Human; gene therapy; tumour suppressor; HTP1; chromosome 10p12.1;
XX human testis expressed Patched like protein; testis; adrenal; liver;
XX male germ cell development; bone marrow; brain; kidney; lung; placenta;
XX prostate; skeletal muscle; colon; male infertility; cancer; ss.
OS
XX Homo sapiens.
XX
XX EP1229046-A2.
XX
XX 07-AUG-2002.
PD
XX 28-JAN-2002; 2002EP-00001167.
PF
XX 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.

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PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 23-MAY-2001; 2001US-00864761.
PR 09-OCT-2001; 2001US-0327898P.
PA (AEOM-) AEOMICA INC.
XX Zhan J;
XX WPI; 2002-676582/73.
XX
XX Novel isolated human testis expressed Patched like protein (HTPL), useful
XX for identifying agonist and antagonist and specific binding partners, and
XX for treating subjects having defects in HTPL.
XX
XX Example 2; Page 623; 718pp; English.
XX
XX The present invention relates to human testis expressed patched like
XX protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
XX has two isoforms, with a few single base pair differences between the
XX two. One of the single base pair changes introduces a premature stop
XX codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
XX shares an overall structure organisation with the Patched protein. The
XX shared structural features strongly imply that HTPL plays a role similar
XX to that of Patched, and is a potential tumour suppressor. HTPL is
XX important in regulating male germ cell development, and the HTPL gene was
XX mapped to human chromosome 10p12.1. HTPL and its coding sequence are
XX useful for diagnosing a disorder caused by mutation in HTPL, and in
XX therapy and manufacture of a medicament for treatment or prevention of
XX such disorder associated with decreased expression or activity of human
XX HTPL. Such disorders include disorders of testis, or adrenal, adult and
XX foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
XX skeletal muscle or colon function. HTPL proteins and nucleic acids are
XX clinically useful diagnostic markers and potential therapeutic agents for
XX male infertility and cancer. The present oligonucleotide was used in an
XX example from the invention
XX
XX Sequence 17 BP; 2 A; 5 C; 7 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 2.8e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1089 GGCATGAGCTCCACCA 1105
XX 17 GGCATGAGCTGCCCA 1
XX
XX RESULT 393
XX ABV90740/C
XX ID ABV90740 standard; DNA; 17 BP.
XX
XX AC ABV90740;
XX
XX DT 23-DEC-2002 (first entry)
XX
XX DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1453.
XX
XX KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
XX Rho GTPase; signal transduction; gene expression; cancer; vaccine;
XX gene therapy; transgenic; ss.
XX
XX OS Homo sapiens.
XX
XX PN EP1239051-A2.
XX
XX PD 11-SEP-2002.
XX
XX PF 28-JAN-2002; 2002EP-00001165.
XX
XX PR 30-JAN-2001; 2001WO-US000663.
XX
XX PR 30-JAN-2001; 2001WO-US000664.
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PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 10-OCT-2001; 2001US-0328205P.
PA (AEOM-) AEOMICA INC.
XX Shannon M;
XX WPI; 2002-684061/74.
XX
XX Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL
XX -1, useful for treating disorders associated with decreased expression or
XX activity of human POSHL1.
XX
XX Example 2; SEQ ID NO 1453; 60pp + Sequence Listing; English.
XX
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
XX protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
XX acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
XX (S1) having 95% deviations, especially conservative substitutions or a
XX fragment of the sequences comprising at least 8 contiguous amino acids.
XX Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
XX adaptor protein that interacts with Rho family small GTPases as well as
XX downstream components of the signal transduction pathway. (I) is useful
XX for identifying a specific binding partner. (I) and nucleic acids (II)
XX encoded by altered expression of human POSHL1 including diagnosing and
XX caused by altered expression of human POSHL1 including diagnosing and
XX treating cancer, they useful in the development of vaccines and (II) is
XX useful in gene therapy. (II) is useful for constructing microarrays which
XX are useful for measuring and for surveying gene expression and creating
XX transgenic non-human animals capable of producing the proteins. The
XX present sequence is that of a scanning oligonucleotide useful in examples
XX of the invention. Note: The present sequence did not form part of the
XX printed specification, but is based on sequence information supplied to
XX Derwent by the European Patent Office
XX
XX Sequence 17 BP; 5 A; 4 C; 6 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 2.8e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1444 CTTTGGCAGGTGCAGC 1460
XX 17 CTTTGGCAGGTGCAGC 1
XX
XX RESULT 394
XX ABL31550
XX ID ABL31550 standard; DNA; 17 BP.
XX
XX AC ABL31550;
XX
XX DT 21-MAR-2002 (first entry)
XX
XX DE Human HLA genotyping oligonucleotide SEQ ID NO 1039.
XX
XX KW Human; human leukocyte antigen; HLA; genotype; polymorphism;
XX immunogenetic; transplantation; genetic disease; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200192572-A1.
XX
XX PD 06-DEC-2001.
XX
XX PF 01-JUN-2001; 2001WO-JP004662.
XX
```


PR 01-JUN-2000; 2000JP-00164798.
XX (N1SN) NISSHINO IND INC.
PA (SYST-) SYSTEM RES INC.
XX Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;
DR WPI; 2002-122074/16.
XX Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of
PT individuals e.g. by determining immunogenetic differences when
XX transplanting between them.
PS Claim 10; Page 290; 345pp; Japanese.
XX The invention relates to a typing kit for judging human leukocyte antigen
CC (HLA) genotype of a sample by hybridising a substrate on which 10-24 base
CC oligonucleotides (ABL30512-ABL31809) originating in the sequences of
CC genes e.g. belonging to HLA class I antigens on human genome and
CC containing gene polymorphisms as alloantigens have been immobilised as
CC primers for amplification of cleaved nucleic acids relating to gene
CC polymorphisms. The method is useful for judging HLA genotypes of
CC individuals by determining immunogenetic differences before transplanting
CC between them, providing genetic information to decide compatibility of
CC organ and tissue for transplantation e.g. of bone marrow, kidney, liver,
CC pancreas, langerhans islet in pancreas and cornea, susceptibility
CC diagnosis of genetic diseases and identifying individuals
SQ Sequence 17 BP; 3 A; 5 C; 8 G; 1 T; 0 U; 0 Other;
Qy Query Match 0.84; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.24; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1299 GGGCCACGAGGAGGAC 1315
Db 1 GGGCCATGAGCGGAGC 17
RESULT 395
ABQ76743/C
ID ABQ76743 standard; DNA; 17 BP.
XX
AC ABQ76743;
XX
DT 03-MAR-2003 (first entry)
XX
DE TNF-associated PCR primer #2.
XX
KM Shine-Dalgarno; exogenous gene expression; filamentous blue-green algae;
KM promoter; PCR; primer; ss.
XX
OS Unidentified.
XX
PN CNI353189-A.
XX
PD 12-JUN-2002.
XX
PF 14-NOV-2000; 2000CN-00132268.
XX
PR 14-NOV-2000; 2000CN-00132268.
XX
PA (PHYT-) INST PHYTOLOGY CHINESE ACAD SCI.
XX
PI Shi D, Ran L, Li Y;
XX
DR WPI; 2002-751432/82.
XX
PT Efficient expression box of filamentous blue-green algae.
XX
PS Example; Page 4 (Disclosure); 9pp; Chinese.
XX
CC This invention describes a novel, efficient expression box for

CC effectively expressing an exogenous gene in filamentous blue-green algae.
CC The box includes a promoter, a Shine-Dalgarno (SD) sequence and a target
CC gene. This sequence represents a PCR primer associated with the
CC amplification of TNF, described in the disclosure of the invention
XX
SQ Sequence 17 BP; 4 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
Qy Query Match 0.84; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.24; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 891 GATCCCGGAGACTCCT 907
Db 17 GATCCCGGAGATTCT 1
RESULT 396
ACN01554
ID ACN01554 standard; RNA; 17 BP.
XX
AC ACN01554;
XX
DT 22-APR-2004 (first entry)
XX
DE MNV Inozyme substrate SEQ ID NO 1544.
XX
KM MNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KM virucide; neuroprotective; antibacterial; replication; pancreatitis;
KM encephalitis; myocarditis; meningitis; infection; hepatitis;
KM liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
KM Amberzyme; Zinzyme; ss.
XX
OS West Nile Virus.
XX
PN W0200268637-A2.
XX
PD 06-SEP-2002.
XX
PF 19-OCT-2001; 2001WO-US048350.
XX
PR 20-OCT-2000; 2000US-0242411P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGEN J A.
XX
PI Blatt L, Mcswiggen JA;
XX
DR WPI; 2002-706994/76.
XX
PT New nucleic acid molecule that modulates replication of West Nile Virus
PT (MNV), useful for treating a condition related to MNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
PS Claim 23; SEQ ID NO 1544; 495pp; English.
XX
CC The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (MNV). The nucleic acid molecules are useful for
CC treating a condition related to MNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
SQ Sequence 17 BP; 6 A; 7 C; 4 G; 0 T; 0 U; 0 Other;


```
XX 22-APR-2004 (first entry)
DT
XX
DE MNV Hammerhead Ribozyme substrate SEQ ID NO 1263.
XX
XX MNV; West Nile Virus; antiinflammatory; cyostatic; hepatotropic;
KM virucide; neuroprotective; antibacterial; replication; pancreatitis;
KM encephalitis; myocarditis; meningitis; infection; hepatitis;
KM liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
KM Amberzyme; Zinzyne; ss.
XX
XX West Nile Virus.
OS
XX
XX WO200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGEN J A.
XX
XX Blatt L, Mcswiggen JA;
PI
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
PT (MNV), useful for treating a condition related to MNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 23; SEQ ID NO 1263; 495bp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (MNV). The nucleic acid molecules are useful for
CC treating a condition related to MNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyne. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3', inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
XX Sequence 17 BP; 7 A; 5 C; 1 G; 0 T; 4 U; 0 Other;
SQ
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 2.8e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1641 CAAACCAATCATCTGAA 1657
DB 1 CAAACCAUUCACUGAA 17
RESULT 400
ACN07407
ID ACN07407 standard; RNA; 17 BP.
XX
XX ACN07407;
AC
XX 22-APR-2004 (first entry)
DT
XX
XX MNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 7410.
XX
XX MNV; West Nile Virus; antiinflammatory; cyostatic; hepatotropic;
KM virucide; neuroprotective; antibacterial; replication; pancreatitis;
KM virucide; neuroprotective; antibacterial; replication; pancreatitis;
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KM encephalitis; myocarditis; meningitis; infection; hepatitis;
KM liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
KM Amberzyme; Zinzyne; ss.
XX
XX West Nile Virus.
OS
XX
XX WO200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGEN J A.
XX
XX Blatt L, Mcswiggen JA;
PI
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
PT (MNV), useful for treating a condition related to MNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 23; SEQ ID NO 7410; 495bp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (MNV). The nucleic acid molecules are useful for
CC treating a condition related to MNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyne. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3', inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
XX Sequence 17 BP; 2 A; 7 C; 4 G; 0 T; 4 U; 0 Other;
SQ
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 2.8e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 897 CGGGGACTCCTCGACC 913
DB 1 CGGGGUCUCUCUAAAC 17
RESULT 401
ACN12112/C
ID ACN12112 standard; RNA; 17 BP.
XX
XX ACN12112;
AC
XX 22-APR-2004 (first entry)
DT
XX
XX MNV minus strand Inozyme substrate SEQ ID NO 12115.
XX
XX MNV; West Nile Virus; antiinflammatory; cyostatic; hepatotropic;
KM virucide; neuroprotective; antibacterial; replication; pancreatitis;
KM encephalitis; myocarditis; meningitis; infection; hepatitis;
KM liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
KM Amberzyme; Zinzyne; ss.
XX
XX West Nile Virus.
OS
XX
XX WO200268637-A2.
XX
```

XX 06-SEP-2002.
 PD ACN07336/C
 XX 19-OCT-2001; 2001WO-US048350.
 PF
 XX 20-OCT-2000; 2000US-0242411P.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 PI Blatt L, Mcswiggen JA;
 PI WPI; 2002-706994/76.
 DR
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (MNV), useful for treating a condition related to MNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 PT
 PS Claim 23; SEQ ID NO 12115; 495bp; English.
 XX
 XX The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (MNV). The nucleic acid molecules are useful for
 CC treating a condition related to MNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention
 CC
 SQ Sequence 17 BP; 2 A; 5 C; 4 G; 0 T; 6 U; 0 Other;
 Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 1252 GTGTACAAAGTCAGCCG 1268
 Db 17 GTGCACAAAGTCAGCAG 1
 RESULT 402
 ACN07336/C
 ID ACN07336 standard; RNA; 17 BP.
 XX
 XX ACN07336;
 AC
 XX 22-APR-2004 (first entry)
 DT
 XX MNV Amberzyme substrate SEQ ID NO 7339.
 DE
 XX MNV, West Nile Virus; antiinflammatory; cyrostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
 KW Amberzyme; Zinzyme; ss.
 KW
 XX West Nile Virus.
 OS
 XX WO200268637-A2.
 PN
 XX 06-SEP-2002.
 PD
 XX 19-OCT-2001; 2001WO-US048350.
 PF
 XX 20-OCT-2000; 2000US-0242411P.
 PR
 XX

PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 PI Blatt L, Mcswiggen JA;
 PI WPI; 2002-706994/76.
 DR
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (MNV), useful for treating a condition related to MNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 PT
 PS Claim 23; SEQ ID NO 7339; 495bp; English.
 XX
 XX The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (MNV). The nucleic acid molecules are useful for
 CC treating a condition related to MNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention
 CC
 SQ Sequence 17 BP; 4 A; 4 C; 7 G; 0 T; 2 U; 0 Other;
 Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 897 CGGGGACTCCTCTGACC 913
 Db 17 CGGGGCTCCTCTGACC 1
 RESULT 403
 ACN09339/C
 ID ACN09339 standard; RNA; 17 BP.
 XX
 XX ACN09339;
 AC
 XX 22-APR-2004 (first entry)
 DT
 XX MNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 9342.
 DE
 XX MNV, West Nile Virus; antiinflammatory; cyrostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
 KW Amberzyme; Zinzyme; ss.
 KW
 XX West Nile Virus.
 OS
 XX WO200268637-A2.
 PN
 XX 06-SEP-2002.
 PD
 XX 19-OCT-2001; 2001WO-US048350.
 PF
 XX 20-OCT-2000; 2000US-0242411P.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 PI Blatt L, Mcswiggen JA;
 PI WPI; 2002-706994/76.
 DR

XX New nucleic acid molecule that modulates replication of West Nile Virus
PT (MNV), useful for treating a condition related to MNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
PS Claim 23; SEQ ID NO 9342; 495bp; English.
XX
CC The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (MNV). The nucleic acid molecules are useful for
CC treating a condition related to MNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
CC
SQ Sequence 17 BP; 0 A; 3 C; 7 G; 0 T; 7 U; 0 Other;
XX
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1322 ACCGCCCAAGGCCACA 1338
Db 17 ACAGCACCAAGGCCACA 1
RESULT 404
ACN13675/c
ID ACN13675 standard; RNA; 17 BP.
XX
AC ACN13675;
XX
DT 22-APR-2004 (first entry)
XX
DE MNV minus strand DNazyme substrate SEQ ID NO 13678.
XX
XX MNV; West Nile Virus; antiinflammatory; cytoprotic; hepatotropic;
KM virucide; neuroprotective; antibacterial; replication; pancreatitis;
KM encephalitis; myocarditis; meningitis; infection; hepatitis;
KM liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KM Amberzyme; Zinzyne; ss.
XX
XX West Nile Virus.
XX
XX WO200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGEN J A.
XX
XX Blatt L, Mcswigen JA;
PT
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
PT (MNV), useful for treating a condition related to MNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 23; SEQ ID NO 13678; 495bp; English.

CC The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (MNV). The nucleic acid molecules are useful for
CC treating a condition related to MNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
CC
SQ Sequence 17 BP; 5 A; 1 C; 5 G; 0 T; 6 U; 0 Other;
XX
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1640 TCAAACCAATCACTGA 1656
Db 17 TCAAACCAATTCACCTGA 1
RESULT 405
ACN03237
ID ACN03237 standard; RNA; 17 BP.
XX
AC ACN03237;
XX
DT 22-APR-2004 (first entry)
XX
DE MNV Inozyme substrate SEQ ID NO 3240.
XX
XX MNV; West Nile Virus; antiinflammatory; cytoprotic; hepatotropic;
KM virucide; neuroprotective; antibacterial; replication; pancreatitis;
KM encephalitis; myocarditis; meningitis; infection; hepatitis;
KM liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KM Amberzyme; Zinzyne; ss.
XX
XX West Nile Virus.
XX
XX WO200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGEN J A.
XX
XX Blatt L, Mcswigen JA;
PT
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
PT (MNV), useful for treating a condition related to MNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 23; SEQ ID NO 3240; 495bp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (MNV). The nucleic acid molecules are useful for
CC treating a condition related to MNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The

CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3', inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
SQ Sequence 17 BP; 5 A; 6 C; 1 G; 0 T; 5 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 2.8e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1639 CTCGAACCAATCACTG 1655
DB 1 CUCAAACCAUUCACUG 17
RESULT 406
ACN15211/C
ID ACN15211 standard; RNA; 17 BP.
XX
XX ACN15211;
XX
XX 22-APR-2004 (first entry)
XX
XX MNV minus strand Amberzyme substrate SEQ ID NO 15214.
XX
XX MNV, West Nile Virus; antiinflammatory; cyostatic; hepatotropic;
XX vircide; neuroprotective; antibacterial; replication; pancreatitis;
XX encephalitis; myocarditis; meningitis; infection; hepatitis;
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
XX Amberzyme; Zinzyme; ss.
XX
XX West Nile Virus.
XX
XX WO200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-024211P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX PA (BLAT/) BLATT L.
XX PA (MCSW/) MCSWIGEN J A.
XX
XX Blatt L, Mcswigen JA;
XX
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
XX (MNV), useful for treating a condition related to MNV infection e.g.
XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 23; SEQ ID NO 15214; 495bp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
XX of the West Nile Virus (MNV). The nucleic acid molecules are useful for
XX treating a condition related to MNV infection e.g. pancreatitis,
XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
XX molecule is selected from the group of ribozymes consisting of
XX Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
XX nucleic acid molecules further comprise at least five ribose residues, at
XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at
XX least three of the 5' terminal nucleotides and a 3' end modification of a
XX 3'-3', inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
XX in the specification. The present sequence is that of a nucleic acid
XX molecule of the invention

XX
SQ Sequence 17 BP; 0 A; 4 C; 7 G; 0 T; 6 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1321 GACGCCCCAAGCCAC 1337
DB 17 GACAGCAGCCAGGCGAC 1
RESULT 407
ACD00505
ID ACD00505 standard; DNA; 17 BP.
XX
XX ACD00505;
XX
XX 28-JUL-2003 (first entry)
XX
XX G-protein coupled receptor GPCR-A-1 analysis oligonucleotide #978.
XX
XX Human; G-protein coupled receptor; GPCR-A-1; cancer; tumour;
XX G-protein-Agonist; G-protein-Antagonist; gene therapy; cyostatic; ss.
XX
XX Homo sapiens.
XX
XX WO2003031621-A2.
XX
XX 17-APR-2003.
XX
XX 11-OCT-2002; 2002WO-US032599.
XX
XX 12-OCT-2001; 2001US-0329000P.
XX
XX (AMSH) AMERSHAM BIOSCIENCES SV CORP.
XX
XX Zhang J;
XX
XX WPI; 2003-381720/36.
XX
XX New GPCR-A-1 nucleic acid and polypeptide, useful for diagnosing,
XX investigating and/or treating disorders associated with aberrant
XX expression or activity of GPCR-A-1, such as tumors and cancers.
XX
XX Example 2; SEQ ID NO 1002; 156bp; English.
XX
XX The invention describes an isolated nucleic acid encoding a G protein
XX coupled receptor (GPCR), mutations of which cause cancer, comprising a
XX 2225 or 1921 base pair sequence, or their degenerate variants, encoding a
XX 409 residue amino acid sequence, all given in the specification, with or
XX without conservative amino acid substitutions, or complements of the
XX sequence of them. The encoding nucleic acid is not more than 100 kbase in
XX length. The methods and compositions of the present invention are useful
XX for diagnosing, investigating and/or treating disorders associated with
XX aberrant expression or activity of GPCR-A-1, such as tumours and cancers.
XX This sequence represents an oligonucleotide used to analyse the gene
XX encoding human G-protein coupled receptor GPCR-A-1
XX
SQ Sequence 17 BP; 3 A; 4 C; 3 G; 7 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 455 CTGCATTCATCACTG 471
DB 1 CTGCATTCATCACTG 17
RESULT 408
ACA99879
ID ACA99879 standard; DNA; 17 BP.

XX AC A99879;
XX DT 28-JUL-2003 (first entry)
XX DE G-protein coupled receptor GPCR-A-1 analysis oligonucleotide #372.
XX KM Human; G-protein coupled receptor; GPCR-A-1; cancer; tumour;
XX KM G-Protein-Agonist; G-Protein-Antagonist; gene therapy; cytostatic; ss.
XX OS Homo sapiens.
XX PN WO2003031621-A2.
XX PD 17-APR-2003.
XX PF 11-OCT-2002; 2002MO-US032599.
XX PR 12-OCT-2001; 2001US-0329000P.
XX PA (AMSH) AMERSHAM BIOSCIENCES SV CORP.
XX PI Zhang J;
XX DR WPI; 2003-381720/36.
XX PT New GPCR-A-1 nucleic acid and polypeptide, useful for diagnosing,
XX PT investigating and/or creating disorders associated with aberrant
XX PT expression or activity of GPCR-A-1, such as tumors and cancers.
XX PS Example 2; SEQ ID NO 396; 156bp; English.
XX CC The invention describes an isolated nucleic acid encoding a G protein
XX CC coupled receptor (GPCR), mutations of which cause cancer, comprising a
XX CC 2225 or 1921 base pair sequence, or their degenerate variants, encoding a
XX CC 409 residue amino acid sequence, all given in the specification, with or
XX CC without conservative amino acid substitutions, or complements of the
XX CC sequence of them. The encoding nucleic acid is not more than 100 kbase in
XX CC length. The methods and compositions of the present invention are useful
XX CC for diagnosing, investigating and/or treating disorders associated with
XX CC aberrant expression or activity of GPCR-A-1, such as tumors and cancers.
XX CC This sequence represents an oligonucleotide used to analyse the gene
XX CC encoding human G-protein coupled receptor GPCR-A-1
XX SQ Sequence 17 BP; 5 A; 3 C; 6 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 2.8e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1536 CTGGGACTTGCAAAAG 1552
XX 1 CTGGGACTGCAAAATAG 17
XX DB
XX
XX RESULT 409
XX ACA99880
XX ID ACA99880 standard; DNA; 17 BP.
XX AC ACA99880;
XX XX
XX DT 28-JUL-2003 (first entry)
XX DE G-protein coupled receptor GPCR-A-1 analysis oligonucleotide #373.
XX KM Human; G-protein coupled receptor; GPCR-A-1; cancer; tumour;
XX KM G-Protein-Agonist; G-Protein-Antagonist; gene therapy; cytostatic; ss.
XX OS Homo sapiens.
XX PN WO2003031621-A2.
XX PD 17-APR-2003.

XX PF 11-OCT-2002; 2002MO-US032599.
XX XX
XX PR 12-OCT-2001; 2001US-0329000P.
XX XX
XX PA (AMSH) AMERSHAM BIOSCIENCES SV CORP.
XX PI Zhang J;
XX DR WPI; 2003-381720/36.
XX PT New GPCR-A-1 nucleic acid and polypeptide, useful for diagnosing,
XX PT investigating and/or treating disorders associated with aberrant
XX PT expression or activity of GPCR-A-1, such as tumors and cancers.
XX PS Example 2; SEQ ID NO 397; 156bp; English.
XX CC The invention describes an isolated nucleic acid encoding a G protein
XX CC coupled receptor (GPCR), mutations of which cause cancer, comprising a
XX CC 2225 or 1921 base pair sequence, or their degenerate variants, encoding a
XX CC 409 residue amino acid sequence, all given in the specification, with or
XX CC without conservative amino acid substitutions, or complements of the
XX CC sequence of them. The encoding nucleic acid is not more than 100 kbase in
XX CC length. The methods and compositions of the present invention are useful
XX CC for diagnosing, investigating and/or treating disorders associated with
XX CC aberrant expression or activity of GPCR-A-1, such as tumors and cancers.
XX CC This sequence represents an oligonucleotide used to analyse the gene
XX CC encoding human G-protein coupled receptor GPCR-A-1
XX SQ Sequence 17 BP; 5 A; 2 C; 7 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 2.8e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1537 TGGGACTTGCAAAAG 1553
XX 1 TGGGACTGCAAAATAG 17
XX DB
XX
XX RESULT 410
XX ABT35050/c
XX ID ABT35050 standard; DNA; 17 BP.
XX AC ABT35050;
XX XX
XX DT 12-JUN-2003 (first entry)
XX DE Tumour suppression related human fukutin oligo SEQ ID NO 687.
XX KM Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX KM antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX KM schizophrenia; protein chip; gene therapy; tumour suppression;
XX KM human fukutin; de.
XX OS Homo sapiens.
XX PN WO2003025175-A2.
XX PD 27-MAR-2003.
XX PF 17-SEP-2002; 2002MO-IB004208.
XX PR 17-SEP-2001; 2001FR-00011978.
XX PA (MOLE-) MOLECULAR ENGINES LAB.
XX PI Telerman A, Amson R, Tuijnder M;
XX DR WPI; 2003-313353/30.
XX PT New isolated nucleic acid, useful for treating viral diseases associated
XX PT with tumors and cell degeneration, also related polypeptides, antibodies

PT and transfected cells.
XX
PS Disclosure; Page 114; 720pp; French.
XX
XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, or the complement
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterized by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression and/or prognosis of these
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX
SQ Sequence 17 BP; 4 A; 4 C; 3 G; 6 T; 0 U; 0 Other;
XX
XX
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 788 AGAAGTGTCACGATC 804
DB 17 AGAAGTGTCGATC 1
RESULT 411
ABT36411/c
ID ABT36411 standard; DNA; 17 BP.
XX
XX ABT36411;
AC
XX
XX 12-JUN-2003 (first entry)
DT
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 2048.
XX
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX anti-sense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX schizophrenia; protein chip; gene therapy; tumour suppression;
XX human fukutin; ds.
XX
XX Homo sapiens.
OS
XX
XX WO2003025175-A2.
PN
XX
XX 27-MAR-2003.
PD
XX
XX 17-SEP-2002; 2002WO-IB004208.
PE
XX
XX 17-SEP-2001; 2001FR-00011978.
PR
XX
XX (MOIE-) MOLECULAR ENGINES LAB.
PA
XX
XX Telerman A, Amson R, Tuijnder M,
PI
XX
XX WPI; 2003-313353/30.
DR
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX

PS Disclosure; Page 272; 720pp; French.
XX
XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, or the complement
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterized by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression and/or prognosis of these
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX
SQ Sequence 17 BP; 5 A; 6 C; 3 G; 3 T; 0 U; 0 Other;
XX
XX
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 806 GTGTGACTGTGTGATC 822
DB 17 GTGTGACTGTGTGATC 1
RESULT 412
ACA06517
ID ACA06517 standard; RNA; 17 BP.
XX
XX ACA06517;
AC
XX
XX 03-JUN-2003 (first entry)
DT
XX
DE NFKB sub-unit modulating inozyme substrate #336.
XX
XX Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;
XX G-cleaver; amberyne; cancer; REL-A activity; breast cancer; human;
XX lung cancer; prostate cancer; colorectal cancer; brain cancer;
XX oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
XX cervical cancer; head and neck cancer; ovarian cancer; melanoma;
XX lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
XX chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
XX cyclophosphamide; doxorubicin; fluorouracil carboplatin; edatrexate;
XX gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
XX rheumatoid arthritis; retinosis; Crohn's disease; obesity; ischaemia;
XX gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
XX transplant/graft rejection; reperfusion injury; glomerulonephritis;
XX allergic airway inflammation; inflammatory bowel disease; infection; ss.
OS
XX
XX Homo sapiens.
XX
XX US2002177568-A1.
PN
XX
XX 28-NOV-2002.
PD
XX
XX 23-MAY-2001; 2001US-00864785.
PE
XX
XX 07-DEC-1992; 92US-00987132.
PR 18-MAY-1994; 94US-00245466.
PR 15-AUG-1994; 94US-00291932.
PR 23-DEC-1996; 96US-00777916.
XX

PA (STIN/) STINCHOMB D T.
PA (MCSW/) MCSWIGGEN J.
PA (DRAP/) DRAPER K G.
PI Stinchcomb DT, Mcawiggen J, Draper KG;
DR WPI; 2003-340953/32.
XX
XX Novel enzymatic nucleic acid molecules which down regulates expression of
PT a sequence encoding a subunit of nuclear factor kappa B useful for
PT treating cancer, inflammatory disorders and autoimmune diseases.
XX
PS Claim 3; Page 32; 72pp; English.
XX
XX The invention describes an enzymatic nucleic acid molecule (I) which down
CC regulates expression of a sequence encoding a subunit of nuclear factor
CC kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or amberyzyme
CC configuration. The enzymatic nucleic acid molecule is adapted to treat
CC cancer and is useful for down-regulating RBL-A activity in a cell, for
CC treating a patient having a condition associated with the level of RBL-A.
CC (1) is useful for cleaving RNA comprising a sequence of RBL-A gene, in
CC the presence of a divalent cation, especially Mg²⁺. The enzymatic and
CC antisense nucleic acid molecules are useful for treating breast, lung,
CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
CC multidrug resistant cancer. The method involves use of other drug
CC therapies such as monoclonal antibodies, RBL-A-specific inhibitors or
CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,
CC cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate,
CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic
CC acid molecules are also useful for treating inflammatory disease such as
CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
CC rejection, gene therapy applications, ischaemia/reperfusion injury
CC (central nervous system (CNS) and myocardial), glomerulonephritis,
CC sepsis, allergic airway inflammation, inflammatory bowel disease or
CC infection. This sequence represents the substrate of a novel enzymatic
CC nucleic acid molecule
XX
SQ Sequence 17 BP; 2 A; 11 C; 3 G; 0 T; 1 U; 0 Other;
XX
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 135 CCCGAGCGCCGAC 151
DB 1 CCCGAGCGCCGAC 17
XX
RESULT 413
ADA99853
ID ADA99853 standard; DNA; 17 BP.
XX
AC ADA99853;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human MD23 scanning oligonucleotide SEQ ID 842.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KM zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KM chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KM developmental disorder; ss.
XX
XX Homo sapiens.
XX
XX EPI281758-A2.
XX
XX 05-FEB-2003.
XX
XX 30-JUL-2002; 2002EP-00016874.
XX

PR 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
PI
XX
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
XX
PS Example 8; SEQ ID NO 842; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
XX
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 429 CCTGGCCTTCGCGAGG 445
DB 1 CCTGGCCTTCGCGAGG 17
XX
RESULT 414
ADB03782
ID ADB03782 standard; DNA; 17 BP.
XX
AC ADB03782;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human MD27 scanning oligonucleotide SEQ ID 4768.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KM zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KM chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KM developmental disorder; ss.
XX
XX Homo sapiens.
XX
XX EPI281758-A2.
XX
XX 05-FEB-2003.
XX
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
PI
XX
XX WPI; 2003-423107/40.
XX

PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS Example 8; SEQ ID NO 4768; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 0 A; 8 C; 2 G; 7 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 684 TCTCCTGCTGCGCTTCC 700
DB 1 TCTTCTCCTGCGCTTCC 17
RESULT 415
ACDS5641
ID ACDS5641 standard; RNA; 17 BP.
XX
AC ACDS5641;
XX
DT 23-SEP-2003 (first entry)
XX
DE HBV amberzyme substrate sequence #151.
XX
KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW RNA stability; RNA expression; RNA synthesis; antisense;
KW enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; zinczyme;
KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW HBV reverse transcriptase; Enhancer I region; viral replication;
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW virucide; antiinflammatory; substrate; ss.
XX
OS Hepatitis B virus.
XX
PN WO200281494-A1.
XX
PD 17-OCT-2002.
XX
PF 26-MAR-2002; 2002WO-US009187.
XX
PR 26-MAR-2001; 2001US-00817879.
PR 08-JUN-2001; 2001US-00877478.
PR 08-JUN-2001; 2001US-0286876P.
PR 24-OCT-2001; 2001US-0335059P.
PR 05-DEC-2001; 2001US-0337055P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MACE/) MACEJAK D.
PA (MCSW/) MCSWIGEN J.
PA (MORR/) MORRISSEY D.
PA (PAVC/) PAVCO P.

PA (LEEP/) LEE P.
PA (DRAP/) DRAPER K.
PA (ROBB/) ROBERTS E.
XX
PI Blatt L., Macejak D., Mcswigen J., Morrissey D., Pavco P., Lee P;
PI Draper K., Roberts E,
XX
DR WPI; 2003-229207/22.
XX
PT Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.
XX
XX Example 1; Page 206; 387pp; English.
PS
XX The present invention relates to nucleic acid molecules which modulate
XX the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
XX Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
XX and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes,
XX inozymes, zinczymes, amberzymes, and G-cleaver ribozymes. Also disclosed
XX are nucleic acid decoy molecules and aptamers that bind to HBV reverse
XX transcriptase and/or HBV reverse transcriptase primer sequences, as well
XX as oligonucleotides that specifically bind the Enhancer I region of HBV
XX DNA. The nucleic acids may be used to modulate the expression of HBV
XX genes and HBV viral replication. Also disclosed is a method for screening
XX compounds and/or potential therapies directed against HBV, and compounds
XX that modulate the expression and/or replication of HCV. The compounds and
XX methods of the invention are useful for the treatment of degenerative and
XX disease states related to HBV and HCV infection, replication and gene
XX expression such as cirrhosis, liver failure, and hepatocellular
XX carcinoma. The present sequence represents a substrate for one of the HBV
XX ribozyme, inozyme, G-cleaver, zinczyme, DNAzyme or amberzyme sequences
XX disclosed in the present invention
XX
SQ Sequence 17 BP; 4 A; 6 C; 5 G; 0 T; 2 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 2.8e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1267 CGCCTGGAGACACCAT 1283
DB 1 CGCAUGGAGACACCGU 17
RESULT 416
ACDS5640
ID ACDS5640 standard; RNA; 17 BP.
XX
AC ACDS5640;
XX
DT 23-SEP-2003 (first entry)
XX
DE HBV amberzyme substrate sequence #150.
XX
KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW RNA stability; RNA expression; RNA synthesis; antisense;
KW enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; zinczyme;
KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW HBV reverse transcriptase; Enhancer I region; viral replication;
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW virucide; antiinflammatory; substrate; ss.
XX
OS Hepatitis B virus.
XX
PN WO200281494-A1.
XX
PD 17-OCT-2002.
XX
PF 26-MAR-2002; 2002WO-US009187.
XX
PR 26-MAR-2001; 2001US-00817879.

PR 08-JUN-2001; 2001US-00877478.
PR 08-JUN-2001; 2001US-0296876P.
PR 24-OCT-2001; 2001US-0335059P.
PR 05-DEC-2001; 2001US-0337055P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MACE/) MACEJAK D.
PA (MCSW/) MCSWIGGEN J.
PA (MORR/) MORRISSEY D.
PA (PAVCO/) PAVCO P.
PA (LEEP/) LEE P.
PA (DRAP/) DRAPER K.
PA (ROBE/) ROBERTS E.
XX
XX Blatt L, Macejak D, Mcswigen J, Morrissey D, Pavco P, Lee P,
PI Draper K, Roberts E;
DR WPI; 2003-229207/22.
XX
XX Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.
XX
XX Example 1; Page 206; 387pp; English.
XX
XX The present invention relates to nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the Enhancer I region of HBV
CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents a substrate for one of the HBV
CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberzyme sequences
CC disclosed in the present invention
XX
XX Sequence 17 BP; 4 A; 6 C; 5 G; 0 T; 2 U; 0 Other;
SQ
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.8e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1265 GCCGCGCTGGAGACCACC 1281
DB 1 GUGCGAUGAGACACC 17
ACD58714/c
ID ACD58714 standard; RNA; 17 BP.
XX
XX ACD58714;
XX
XX 24-SEP-2003 (first entry)
XX
XX HCV DNAzyme substrate sequence #964.
XX
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KM RNA stability; RNA expression; RNA synthesis; antisense;
KM enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
KM amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KM HBV reverse transcriptase; Enhancer I region; viral replication;
KM degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KM liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;

KM virucide; antiinflammatory; substrate; ss.
XX
XX Hepatitis C virus.
OS
XX
XX W0200281494-A1.
XX
XX
XX 17-OCT-2002.
PD
XX
XX 26-MAR-2002; 2002WO-US009187.
XX
XX
XX 26-MAR-2001; 2001US-00817879.
XX
XX 08-JUN-2001; 2001US-00877478.
PR 08-JUN-2001; 2001US-0296876P.
PR 24-OCT-2001; 2001US-0335059P.
PR 05-DEC-2001; 2001US-0337055P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MACE/) MACEJAK D.
PA (MCSW/) MCSWIGGEN J.
PA (MORR/) MORRISSEY D.
PA (PAVCO/) PAVCO P.
PA (LEEP/) LEE P.
PA (DRAP/) DRAPER K.
PA (ROBE/) ROBERTS E.
XX
XX Blatt L, Macejak D, Mcswigen J, Morrissey D, Pavco P, Lee P,
PI Draper K, Roberts E;
DR WPI; 2003-229207/22.
XX
XX Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.
XX
XX Claim 1; Page 251; 387pp; English.
XX
XX The present invention relates to nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the Enhancer I region of HBV
CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents a substrate for one of the HCV
CC DNazyme or minus strand DNazyme sequences disclosed in the present
CC invention
XX
XX Sequence 17 BP; 2 A; 3 C; 7 G; 0 T; 5 U; 0 Other;
SQ
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1254 GTACAAAGTCAGCGGCC 1270
DB 17 GTACAAAGTCAGCGGCC 1
ACD62777
ID ACC62777 standard; DNA; 17 BP.
XX
XX ACC62777;
XX

PT	useful e.g. for treatment of tumors and viral infection, also related
PT	polypeptide and antibodies.
XX	
PS	Disclosure; Page 420; 771pp; French.
XX	
CC	The invention relates to the isolation of 6327 nucleotide sequences,
CC	fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC	sequence having at least 80% identity, after optimal alignment, with the
CC	nucleotide, a sequence that hybridizes under stringent conditions with
CC	the nucleotides, or the complement, or corresponding RNA, of the
CC	nucleotides. The nucleotides are used as probes or primers for detecting,
CC	identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC	sense and antisense sequences, of nucleotides involved in tumour
CC	suppression or reversion, apoptosis and or viral resistance, to produce
CC	recombinant polypeptides, and to prepare transgenic animals, as
CC	experimental models. The nucleotides (also vectors containing them and
CC	cells containing the vectors), the encoded polypeptides and antibodies
CC	(Ab) against the polypeptides are useful for prevention and/or treatment
CC	of viral infections or diseases characterized by development of tumours
CC	or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC	Analysis of the expression of the nucleotides can be used for diagnosis
CC	and/or prognosis of these diseases. The nucleotides and polypeptides can
CC	also be used to screen for their specific interactive molecules,
CC	potentially useful for treating diseases associated with abnormal
CC	expression of the nucleotides.
XX	
SQ	Sequence 17 BP; 7 A; 6 C; 2 G; 2 T; 0 U; 0 Other;
	Query Match 0.8%; Score 13.8; DB 1; Length 17;
	Best Local Similarity 88.2%; Pred. No. 2.8e+02;
	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY	375 GATCATCTTAGCCCA 391
DB	1 GATCATCAAGCCACA 17
RESULT 421	
ADFe4140/C	
ID	ADFe4140 standard; DNA; 17 BP.
XX	
AC	ADFe4140;
XX	
DT	12-FEB-2004 (first entry)
XX	
DE	Human PCCP1 DNA fragment SEQ ID 8-directed probe - SEQ ID 2044.
XX	
KM	chromatin organisation modifier; CHROMO domain; cytosratic; PCCP1;
KW	prostate cancer candidate protein 1; tumour; gene therapy; vaccine;
KW	human; ss; probe.
XX	
OS	Homo sapiens.
XX	
PN	WO2003050284-A1.
XX	
PD	19-JUN-2003.
XX	
PF	22-NOV-2002; 2002MO-US037506.
XX	
PR	10-DEC-2001; 2001US-0339764P.
XX	
PA	(AMSH) AMERSHAM BIOSCIENCES SV CORP.
XX	
P1	Guo J;
XX	
DR	WPI; 2003-532916/50.
XX	
PT	New prostate cancer candidate protein 1 (PCCP1), useful for preparing a
PT	composition for treating or preventing a disorder associated with
PT	decreased or increased expression or activity of PCCP1 e.g., tumor.
XX	
PS	Example 2; SEQ ID NO 2044; 164dp; English.
XX	

```

CC The invention relates to a novel isolated nucleic acid that encodes a
CC protein with a chromatin organisation modifier (CHROMO) domain. The
CC polynucleotide of the invention demonstrates cytostatic activity and may
CC be useful for preparing a composition for treating or preventing a
CC disorder associated with decreased or increased expression or activity of
CC PCCP1 (prostate cancer candidate protein 1), such as a tumour, as well as
CC PCCP1 (prostate cancer candidate protein 1), such as a tumour, as well as
CC during gene therapy and vaccine production procedures. The current
CC sequence is that of the human PCCP1-related DNA fragment SEQ ID 8-
CC directed probe of the invention. Note: The current sequence is not shown
CC within the specification per se but was retrieved from the Wipoweb
CC database.
CC
XX
SQ Sequence 17 BP; 3 A; 2 C; 8 G; 4 T; 0 U; 0 Other;
XX
XX
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 255 CTCGACTAAGACCTCCG 271
DB 17 CTCCTTAACACACGCG 1
XX
XX
RESULT 422
ADFC63951
ID ADF63951 standard; DNA; 17 BP.
XX
XX ADF63951;
XX
XX 12-FEB-2004 (first entry)
XX
DE Human PCCP1 DNA fragment SEQ ID 8-directed probe - SEQ ID 1855.
XX
XX chromatin organisation modifier; CHROMO domain; cytostatic; PCCP1;
KW prostate cancer candidate protein 1; tumour; gene therapy; vaccine;
KW human; ss; probe.
XX
XX Homo sapiens.
OS
XX WO2003050284-A1.
PN
XX 19-JUN-2003.
PD
XX 22-NOV-2002; 2002WO-US037506.
PF
XX 10-DEC-2001; 2001US-0339764P.
PR
XX (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
PA
XX
XX Guo J;
PI
XX
XX WPI; 2003-532916/50.
DR
XX
XX The invention relates to a novel isolated nucleic acid that encodes a
CC protein with a chromatin organisation modifier (CHROMO) domain. The
CC polynucleotide of the invention demonstrates cytostatic activity and may
CC be useful for preparing a composition for treating or preventing a
CC disorder associated with decreased or increased expression or activity of
CC PCCP1 (prostate cancer candidate protein 1), such as a tumour, as well as
CC during gene therapy and vaccine production procedures. The current
CC sequence is that of the human PCCP1-related DNA fragment SEQ ID 8-
CC directed probe of the invention. Note: The current sequence is not shown
CC within the specification per se but was retrieved from the Wipoweb
CC database.
XX
XX Sequence 17 BP; 0 A; 8 C; 4 G; 5 T; 0 U; 0 Other;

```

Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 987 CTGCTGAGTGCCTTCC 1003
 DB 1 CTGCTGAGTGCCTTCC 17

RESULT 423
 ADF62472
 ID ADF62472 standard; DNA; 17 BP.
 AC ADF62472;
 DT 12-FEB-2004 (first entry)
 DE Human PCCP1 DNA fragment SEQ ID 4-directed probe - SEQ ID 376.
 XX chromatin organisation modifier; CHROMO domain; cytosolic; PCCP1;
 KM prostate cancer candidate protein 1; tumour; gene therapy; vaccine;
 KM human; ss; probe.
 XX Homo sapiens.
 XX MO2003050284-A1.
 XX 19-JUN-2003.
 XX 22-NOV-2002; 2002WO-US037506.
 XX 10-DEC-2001; 2001US-0339764P.
 XX (AMSH) AMERSHAM BIOSCIENCES SV CORP.
 PA Guo J;
 PI WPI; 2003-532916/50.
 DR New prostate cancer candidate protein 1 (PCCP1), useful for preparing a
 PT composition for treating or preventing a disorder associated with
 PT decreased or increased expression or activity of PCCP1 e.g., tumor.
 XX Example 2; SEQ ID NO 376; 164pp; English.
 PS The invention relates to a novel isolated nucleic acid that encodes a
 CC protein with a chromatin organisation modifier (CHROMO) domain. The
 CC polynucleotide of the invention demonstrates cytosolic activity and may
 CC be useful for preparing a composition for treating or preventing a
 CC disorder associated with decreased or increased expression or activity of
 CC PCCP1 (prostate cancer candidate protein 1), such as a tumour, as well as
 CC during gene therapy and vaccine production procedures. The current
 CC sequence is that of the human PCCP1-related DNA fragment SEQ ID 4-
 CC directed probe of the invention. Note: The current sequence is not shown
 CC within the specification per se but was retrieved from the Wipoweb
 CC database.
 CC
 SQ Sequence 17 BP; 6 A; 5 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 786 TGAGAAAGTGACCA 802
 DB 1 TGAGAAAGTGACCA 17

RESULT 424
 ADI51353/C
 ID ADI51353 standard; DNA; 17 BP.
 AC ADI51353;

XX 15-APR-2004 (first entry)
 DT Human tumour suppression/reversion-related DNA sequence SeqID3856.
 XX tumour suppression; tumour reversion; apoptosis; virus resistance;
 KM cytosolic; vironucle; neuroprotective; neurotropic; neuroleptic; probe;
 KM primer; PCR; gene chip; antisense; viral disease; tumour;
 KM cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
 XX Homo sapiens.
 XX MO2003025177-A2.
 XX 27-MAR-2003.
 XX 17-SEP-2002; 2002WO-IB004523.
 XX 17-SEP-2001; 2001PR-00011980.
 XX (MOLE-) MOLECULAR ENGINES LAB.
 PA Telerman A, Amson R, Tuijnder M;
 PI WPI; 2003-313354/30.
 DR New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX Disclosure; SEQ ID NO 3856; 30pp; French.
 PS This invention relates to novel isolated nucleic acid sequences involved
 CC in the phenomena of tumour suppression, tumour reversion, apoptosis
 CC and/or resistance to viruses. The invention may be useful for the
 CC development of compounds with a cytosolic, vironucle, neuroprotective,
 CC neurotropic or neuroleptic activity. The DNA sequences may be useful as
 CC probes and primers for detecting, identifying, quantifying and/or
 CC amplifying nucleic acid, for example as one component of a gene chip, in
 CC vitro as antisense reagents and for production of recombinant
 CC polypeptides. The invention may therefore be useful for preparation of
 CC pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration. The
 CC specifically cancer but also Alzheimer's disease and schizophrenia. The
 CC present sequence is that of a nucleic acid sequence of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/publshdepct_sequences

SQ Sequence 17 BP; 5 A; 7 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 806 GTGTGACTGTGTGATC 822
 DB 17 GTGTGACTGTGTGATC 1

RESULT 425
 ACC53250
 ID ACC53250 standard; DNA; 17 BP.
 AC ACC53250;
 DT 27-JUN-2003 (first entry)
 DE Human tumour suppressor sequence #2017.
 XX ss; tumour suppressor; antitumour; cytosolic; tumour suppression;
 KM tumour regression; apoptosis; virus resistance; diagnosis;
 KM cellular degeneration.

XX OS Homo sapiens.
XX PN FR2826373-A1.
XX PS 27-DEC-2002.
XX PD 20-JUN-2001; 2001FR-00008139.
XX PF 20-JUN-2001; 2001FR-00008139.
XX PR 20-JUN-2001; 2001FR-00008139.
XX PS (MOLE-) MOLECULAR ENGINES LAB SA.
PI Tuijnder M, Tejerman A, Amson R;
XX WPI; 2003-250498/25.
XX DR WPI; 2003-250498/25.
XX PT New nucleic acid sequences associated with tumor suppression, regression,
PT apoptosis or virus resistance are useful to diagnose and treat viral
PT disease, development of tumor cells and cell degeneration.
PS Claim 1; Page 506; 798bp; French.
XX CC This sequence represents an isolated nucleic acid sequence associated
CC with tumour suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%
CC identity to them, and polypeptides encoded by the sequences or
CC polypeptides having 80% identity to the polypeptide sequences. The
CC invention is used to diagnose or treat viral disease or disease
CC characterized by development of tumour cells or cellular degeneration
XX Sequence 17 BP; 9 A; 2 C; 1 G; 5 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1665 GAGCCTGTAAATATAA 1681
Db 1 GATCCTTTAAATAATAA 17
RESULT 426
ACCS3982/C
ID ACCS3982 standard; DNA; 17 BP.
XX AC ACCS3982;
XX DT 27-JUN-2003 (first entry)
XX DE Human tumour suppressor sequence #2749.
XX KM 89; tumour suppressor; antitumour; cytostatic; tumour suppression;
KM tumour regression; apoptosis; virus resistance; diagnosis;
KM cellular degeneration.
XX OS Homo sapiens.
XX PN FR2826373-A1.
XX PD 27-DEC-2002.
XX PF 20-JUN-2001; 2001FR-00008139.
XX PR 20-JUN-2001; 2001FR-00008139.
XX PS (MOLE-) MOLECULAR ENGINES LAB SA.
PI Tuijnder M, Tejerman A, Amson R;
XX WPI; 2003-250498/25.
XX DR WPI; 2003-250498/25.
XX PT New nucleic acid sequences associated with tumor suppression, regression,

PT apoptosis or virus resistance are useful to diagnose and treat viral
PT disease, development of tumor cells and cell degeneration.
XX PS Claim 1; Page 675; 798bp; French.
XX CC This sequence represents an isolated nucleic acid sequence associated
CC with tumour suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%
CC identity to them, and polypeptides encoded by the sequences or
CC polypeptides having 80% identity to the polypeptide sequences. The
CC invention is used to diagnose or treat viral disease or disease
CC characterized by development of tumour cells or cellular degeneration
XX Sequence 17 BP; 5 A; 7 C; 3 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 806 GTGTGACTGTGCTGATC 822
Db 17 GTGTGCTGTGCTGATC 1
RESULT 427
ADL46848
ID ADL46848 standard; RNA; 17 BP.
XX AC ADL46848;
XX DT 20-MAY-2004 (first entry)
XX DE Human NOCO receptor inozyme substrate sequence #281.
XX KM antisense oligonucleotide; neurite growth inhibitor; NOCO;
KM prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
KM protein kinase PKR; cerebrovascular accident;
KM central nervous system injury; CNS injury; spinal cord injury; cancer;
KM melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
KM restenosis; asthma; Crohn's disease; diabetes; obesity;
KM autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KM graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KM allergy; asthma; allergic rhinitis; atopic dermatitis;
KM NOCO receptor inozyme; substrate; ds.
XX OS Unidentified.
XX PN WO200281628-A2.
XX PD 17-OCT-2002.
XX PF 03-APR-2002; 2002MO-US010512.
XX PR 05-APR-2001; 2001US-00827395.
XX PR 29-MAY-2001; 2001US-0294412P.
XX PR 28-AUG-2001; 2001US-0315315P.
XX PA (RIBO-) RIBOZYME PHARM INC.
PI Blatt L, Chowrira B, Haeblerl P, Mcawiggen J, Fossnaugh K;
XX WPI; 2003-058513/05.
XX DR WPI; 2003-058513/05.
XX PT Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
PT protein kinase PKR genes, for treating cancer and inflammatory disease.
XX Claim 9; SEQ ID NO 381; 317bp; English.
XX CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOCO, prostaglandin D2 receptor (PTGDR),
CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the

invention are useful for treating: cerebrovascular accident, central nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma, lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis, Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft rejection, ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic conditions (e.g. asthma, allergic rhinitis or atopic dermatitis)). The nucleic acids of the invention are also useful for down-regulating the expression of a target gene and as a diagnostic tool to examine genetic drifts and mutations within diseased cells or to detect the presence of a target RNA in a cell. The present RNA sequence represents a human NCOO receptor inozyme substrate sequence.

Sequence 17 BP; 1 A; 6 C; 6 G; 0 T; 4 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 2.8e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

1084 TGGCTGGCGCATGAGCTC 1100
:||||:||||:||||:
Db 1 UGGCUGGCCGUGACCTC 17

RESULT 428

ADL48696/C
ID ADL48696 standard; RNA; 17 BP.

ADL48696;

20-MAY-2004 (first entry)

Human IKK-gamma substrate sequence #1206.

antisense oligonucleotide; neurite growth inhibitor; NCOO;
prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
central nervous system injury; CNS injury; spinal cord injury; cancer;
melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
restenosis; asthma; Crohn's disease; diabetes; obesity;
autoimmune disease; lupus; multiple sclerosis; transplant rejection;
graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
allergy; asthma; allergic rhinitis; atopic dermatitis; Human IKK-gamma;
substrate; ds.

Unidentified.

WO200281628-A2.

17-OCT-2002.

03-APR-2002; 2002WO-US010512.

05-APR-2001; 2001US-00827395.

29-MAY-2001; 2001US-0294412P.

28-AUG-2001; 2001US-0315315P.

(RIBO-) RIBOZYME PHARM INC.

Blatt L, Chowrira B, Haerberli P, Mcswiggen J, Fosnaugh K;

WPI; 2003-058513/05.

Novel enzymatic nucleic acid that down-regulates expression of neurite growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or protein kinase PKR genes, for treating cancer and inflammatory disease.

Claim 59; SEQ ID NO 2229; 317pp; English.

The invention comprises nucleic acids (e.g. antisense oligonucleotides) that down regulate the expression or inhibit the function of a receptor (PTGDR), for a neurite growth inhibitor, NCOO, prostaglandin D2 receptor (PTGDR), Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the

invention are useful for treating: cerebrovascular accident, central nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma, lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis, Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft rejection, ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic conditions (e.g. asthma, allergic rhinitis or atopic dermatitis)). The nucleic acids of the invention are also useful for down-regulating the expression of a target gene and as a diagnostic tool to examine genetic drifts and mutations within diseased cells or to detect the presence of a target RNA in a cell. The present RNA sequence represents a human IKK-gamma substrate sequence.

Sequence 17 BP; 7 A; 1 C; 8 G; 0 T; 1 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1402 AGCTTCAGCTTCCTCC 1418
:||||:||||:||||:
Db 17 AGCTTCCTCTCTCTCTC 1

RESULT 429

ADM60211
ID ADM60211 standard; RNA; 17 BP.

ADM60211;

03-JUN-2004 (first entry)

Hepatitis B virus (HBV) RNA target sequence #2345.

Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage;
hepatitis B virus infection; hepatitis; hepatocellular carcinoma;
cirrhosis; liver failure; lamivudine; interferon; genetic drift;
viral; hepatotropic; antiinflammatory; cytostatic.

Hepatitis B virus.

US2004054156-A1.

18-MAR-2004.

15-JAN-2003; 2003US-00342902.

14-MAY-1992; 92US-00882712.

07-FEB-1994; 94US-00193627.

08-NOV-1999; 99US-00436430.

20-MAR-2000; 2000US-00531025.

09-AUG-2000; 2000US-00636385.

24-OCT-2000; 2000US-00696347.

08-JUN-2001; 2001US-00877478.

(DRAP/) DRAPER K.

(BLAT/) BLATT L.

(MCSW/) MCSWIGGEN J A.

(MORR/) MORRISSEY D.

Draper K, Blatt L, Mcswiggen JA, Morrissey D;

WPI; 2004-247781/23.

Novel enzymatic nucleic acid molecule such as DNazymes and inozymes specifically cleaving RNA derived from hepatitis B virus and comprising one or more binding arms, useful for treating hepatitis and cirrhosis.

Disclosure; SEQ ID NO 2345; 122pp; English.

The invention relates to an enzymatic nucleic acid molecule that specifically cleaves RNA derived from hepatitis B virus (HBV) and comprising one or more binding arms, without requiring the presence of a

CC 2'-OH group within the molecule for activity. The nucleic acids are
CC useful for treating hepatitis B virus infection, hepatitis,
CC hepatocellular carcinoma, cirrhosis and liver failure, either alone or in
CC combination with other therapies such as lamivudine and interferons. The
CC nucleic acids are useful as diagnostic tools to examine genetic drift and
CC mutations within diseased cells, for detecting the presence of HBV RNA in
CC a cell, for the study of RNA and for down-regulating gene expression of
CC target genes in bacterial, fungal, viral, plant or mammalian cells. This
CC sequence represents an HBV RNA target sequence, used in the scope of the
CC invention. Note: The sequence data for this patent is also available in
CC electronic format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 17 BP; 4 A; 6 C; 5 G; 0 T; 2 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.8e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1265 GCGCGCTGGAGACCAACC 1281
Db 1 GCGCGAUGGAGACCAACC 17
RESULT 430
ADM60212
ID ADM60212 standard; RNA; 17 BP.
XX
AC ADM60212;
XX
DT 03-JUN-2004 (first entry)
XX
DE Hepatitis B virus (HBV) RNA target sequence #2346.
XX
KM Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage;
KM hepatitis B virus infection; hepatitis; hepatocellular carcinoma;
KM cirrhosis; liver failure; lamivudine; interferon; genetic drift;
KM virucide; hepatotropic; antiinflammatory; cytostatic.
XX
OS Hepatitis B virus.
XX
PN US2004054156-A1.
XX
PD 18-MAR-2004.
XX
PF 15-JAN-2003; 2003US-00342902.
XX
PR 14-MAY-1992; 92US-00882712.
PR 07-FEB-1994; 94US-00193627.
PR 08-NOV-1999; 99US-00436430.
PR 20-MAR-2000; 2000US-00531025.
PR 09-AUG-2000; 2000US-00636385.
PR 24-OCT-2000; 2000US-00696347.
PR 08-JUN-2001; 2001US-00877478.
XX
PA (DRAP/) DRAPER K.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGEN J A.
PA (MORR/) MORRISSEY D.
XX
PI Draper K, Blatt L, Mcswigen JA, Morrissey D;
XX
DR WPI; 2004-247781/23.
XX
PT Novel enzymatic nucleic acid molecule such as DNAsymes and inozymes
PT specifically cleaving RNA derived from hepatitis B virus and comprising
PT one or more binding arms, useful for treating hepatitis and cirrhosis.
XX
PS Disclosure; SEQ ID NO 2346; 122bp; English.
XX
CC The invention relates to an enzymatic nucleic acid molecule that
CC specifically cleaves RNA derived from hepatitis B virus (HBV) and
CC comprising one or more binding arms, without requiring the presence of a
2'-OH group within the molecule for activity. The nucleic acids are

CC useful for treating hepatitis B virus infection, hepatitis,
CC hepatocellular carcinoma, cirrhosis and liver failure, either alone or in
CC combination with other therapies such as lamivudine and interferons. The
CC nucleic acids are useful as diagnostic tools to examine genetic drift and
CC mutations within diseased cells, for detecting the presence of HBV RNA in
CC a cell, for the study of RNA and for down-regulating gene expression of
CC target genes in bacterial, fungal, viral, plant or mammalian cells. This
CC sequence represents an HBV RNA target sequence, used in the scope of the
CC invention. Note: The sequence data for this patent is also available in
CC electronic format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 17 BP; 4 A; 6 C; 5 G; 0 T; 2 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 2.8e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1267 GCGCTGGAGACCAACC 1283
Db 1 GCGAUGGAGACCACCG 17
RESULT 431
ACN70772/C
ID ACN70772 standard; DNA; 17 BP.
XX
AC ACN70772;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human GDMPL-1 probe SEQ ID NO:7674.
XX
KM Human; ss; probe; myosin-like protein-1; hGDMPL-1;
KM hGDMPL-1 agonist hGDMPL antagonist; hGDMPL inhibitor; heart disorder;
KM skeletal muscle function.
XX
OS Homo sapiens.
XX
PN US2004137589-A1.
XX
PD 15-JUL-2004.
XX
PF 26-NOV-2003; 2003US-00723361.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
PR 25-MAY-2001; 2001US-00866108.
XX
PA (GUY/) GU Y.
PA (JY/) JI Y.
PA (PENN/) PENN S G.
PA (HANZ/) HANZEL D K.
PA (RANK/) RANK D.
PA (CHEN/) CHEN W.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
XX
DR WPI; 2004-533378/51.
XX

PT Novel myosin-like protein-1, useful for treating or preventing disorder
PT associated with decreased expression or activity of human genome-derived
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT function.
XX
PS Disclosure; SEQ ID NO 7674; Opp; English.
XX
CC The invention relates to a novel polypeptide (I) comprising a sequence
CC (S1) of myosin-like protein-1 (hGDMPL-1) having 2568 amino acids fully
CC defined in the specification, a fragment of at least 8 amino acids of
CC (S1), 95% deviation from (S1) which are conservative substitutions, and
CC 65% identity to (S1). A polypeptide of the invention acts as a agonist or
CC antagonist of hGDMPL-1, or as an inhibitor of hGDMPL-1 activity. A
CC pharmaceutical composition of the invention is useful for treating or
CC preventing a disorder associated with decreased expression or activity of
CC hGDMPL-1, such as a disorder of heart and/or skeletal muscle function.
CC The present sequence represents a 17-mer nucleotide, used in the
CC invention for scanning the sequence represented in ACN63103
CC
XX
SQ Sequence 17 BP; 8 A; 1 C; 7 G; 1 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.8e+02; Mismatches 0; Gaps 0;
Matches 15; Conservative 0; Indels 2; Indels 0;
QY 1404 CTTGAGCTTCTCTCCCA 1420
Db 17 CTTCTGCTTCTTCTCCA 1
RESULT 432
ACN65854
ID ACN65854 standard; DNA; 17 BP.
XX ACN65854;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human GDMPL-1 probe SEQ ID NO:2756.
XX
KW Human; ss; probe; myosin-like protein-1; hGDMPL-1;
KW hGDMPL-1 agonist hGDMPL antagonist; hGDMPL inhibitor; heart disorder;
KW skeletal muscle function.
XX
OS Homo sapiens.
XX
PN US2004137589-A1.
XX
PD 15-JUL-2004.
XX
PF 26-NOV-2003; 2003US-00723361.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-026686OP.
PR 25-MAY-2001; 2001US-00866108.
XX
XX (GUY/) GU Y.
PA (JUY/) JT Y.
PA (PENN/) PENN S G.
PA (HANZ/) HANZEL D K.

PA (RANK/) RANK D.
PA (CHEN/) CHEN W.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
XX WPI, 2004-533378/51.
DR
XX
XX Novel myosin-like protein-1, useful for treating or preventing disorder
PT associated with decreased expression or activity of human genome-derived
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT function.
XX
PS Disclosure; SEQ ID NO 2756; Opp; English.
XX
CC The invention relates to a novel polypeptide (I) comprising a sequence
CC (S1) of myosin-like protein-1 (hGDMPL-1) having 2568 amino acids fully
CC defined in the specification, a fragment of at least 8 amino acids of
CC (S1), 95% deviation from (S1) which are conservative substitutions, and
CC 65% identity to (S1). A polypeptide of the invention acts as a agonist or
CC antagonist of hGDMPL-1, or as an inhibitor of hGDMPL-1 activity. A
CC pharmaceutical composition of the invention is useful for treating or
CC preventing a disorder associated with decreased expression or activity of
CC hGDMPL-1, such as a disorder of heart and/or skeletal muscle function.
CC The present sequence represents a 17-mer nucleotide, used in the
CC invention for scanning the sequence represented in ACN63102
CC
XX
SQ Sequence 17 BP; 4 A; 2 C; 8 G; 3 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.8e+02; Mismatches 0; Gaps 0;
Matches 15; Conservative 0; Indels 2; Indels 0;
QY 1196 GCGACTATGAGGAGCTG 1212
Db 1 GCGAGTAGAGGAGCTG 17
RESULT 433
ADM29146
ID ADM29146 standard; DNA; 17 BP.
XX ADM29146;
XX
DT 24-MAR-2005 (first entry)
XX
DE Gastric cancer related gene GSTP1 primer SEQ ID NO 79.
XX
KW diagnosis; gene expression; stomach tumor; gastrointestinal disease;
KW neoplasm; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO2005001126-A1.
XX
PD 06-JAN-2005.
XX
PF 25-MAR-2004; 2004WO-KR000677.
XX
PR 12-JUN-2003; 2003KR-00038034.
PR 25-NOV-2003; 2003KR-00084001.
XX
XX (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX
PA Kim N, Kim YS, Lee J, Oh J, Park H, Ahn H, Yoon S, Han Y,
PI Kim S, Kim J, Byun S, Noh S, Song K, Yoo HS;
XX WPI, 2005-075581/08.
DR
XX Diagnosing gastric cancer or metastatic gastric cancer comprises
PT measuring the expression levels of RNA or protein of any of the up-
PT and/or down-regulated genes in gastric cancers or metastatic gastric
PT cancer.

XX Example 3; SEQ ID NO 79; 112bp; English.
PS The invention describes a method of diagnosing gastric cancer or
XX metastatic gastric cancer comprising measuring the expression levels of
CC RNA or protein of at least one gene, e.g. up- and/or down-regulated genes
CC in gastric cancers or metastatic gastric cancer. Also described are: a
CC kit, for diagnosing gastric cancer and/or metastatic gastric cancer,
CC comprising: a sense primer and an anti-sense primer of; a probe
CC corresponding to; and an antibody that recognizes the protein encoded by
CC at least one of the cited up- and down-regulated genes; and screening a
CC suppressor of gastric cancer or metastatic gastric cancer. The methods
CC and kits are useful for diagnosing gastric cancer or metastatic gastric
CC cancer. Expression levels for gastric cancer-related marker genes were
CC identified in the 4 pairs of patient samples with gastric cancer.
CC tissues/normal tissues taken from 4 patients with gastric cancer.
CC Competitive RT-PCR was performed to determine the amount of the gene
CC expression of any of the up- and down-regulated genes in gastric cancer.
CC In addition, expression level of any of the up- and down-regulated genes
CC in metastatic gastric cancer was also identified. The amount of
CC competitive RT-PCR products of up- and down-regulated genes in metastatic
CC gastric cancer was higher in most tested metastatic cancer tissues than
CC those of primary cancer tissues. This sequence represents a primer used
CC in competitive PCR to establish which genes are up and/or down regulated
CC in gastric and metastatic cancers.
XX Sequence 17 BP; 2 A; 5 C; 6 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 432 GGCCTTCGCGAGGCT 448
Db 1 GGCCTTCGCTGAGGACT 17
RESULT 434
AEB23914
ID AEB23914 standard; DNA; 17 BP.
XX
AC AEB23914;
XX
DT 22-SEP-2005 (first entry)
XX
DE HLA-C allele identification-related oligonucleotide probe SeqID55.
XX
KM HLA-C; human leukocyte antigen; diagnostic; SNP detection; DNA detection;
KM transplant rejection; cancer; diabetes; probe; ss.
XX
OS Homo sapiens.
XX
PN JP2005185174-A.
XX
PD 14-JUL-2005.
XX
PF 25-DEC-2003; 2003JP-00430556.
XX
PR 25-DEC-2003; 2003JP-00430556.
XX
PA (CANO) CANON KK.
XX
PI Tsukada M;
XX
DR WPI; 2005-483348/49.
XX
PT Probe set for identifying human leukocyte antigen (HLA)-C allele in test
PT substance in patients with organ transplant, cancer, diabetes, comprises
PT probes such as CW.0102, CW.0104, CW.0206, CW.03042, CW.0314, CW.0408,
XX
PS Claim 2; SEQ ID NO 180; 51bp; Japanese.
XX

CC This invention relates to a novel probe set for identifying HLA-C (human
CC leukocyte antigen-C) alleles in a test substance. The invention enables
CC identification of HLA-C alleles in patients with organ transplant,
CC cancer, diabetes and other multiple-factor diseases, and thus provides
CC tailored medical treatment to individual patients. The present sequence
CC is that of an oligonucleotide probe which is used in the HLA-C probe set
CC of the present invention.
XX
SQ Sequence 17 BP; 5 A; 6 C; 6 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 138 CAGGCCGACGACAGG 154
Db 1 CAGGCCGACGACAGG 17
RESULT 435
AED8144
ID AED8144 standard; DNA; 17 BP.
XX
AC AED8144;
XX
DT 26-JAN-2006 (first entry)
XX
DE Human Leukocyte Antigen B allele identification probe, SEQ ID 27.
XX
KM HLA; Leukocyte; Antigen; transplant rejection; histocompatibility;
KM preclinical testing; cancer; cytostatic; diabetes mellitus; antidiabetic;
KM probe; ss.
XX
OS Homo sapiens.
XX
PN JP2005185172-A.
XX
PD 14-JUL-2005.
XX
PF 25-DEC-2003; 2003JP-00430554.
XX
PR 25-DEC-2003; 2003JP-00430554.
XX
PA (CANO) CANON KK.
XX
PI Tsukada M;
XX
DR WPI; 2006-013379/02.
XX
PT Probe set for specific identification of an HLA-B allele in a sample,
PT useful e.g. in matching transplant donors and recipients, and in
PT determining suitable treatment for patients with conditions such as
PT cancer and diabetes mellitus.
XX
PS Claim 2; SEQ ID NO 27; 152bp; Japanese.
XX
CC The invention relates to a novel probe set for the identification of a
CC Human Leukocyte Antigen (HLA)-B allele in a sample. The invention further
CC includes a method for identifying an HLA-B allele using the probe set.
CC The probe set and method are useful for identifying an HLA-B allele in a
CC sample. The information gained is useful, for example, in matching organ
CC donors and recipients, and in guiding clinical decisions in the treatment
CC of diseases such as cancer and diabetes mellitus. This oligo sequence
CC represents a probe used in the identification of a Human Leukocyte
CC Antigen B allele of the invention.
XX
SQ Sequence 17 BP; 5 A; 6 C; 6 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 138 CAGGCCGACGACAGG 154

Db 1 CAGAGCCGAGCAGG 17

RESULT 436
ID AEF42068/c
AEF42068 standard; DNA; 17 BP.

XX AEF42068;

DT 23-MAR-2006 (first entry)

XX Chicken Pylori LightCycler RT-PCR, reverse PCR primer.

DE DNA microarray; PCR; primer; ss; gene expression; malabsorption syndrome;

KM metabolic; gastrointestinal-gen.; diagnosis; gastrointestinal disease.

XX Gallus gallus.

OS WO2006006853-A2.

XX 19-JAN-2006.

PF 08-JUL-2005; 2005WO-NL000494.

XX 09-JUL-2004; 2004EP-00077001.

PR 16-FEB-2005; 2005EP-00075373.

XX (IDLE-) ID-LEHSTAD INST DIERHOUDERIJ EN DIERGEZ.

XX Niwold JA, Rebel JMJ, Smit MA;

DR WPI; 2006-110237/11.

XX New set of genes or gene sequences comprising at least 20 intestinal
PT genes, and at least 5 enzymes, e.g. caspase, apob, aminopeptidase, etc.,
PT useful for determining intestinal health, and/or disease of an animal or
PT a human.

XX Example 1; Page 22; 88pp; English.

XX The invention relates a set of genes or gene sequences comprising at
CC least 20 genes in table 1, and comprising at least 5 of: Na/glucose
CC transporter, K/Cl channel, I-PABP, L-PABP, Cytochrome P450, caspase, beta
CC -2-microglobulin, guanylyl, calbindin, phosphatase, aldolase, actin,
CC metallopeptidase, aminopeptidase, glycosaminotransferase, glutathion S
CC transferase, maltase/glucosaminidase, sucrase/isomaltase, butyrophilin,
CC apob, and cytochrome C oxidase. Also included are detecting the
CC presence/absence of an intestinal disease in an animal/human (comprising
CC measuring, in a sample of the animal or human, expression levels of a set
CC of genes or gene sequences, or a gene specific fragment of the genes and
CC comparing the expression levels with a reference value), measuring an
CC increase of the intestinal health status of an animal/human (comprising
CC measuring in a series of samples of intestinal tissue of the animal taken
CC at different timepoints, expression levels of a set of genes or gene
CC sequences, or a gene specific fragment of the genes and comparing the
CC expression levels with a reference value), a kit comprising a set of at
CC least 2 oligonucleotide primers capable of specifically hybridizing to a
CC set of genes (or a gene specific fragment of the genes) and a kit
CC containing ingredients to measure protein levels of gene products encoded
CC by genes. The set of genes or gene sequences are useful for determining
CC intestinal health, and/or disease of an animal or a human. Expression of
CC genes in 2 chicken strains (susceptible or resistant to Malabsorption
CC syndrome, MAS) was studied using the differential display method. cDNAs
CC differentially expressed genes were amplified and sequenced. cDNAs
CC representing differentially expressed genes were analyzed for their
CC expression levels using the LightCycler RT-PCR method. The present
CC sequence is a PCR primer for a chicken cDNA or chicken virus sequence,
CC used in the LightCycler PCR experiment (Note, these are not RT-PCR
CC primers, the reverse transcription stage is accomplished using random
CC hexamers as primers).

XX Sequence 17 BP; 1 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.8e-02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 122 GAAGACCCCTGAGCCG 138
DB 17 GAAGACCCCTGAGCCAC 1

RESULT 437
ID AAS19285/c
AAS19285 standard; DNA; 15 BP.

XX AAS19285;

DT 26-MAR-2002 (first entry)

DE Human ASO PCR primer for detecting GPR3 polymorphisms #8.

KM Human; polymorphism; ss; G protein-coupled receptor; GPR3; haplotype;

KW genotyping; adenylate cyclase related disorder; ASO; PCR primer;

KM allele specific oligonucleotide.

XX Homo sapiens.

OS WO200190128-A2.

XX 29-NOV-2001.

XX 24-MAY-2001; 2001WO-US016983.

PR 24-MAY-2000; 2000US-0206857P.

XX (GENA-) GENMAISSANCE PHARM INC.

XX Messer C, Sanchis A, Tanguay DA;

DR WPI; 2002-106170/14.

XX Novel isolated human G protein-coupled receptor 3 polynucleotide, useful
PT for therapeutic purposes, for studying the expression and function of the
PT polynucleotide, and for expressing the receptor protein.

XX Claim 16; Page 12; 63pp; English.

XX The invention relates to an isolated human G protein-coupled receptor 3,
CC (GPR3) polynucleotide comprising a sequence which is a polymorphic
CC variant for a reference sequence for the GPR3 gene or its fragment, or a
CC polymorphic variant of a reference sequence for a GPR3 cDNA or its
CC fragment, and the encoded proteins. Also include are method for
CC genotyping/haplotyping an individual by determining the sequence of both
CC copies of the individuals GPR3 genes and examining the sequence at the
CC polymorphic sites included in the specification, identifying an
CC association between a trait and at least one haplotype or haplotype pair
CC of the GPR3 gene involves comparing the frequency of the haplotype or
CC haplotype pair in a population exhibiting the trait with the frequency of
CC the haplotype or haplotype pair in a reference population, where the
CC haplotype is selected from haplotypes 1-5 defined in the specification,
CC where a higher frequency of the haplotype or haplotype pair in the trait
CC population than in the reference population indicates that the trait is
CC associated with the haplotype or haplotype pair. The GPR3 polynucleotide
CC is useful in studying the expression and function of GPR3, and in
CC expressing GPR3 protein for use in screening for candidate drugs to treat
CC diseases related to GPR3 activity. GPR3 is useful for studying expression
CC of the GPR3 isogenes in vivo, for in vivo screening and testing of drugs
CC targeted against GPR3 protein, and for testing the efficacy of
CC therapeutic agents and compounds for disorders related to defects in
CC adenylate cyclase activation, in a biological system. An anti-GPR3
CC antibody is useful for studying the effect of the variation on the
CC biological activity of GPR3 as well as on the binding affinity of the
CC candidate drugs targeting GPR3 for the treatment of disorders related to
CC defects in adenylate cyclase activation. The present sequence is an ASO

CC (allele specific oligonucleotide) PCR primer for detecting GPR3
CC polymorphisms
XX
SQ Sequence 15 BP; 1 A; 3 C; 7 G; 3 T; 0 U; 1 Other;
Query Match 0.8%; Score 13.6; DB 1; Length 15;
Best Local Similarity 97.9%; Pred. No. 2.2e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 727 ACCATGCCACGACG 740
:|||||
DB 14 RCGATGCCACGACG 1
RESULT 438
AEE77703/C
ID AEE77703 standard; DNA; 20 BP.
XX
AC AEE77703;
XX
DT 09-FEB-2006 (first entry)
XX
XX Human dopamine receptor D2 (DRD2) DNA oligonucleotide SEQ ID NO:1324.
XX
XX Diagnosis; therapeutic; neurological disease; psychiatric disorder;
XX neuropsychologic disorder; dopamine receptor D2; DRD2; ss.
XX
XX Homo sapiens.
XX
XX MO2005118843-A1.
XX
XX 15-DEC-2005.
XX
XX 01-JUN-2005; 2005MO-AU000775.
XX
XX 01-JUN-2004; 2004AU-00902919.
XX
XX (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
XX
XX Morris CP, Van Daal A, Swagell CD, Lawford BR, Young RM;
XX WPI; 2006-047555/05.
XX
XX Identifying genetic profile associated with a neurological, psychiatric,
XX or psychological condition, comprises screening individuals for a
XX polymorphism in a genetic locus comprising the dopamine receptor D2
XX (DRD2) gene.
XX
XX Claim 31; SEQ ID NO 1324; 634bp; English.
XX
XX The invention relates to a method of identifying a genetic profile
XX associated with a neurological, psychiatric or psychological condition,
XX phenotype or state including a sub-threshold neurological, psychiatric or
XX psychological condition, phenotype or state in an individual, comprising
XX screening individuals for a polymorphism in a genetic locus comprising
XX the dopamine receptor D2 (DRD2) gene. The invention also relates to a
XX genetic mutation providing a genetic marker for a neurological,
XX psychiatric, or psychological condition, state or phenotype in an
XX individual, where the presence of a 957C polymorphism is indicative of a
XX predisposition to developing a neurological, psychiatric or psychological
XX condition, phenotype or state. The compositions and methods are useful
XX for identifying a genetic profile associated with a neurological,
XX psychiatric or psychological condition. The method enables clinicians to
XX make a genetic or psychological diagnosis of a neurological, psychiatric or
XX psychological condition and can thereby implement treatment or
XX preventative or symptom-alleviating protocols to reduce the adverse
XX consequences of the condition. This sequence represents a human dopamine
XX receptor D2 (DRD2) DNA oligonucleotide used in the scope of the
XX invention.
XX
XX Sequence 20 BP; 1 A; 8 C; 4 G; 7 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 13.6; DB 1; Length 20;

Best Local Similarity 80.0%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1046 TGAAGAGTTTATCCACGACG 1065
:|||||
DB 20 TGAAGAGGCGACGACGACG 1
RESULT 439
AAX66607
ID AAX66607 standard; RNA; 15 BP.
XX
XX AAX66607;
XX
XX 20-JUL-1999 (first entry)
XX
XX Human CD40 hammerhead ribozyme target SEQ ID NO:1239.
XX
XX Arthritic condition; graft tolerance; immune response; target; cleavage;
XX hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;
XX streptolysin; synovial membrane; joint; arthritis; osteoarthritis;
XX rheumatoid arthritis; autoimmune disease; allergy; inflammation;
XX diagnosis; ss.
XX
XX Homo sapiens.
XX
XX MO9618736-A2.
XX
XX 20-JUN-1996.
XX
XX 22-NOV-1995; 95MO-US015516.
XX
XX 13-DEC-1994; 94US-00354920.
XX
XX 23-DEC-1994; 94US-00363253.
XX
XX 23-DEC-1994; 94US-00363254.
XX
XX 17-FEB-1995; 95US-00390850.
XX
XX 20-APR-1995; 95US-00426124.
XX
XX 02-MAY-1995; 95US-00432874.
XX
XX 04-MAY-1995; 95US-00434509.
XX
XX 07-JUL-1995; 95US-0000951P.
XX
XX 07-JUL-1995; 95US-0000974P.
XX
XX 07-AUG-1995; 95US-00512861.
XX
XX 05-OCT-1995; 95US-00541365.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Belgelman L, Stinchcomb DT, Jarvis T, Draper K, Pavco P;
XX McGwiggan J, Gustofson J, Usman N, Wincott F, Matulic-Adamic J;
XX Karpetsky A, Thompson JD, Modak A, Burgin A;
XX WPI; 1996-300653/30.
XX
XX Enzymatic nucleic acid molecules having a hammer-head motif - used for
XX the treatment of arthritis, induction of graft tolerance or treatment of
XX auto-immune diseases.
XX
XX Claim 10; Page 204; 307bp; English.
XX
XX The present invention describes a novel enzymatic nucleic acid (ENA)
XX having a hammerhead motif (HM) comprising: (i) at least 5 ribose residues
XX (iii) a 2'-C-allyl modification at position 4 of the ENA; (iii) at least
XX ten 2'-O-methyl modifications; and (iv) a 3'-end modification. The ENA's
XX can inhibit collagenase and streptolysin production in the synovial
XX membrane of joints for the treatment or prevention of arthritis,
XX particularly osteoarthritis or rheumatoid arthritis. The ENA's can also
XX be used to treat antigen presenting cells of a donor to induce tolerance
XX in a recipient to an allograft of a donor. They can also be used for
XX enhancing graft tolerance or for treating autoimmune disease, and for
XX treating allergies and other inflammatory conditions. The ENA's can also
XX be used in diagnosis. Ribozyme therapy impacts on the expression of
XX streptolysin without introducing the non-specific effects upon gene
XX expression which accompany treatment with retinoids and dexamethasone.
XX The concentration of ribozyme required to affect a therapeutic treatment

CC is lower than that required of antisense molecules, and is highly
CC specific. The present sequence is used in the exemplification of the
CC present invention

XX Sequence 15 BP; 2 A; 4 C; 2 G; 0 T; 7 U; 0 Other;

SO Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 53.3%; Pred. No. 2.3e+02;
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1411 TTCCTCTCCAATG 1425
:::|:|:|:|:|:|:
Db 1 UUCUUCUCCAUG 15

RESULT 440
AAK6606
ID AAK6606 standard; RNA; 15 BP.

XX AAK6606;

XX 20-JUN-1999 (first entry)

XX Human CD40 hammerhead ribozyme target SEQ ID NO:3238.

XX Arthritic condition; graft tolerance; immune response; target; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;
KW streptolysin; synovial membrane; joint; arthritis; osteoarthritis;
KW rheumatoid arthritis; autoimmune disease; allergy; inflammation;
KW diagnosis; ss.

XX Homo sapiens.

XX W09618736-A2.

XX 20-JUN-1996.

XX 22-NOV-1995; 95WO-US015516.

XX 13-DEC-1994; 94US-00354920.

XX 23-DEC-1994; 94US-00363253.

XX 17-FEB-1994; 94US-00363254.

XX 20-APR-1995; 95US-00308050.

XX 02-MAY-1995; 95US-00426124.

XX 04-MAY-1995; 95US-00432874.

XX 07-JUL-1995; 95US-00434509.

XX 07-JUL-1995; 95US-0000951P.

XX 07-AUG-1995; 95US-0000974P.

XX 05-OCT-1995; 95US-00512861.

XX (RIBO-) RIBOZYME PHARM INC.

XX Beigelman L, Stinchcomb DT, Jarvis T, Draper K, Pavco P;

XX Meswiggen J, Gustofson J, Usman N, Wincott F, Matulic-Adamic J;

XX Karpetsky A, Thompson JD, Modak A, Burgin A;

XX WPI; 1996-300653/30.

XX Enzymatic nucleic acid molecules having a hammer-head motif - used for

XX the treatment of arthritis, induction of graft tolerance or treatment of

XX auto-immune diseases.

XX Claim 10; Page 204; 307pp; English.

CC in a recipient to an alloantigen of a donor. They can also be used for

CC enhancing graft tolerance or for treating autoimmune disease, and for

CC treating allergies and other inflammatory conditions. The ENA's can also

CC be used in diagnosis. Ribozyme therapy impacts on the expression of

CC streptolysin without introducing the non-specific effects upon gene

CC expression which accompany treatment with retinoids and dexamethasone.

CC The concentration of ribozyme required to affect a therapeutic treatment

CC is lower than that required of antisense molecules, and is highly

CC specific. The present sequence is used in the exemplification of the

CC present invention

XX Sequence 15 BP; 2 A; 5 C; 2 G; 0 T; 6 U; 0 Other;

SO Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 60.0%; Pred. No. 2.3e+02;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1409 GCTTCCTCCAATG 1423
||:|:|:|:|:|:
Db 1 GCUUCUCCAUG 15

RESULT 441
AAF49867/c
ID AAF49867 standard; DNA; 15 BP.

XX AAF49867;

XX 30-MAR-2001 (first entry)

XX IGF-I oligonucleotide #827.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;

XX cytostatic; dermatological; cardiac; vitreous; ophthalmological; keloid;

XX skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; psoriasis;

XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; plaritis;

XX growth factor mediated cell proliferation; ichthyosis; seborthosa; ruba;

XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;

XX hyperovascular condition; hyperplasia; kidney disease;

XX neovascular condition of the retina; ss.

XX Homo sapiens.

XX W0200078341-A1.

XX 28-DEC-2000.

XX 21-JUN-2000; 2000WO-AU000693.

XX 21-JUN-1999; 99US-0140345P.

XX (MURDOCH CHILDRENS RES INST.

XX Wraight CJ, Werther GA, Edmondson SR;

XX WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering

XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that

XX inhibits or reduces growth factor mediated cell proliferation and/or

XX inflammation.

XX Example 8; Page 66; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of

XX skin disorders. The method comprises contacting the skin with an

XX antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1

XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of

XX inhibiting or reducing growth factor mediated cell proliferation,

XX inflammation and/or other disorders. The present sequence is an

XX oligonucleotide which can be used to design the antisense

XX oligonucleotides of the present invention (see AAF45151 and AAF45153-

XX F45161). The method is useful for ameliorating the effects of psoriasis,

CC ichtyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 0 A; 8 C; 4 G; 3 T; 0 U; 0 Other;
OY
Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 15 GCGGCGAGCGCGCA 23
15 GCGGCGAGCGCGCA 1
RESULT 442
AAF45173/c
ID AAF45173 standard; DNA, 15 BP.
XX
AC AAF45173;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGFBP2 oligonucleotide #12.
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytoskeletal; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichtyosis; serborrhea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wright CJ, Werther GA, Edmondson SR;
XX
DR WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
PT Example 6; Page 34; 201pp; English.
XX
PS The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichtyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC vessels or any other hyperplasia

CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 6 A; 0 C; 9 G; 0 T; 0 U; 0 Other;
OY
Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 15 CTCTCTCTCTCTCC 1022
15 CTCTCTCTCTCTCC 1
RESULT 443
AAF49642/c
ID AAF49642 standard; DNA, 15 BP.
XX
AC AAF49642;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGF-1 oligonucleotide #602.
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytoskeletal; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichtyosis; serborrhea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wright CJ, Werther GA, Edmondson SR;
XX
DR WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
PT Example 8; Page 64; 201pp; English.
XX
PS The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichtyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 5 A; 2 C; 7 G; 1 T; 0 U; 0 Other;

Query Match	0.8%;	Score 13.4;	DB 1;	Length 15;
Best Local Similarity	93.3%;	Pred. No.2.3e+02;		
Matches 14;	Conservative	0;	Mismatches 1;	Indels 0;
Gaps	0;			
1406 TCAGCTTCTCTCCA	1420			
15 TCGGCTTCTCTCCA	1			
Db				
RESULT 444				
AAFS2680/c				
AAFS2680 standard; DNA; 15 BP.				
AAFS2680;				
30-MAR-2001 (first entry)				
IGF-I oligonucleotide #3640.				
Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;				
cytostatic; dermatological; cardiant; virocid; ophthalmological; keloid;				
skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;				
IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;				
growth factor mediated cell proliferation; ichthyosis; seborrhoea; ruba;				
keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;				
neovascular condition of the retina; ss.				
Homo sapiens.				
MO200078341-A1.				
28-DEC-2000.				
21-JUN-2000; 2000WO-AU000693.				
21-JUN-1999; 99US-0140345P.				
(MURD-) MURDOCH CHILDRENS RES INST.				
Wraight CJ, Werther GA, Edmondson SR;				
WPI; 2001-041421/05.				
Ameliorating the effects of a disorder, e.g. psoriasis, by administering				
UV (ultra-violet) treatment (optional) and an antisense nucleic acid that				
inhibits or reduces growth factor mediated cell proliferation and/or				
inflammation.				
Example 8; Page 84; 201P; English.				
The present invention relates to a method for ameliorating the effects of				
skin disorders. The method comprises contacting the skin with an				
antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1				
receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of				
inhibiting or reducing growth factor mediated cell proliferation,				
inflammation and/or other disorders. The present sequence is an				
oligonucleotide which can be used to design the antisense				
oligonucleotides of the present invention (see AAF45151 and AAF45153-				
FA5161). The method is useful for ameliorating the effects of psoriasis,				
ichthyosis, pityriasis, ruba, pilaris, seborrhoea, keloids, keratosis,				
neoplasias, scleroderma, warts, benign growths, cancers of the skin, a				
hyperneovascular condition such as a neovascular condition of the retina,				
brain or skin, growth factor-mediated malignancies, other sclerotic				
disease, kidney disease, hyperproliferation of the inside of blood				
vessels or any other hyperplasia				
Sequence 15 BP; 0 A; 4 C; 7 G; 4 T; 0 U; 0 Other;				
Query Match	0.8%;	Score 13.4;	DB 1;	Length 15;
Best Local Similarity	93.3%;	Pred. No.2.3e+02;		
Matches 14;	Conservative	0;	Mismatches 1;	Indels 0;
Gaps	0;			

QY	1315	CCACAGAGACGACCCC	1329
DB	15	CCACAGAGACGACCCC	1
RESULT 445			
AF52481			
ID	AF52481	standard; DNA; 15 BP.	
AC	AAFS2481;		
DT	30-MAR-2001	(first entry)	
XX	IGF-I oligonucleotide #3441.		
XX	Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;		
XX	cyrostatic; dermatological; cardiatic; virucide; ophthalmological; keloid;		
KW	skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;		
KW	IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;		
KW	growth factor mediated cell proliferation; ichthyosis; seborrhoea; ruba;		
KW	keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;		
KW	hyperneovascular condition; hyperplasia; kidney disease;		
XX	neovascular condition of the retina; ss.		
OS	Homo sapiens.		
XX	MO200078341-A1.		
XX	28-DEC-2000.		
PF	21-JUN-2000; 2000WO-AU000693.		
XX	21-JUN-1999; 99US-0140345P.		
PA	(MURD-) MURDOCH CHILDRENS RES INST.		
XX	Wraight CJ, Werther GA, Edmondson SR;		
DR	WPI; 2001-041421/05.		
XX	Ameliorating the effects of a disorder, e.g. psoriasis, by administering		
PT	UV (ultra-violet) treatment (optional) and an antisense nucleic acid that		
PT	inhibits or reduces growth factor mediated cell proliferation and/or		
PT	inflammation.		
XX	Example 8; Page 83; 201pp; English.		
XX	The present invention relates to a method for ameliorating the effects of		
CC	skin disorders. The method comprises contacting the skin with an		
CC	antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1		
CC	receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of		
CC	inhibiting or reducing growth factor mediated cell proliferation,		
CC	inflammation and/or other disorders. The present sequence is an		
CC	oligonucleotide which can be used to design to design the antisense		
CC	oligonucleotides of the present invention (see AAF45151 and AAF45153-		
CC	RS161). The method is useful for ameliorating the effects of psoriasis,		
CC	ichthyosis, pityriasis, ruba, pilaris, seborrhoea, keloids, keratosis,		
CC	neoplasia, scleroderma, warts, benign growths, cancers of the skin, a		
CC	hyperneovascular condition such as a neovascular condition of the retina,		
CC	brain or skin, growth factor-mediated malignancies, other sclerotic		
CC	disease, kidney disease, hyperproliferation of the inside of blood		
CC	vessels or any other hyperplasia		
XX	Sequence 15 BP; 4 A; 6 C; 3 G; 2 T; 0 U; 0 Other;		
QY	Query Match	0.8%;	Score 13.4; DB 1; Length 15;
DB	Best Local Similarity	93.3%;	Pred. No. 2.3e+02;
	Matches 14; Conservative	0;	Mismatches 1; Indels 0; Gaps 0
QY	719	CCACAGAGACCATGC	733
DB	1	CCACAGAGACCTTGC	15

RESULT 446
AAFA5224/C
ID AAF45224 standard; DNA, 15 BP.
XX
XX AAF45224;
AC
XX 30-MAR-2001 (first entry)
DT
XX
XX IGFBP2 oligonucleotide #63.
DE
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytoskeletal; dermatological; cardiac; virucide; ophthalmological; keloid;
KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; seborrhoea; rubra;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
XX Homo sapiens.
OS
XX MO200078341-A1.
PN
XX 28-DEC-2000.
PD
XX 21-JUN-2000; 2000WO-AU000693.
PF
XX 21-JUN-1999; 99US-0140345P.
PR
XX (MURD-) MURDOCH CHILDRENS RES INST.
PA
XX (MURD-) MURDOCH CHILDRENS RES INST.
PI
XX Wright CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
DR
XX
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
XX
PS Example 6; Page 34; 201pp; English.
XX
XX The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotide of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, rubra, pilaris, seborrhoea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 0 A; 10 C; 4 G; 1 T; 0 U; 0 Other;
OY Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB 15 GCGGCGGCGGCGCA 29
15 GCGGCGGCGGCGCA 1

ID AAF45223 standard; DNA, 15 BP.
XX
XX AAF45223;
AC
XX 30-MAR-2001 (first entry)
DT
XX
XX IGFBP2 oligonucleotide #62.
DE
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytoskeletal; dermatological; cardiac; virucide; ophthalmological; keloid;
KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; seborrhoea; rubra;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
XX Homo sapiens.
OS
XX MO200078341-A1.
PN
XX 28-DEC-2000.
PD
XX 21-JUN-2000; 2000WO-AU000693.
PF
XX 21-JUN-1999; 99US-0140345P.
PR
XX (MURD-) MURDOCH CHILDRENS RES INST.
PA
XX (MURD-) MURDOCH CHILDRENS RES INST.
PI
XX Wright CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
DR
XX
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
XX
PS Example 6; Page 34; 201pp; English.
XX
XX The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotide of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, rubra, pilaris, seborrhoea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 0 A; 10 C; 4 G; 1 T; 0 U; 0 Other;
OY Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB 15 GCGGCGGCGGCGCAG 30
15 GCGGCGGCGGCGCAG 1

RESULT 447
AAFA5223/C

RESULT 448
AAB53643
ID AEB53643 standard; DNA, 15 BP.
XX
XX AAB53643;
AC

DT 06-OCT-2005 (first entry)
 XX
 DE Human Omi/HtrA2 exon 7 DNA fragment.
 XX ds; Omi/HtrA2; Parkinson's disease; diagnosis; serine protease;
 KW apoptosis; antiparkinsonian; neurological disease; mutant.
 XX
 OS Homo sapiens.
 XX
 PN WO2005071107-A1.
 XX
 PD 04-AUG-2005.
 XX
 PF 20-JAN-2005; 2005WO-EP000503.
 XX
 PR 27-JAN-2004; 2004DE-10004924.
 XX
 PA (UYTU-) UNIV TUEBINGEN EBERHARD-KARLS.
 XX
 PI Krueger R, Strauss K;
 XX
 DR WPI; 2005-534020/54.
 XX
 PT New nucleic acid encoding a mutant Omi/HtrA2 protein, useful for
 PT diagnosis of Parkinson's disease and in screening for potential
 PT therapeutic agents.
 XX
 PS Example 1; Fig 5; 7app; German.
 XX
 CS This invention describes a novel polynucleotide that encodes the human
 CC Omi/HtrA2 protein containing the amino acid substitutions S141A and/or
 CC S339G. These changes are associated with development of Parkinson's
 CC disease and the products of the invention can be used for the diagnosis
 CC of Parkinson's disease or a predisposition for it. Omi/HtrA2 is a
 CC mitochondrial serine protease that is implicated in stress-induced
 CC apoptosis and cells that express the mutated Omi/HtrA2 show a reduction
 CC in mitochondrial membrane potential, i.e. damaged mitochondrial function.
 CC To diagnose Parkinson's disease in humans, a test sample is analyzed for
 CC presence of the mutant Omi/HtrA2 polynucleotide, a fragment of Omi/HtrA2
 CC or the encoded protein. The mutant is detected by PCR, using primers
 CC chosen from ABB53621-ABB53637 and amplicons are analyzed by denaturing
 CC HPLC, heteroduplex methods or direct sequencing. The presence of
 CC amplicons is detected by hybridization with a probe chosen from ABB53638-
 CC ABB53641. The PCR primers and probes of the invention can be incorporated
 CC into a kit for detecting Parkinson's disease or a predisposition to it.
 CC The exon 1 mutation (i.e. S141A) was found in 25 of 414 patients with
 CC Parkinson's disease and the exon 7 mutation (i.e. S339G) was found in 4
 CC of 514 patients. Where the mutations were detected, they were always
 CC heterozygous. The variant proteins described in the invention are used to
 CC screen for specific binding agents useful for treating Parkinson's
 CC disease. This sequence represents a fragment of human Omi/HtrA2 exon 7
 CC which encodes the S339G mutation.
 XX
 SQ Sequence 15 BP; 0 A; 8 C; 3 G; 4 T; 0 U; 0 Other;
 DT Query Match 0.8%; Score 13.4; DB 1; Length 15;
 XX Best Local Similarity 93.3%; Pred. No. 2.3e+02;
 XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 677 TCCGTGCTCTCTGTC 691
 DB 1 TCCGTGCTCTCTCTGTC 15
 RESULT 449
 AED88284
 ID AED88284 standard; DNA; 15 BP.
 AC AED88284;
 XX
 DT 26-JAN-2006 (first entry)
 XX
 DE Human Leukocyte Antigen B allele identification probe, SEQ ID 167.

XX HLA; Leukocyte; Antigen; transplant rejection; histocompatibility;
 KW preclinical testing; cancer; cytostatic; diabetes mellitus; antidiabetic;
 KW probe; ss.
 XX
 OS Homo sapiens.
 XX
 PN JP2005185172-A.
 XX
 PD 14-JUL-2005.
 XX
 PF 25-DEC-2003; 2003JP-00430554.
 XX
 PR 25-DEC-2003; 2003JP-00430554.
 XX
 PA (CANO) CANON KK.
 XX
 PI Tsukada M;
 XX
 DR WPI; 2006-013379/02.
 XX
 PT Probe set for specific identification of an HLA-B allele in a sample,
 PT useful e.g. in matching transplant donors and recipients, and in
 PT determining suitable treatment for patients with conditions such as
 PT cancer and diabetes mellitus.
 XX
 PS Claim 2; SEQ ID NO 167; 152pp; Japanese.
 XX
 CS The invention relates to a novel probe set for the identification of a
 CC Human Leukocyte Antigen (HLA)-B allele in a sample. The invention further
 CC includes a method for identifying an HLA-B allele using the probe set.
 CC The probe set and method are useful for identifying an HLA-B allele in a
 CC sample. The information gained is useful, for example, in matching organ
 CC donors and recipients, and in guiding clinical decisions in the treatment
 CC of diseases such as cancer and diabetes mellitus. This oligo sequence
 CC represents a probe used in the identification of a Human Leukocyte
 CC Antigen B allele of the invention.
 XX
 SQ Sequence 15 BP; 2 A; 7 C; 6 G; 0 T; 0 U; 0 Other;
 DT Query Match 0.8%; Score 13.4; DB 1; Length 15;
 XX Best Local Similarity 93.3%; Pred. No. 2.3e+02;
 XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 132 GAGCCCGAGCGGCCA 146
 DB 1 GAGCCCGAGCGGCCA 15
 RESULT 450
 AAQ95705
 ID AAQ95705 standard; DNA; 16 BP.
 AC AAQ95705;
 XX
 DT 15-FEB-1996 (first entry)
 XX
 DB Primer A (Group 7, set C) for marker D18S66, chromosome 18.
 XX
 KW primer; polymerase chain reaction; PCR; linkage study; locus;
 KW microsatellite marker sequence; automated genotyping; allele;
 KW polymorphism; detection; Homo sapiens; ss.
 XX
 OS Synthetic.
 XX
 PN WO9515400-A1.
 XX
 PD 08-JUN-1995.
 XX
 PF 05-DEC-1994; 94WO-US013945.
 XX
 PR 03-DEC-1993; 93US-00160837.
 XX

PA (UYUO) UNIV JOHNS HOPKINS.
XX
XX Levitt RC;
XX
XX WPI; 1995-215278/28.
XX
XX Kit for automated genotyping contg. pairs of PCR primers - designed to
PT amplify polymorphic nucleotide repeat sequences, arranged in sets each
PT with a characteristic fluorescence label, useful e.g. in detection of
PT disease related genetic rearrangement.
XX
XX Disclosure; Fig 7G-2; 104pp; English.
XX
XX The method aims to provide a collection of highly reproducible
CC microsatellite marker sequences (MMS) at approx. 10-50 cM intervals
CC throughout the human genome which can be detectably labelled. The MMS are
CC polymorphic, simple sequence repeats and can be used in automated
CC genotyping. esp. fluorescence-based. The primers correspond to the unique
CC DNA sequence surrounding each marker, and PCR is used to detect each
CC polymorphism. When the MMS show considerable polymorphism (ie. a
CC difference in the number of repeats) between individuals, the markers can
CC be particularly informative. The MMS can be ideal for linkage studies.
CC Kits comprise at least 4 groups, of at least 3 sets, each comprising
CC labelled primers for PCR amplification of the DNA. Group 7 primer pairs
CC are shown in AAg95687-734. The published size range of the D18S66 allele
CC is 244-262 bp, and the degree of heterozygosity in the population is
CC about 86%
XX
XX Sequence 16 BP; 4 A; 6 C; 4 G; 2 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 922 GAGCAGTCTCTGCC 936
DB 2 GAGCAGTCTCTGCC 16
XX
XX RESULT 451
ADc84377/c
ID ADc84377 standard; DNA; 16 BP.
XX
XX AC ADc84377;
XX
XX DT 01-JAN-2004 (first entry)
XX
XX DE Human papillomavirus type MM7 detection oligonucleotide #11.
XX
XX KW probe; human papilloma virus; HPV; detection; identification; ss.
XX
XX OS Human papillomavirus.
XX
XX PN EP1302550-A1.
XX
XX PD 16-APR-2003.
XX
XX PF 10-OCT-2001; 2001BP-00123379.
XX
XX PR 10-OCT-2001; 2001BP-00123379.
XX
XX PA (KING-) KING CAR FOOD IND CO LTD.
XX
XX PI Lin C, Lin R, You C, Huang H, Lee B, Lee H, Lin Y, Fan C,
PI Hsu H, Shih C, Yeh C, Kao Y, Pan C, Chan P;
XX
XX WPI; 2003-432398/41.
XX
XX Detector for identifying human papilloma virus subtypes, comprises
PT carrier having two parts carrying first and second oligonucleotides that
PT respectively hybridize with DNA contained in first and second subtypes of
PT the virus.
XX

PS Claim 4; SEQ ID NO 607; 221pp; English.
XX
XX The invention comprises oligonucleotides for detecting and identifying
CC subtypes of human papilloma virus (HPV) contained in a sample. The
CC oligonucleotides of the invention are useful for simultaneously detecting
CC and identifying subtypes of HPVs. The present DNA sequence represents an
CC HPV detection oligonucleotide of the invention.
XX
XX Sequence 16 BP; 3 A; 2 C; 4 G; 7 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 601 TACATGGCCATCATTA 615
DB 16 TACATGGCCATCATTA 2
XX
XX RESULT 452
ADf44279/c
ID ADf44279 standard; DNA; 16 BP.
XX
XX AC ADf44279;
XX
XX DT 12-FEB-2004 (first entry)
XX
XX DE HPV MM7 detecting probe MM711.
XX
XX KW detection; human papillomavirus; HPV subtype; probe; ss.
XX
XX OS Human papillomavirus.
XX
XX PN JP2002360271-A.
XX
XX PD 17-DEC-2002.
XX
XX PF 28-NOV-2001; 2001BP-00362595.
XX
XX PR 04-MAY-2001; 2001TW-00110785.
XX
XX PA (KING-) KING CAR FOOD IND CO LTD.
XX
XX WPI; 2003-600935/57.
XX
XX DT A detecting apparatus and a detecting method for identifying the subtypes
XX of many species of human papilloma viruses at the same time and a
PT composition for the detection.
XX
XX PS Claim 1; SEQ ID NO 636; 166pp; Japanese.
XX
XX This invention describes a novel detecting apparatus for identifying the
CC subtypes of human papillomaviruses (HPV) contained in a sample which
CC comprises a carrier which can load sample, a first oligonucleotide loaded
CC on first part of the carrier and a second oligonucleotide loaded on
CC second part of carrier, in which first and second oligonucleotides
CC hybridise with the DNA of the first and the second HPV subtype and can
CC identify HPV subtype contained in sample at the same time. ADf43644-
CC ADf44289 represent oligonucleotide probes used in the method of the
CC invention.
XX
XX Sequence 16 BP; 3 A; 2 C; 4 G; 7 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 601 TACATGGCCATCATTA 615
DB 16 TACATGGCCATCATTA 2
XX
XX RESULT 453

```

ADU76209
ID ADU76209 standard; DNA; 16 BP.
XX
XX AC ADU76209;
XX
XX DT 10-FEB-2005 (first entry)
XX
XX DE V segment TCR beta primer SEQ ID NO 225.
XX
XX KM ss; primer; genetic marker; neoplasia; cytostatic; leukemia.
XX
XX OS Synthetic.
XX
XX PN WO2004101815-A1.
XX
XX PD 25-NOV-2004.
XX
XX PF 13-MAY-2004; 2004WO-AU000625.
XX
XX PR 13-MAY-2003; 2003AU-00902299.
XX
XX PA (MONO-) MONOQUANT PTY LTD.
XX
XX PI Morley AA, Brisco M, Sykes P;
XX
XX DR WPI; 2004-821897/81.
XX
XX PT Analyzing a marker nucleic acid region of a clonal population of cells
XX PT that is flanked on one or both sides by members of distinct repeated
XX PT sequences by identifying nucleic acid sequence regions flanking the
XX PT marker nucleic acid region.
XX
XX PS Example 3; SEQ ID NO 225; 99pp; English.
XX
XX CC The invention relates to a method of analyzing a marker nucleic acid
XX CC region of a clonal population of cells that is flanked on one or both
XX CC sides by members of a family of distinct repeated sequences comprises
XX CC identifying one or more of the nucleic acid sequence regions flanking the
XX CC marker nucleic acid region. The method is useful in diagnosing and/or
XX CC monitoring a mammalian disease condition, the condition is a neoplastic
XX CC condition, e.g. malignant or non-malignant neoplastic condition. The
XX CC condition is an immunodeficiency and the screening is directed to
XX CC detecting specific immune cell expansion. The condition is an immune
XX CC response and the screening is directed to detecting specific immune cell
XX CC expansion. The method is useful for analyzing a marker nucleic acid
XX CC region of a clonal population of cells that is flanked on one or both
XX CC sides by members of distinct repeated sequences. The present sequence
XX CC represents a V segment TCR beta primer.
XX
XX SQ Sequence 16 BP; 4 A; 6 C; 5 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 13.4; DB 1; Length 16;
XX Best Local Similarity 93.3%; Pred. No. 2.7e+02;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1324 GGGCCCAAGGCCCA 1338
XX |||||
XX DB 2 GGCTCCAAGGCCCA 16
XX
XX RESULT 454
XX ABB56195/c
XX ID ABB56195 standard; DNA; 16 BP.
XX
XX AC ABB56195;
XX
XX DT 20-OCT-2005 (first entry)
XX
XX DE HPV MM7 probe SEQ ID NO 419.
XX
XX KM human papilloma virus; probe; ss; diagnosis; DNA microarray; biochip.
XX
XX OS Human papillomavirus.

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XX
XX PN US2005175989-A1.
XX
XX PD 11-AUG-2005.
XX
XX PF 23-JUN-2003; 2003US-00601497.
XX
XX PR 20-JUN-2001; 2001US-00885799.
XX
XX PA (LINC/) LIN C.
XX PA (LINR/) LIN R.
XX PA (YOUNC/) YOU C.
XX PA (YOUNR/) YOU R.
XX PA (YANC/) YAN C.
XX PA (YANR/) YAN R.
XX PA (LEEB/) LEE B.
XX PA (LEER/) LEE R.
XX PA (LEEH/) LEE H.
XX PA (LINY/) LIN Y.
XX PA (PANC/) PAN C.
XX PA (HSUH/) HSU H.
XX PA (SHIH/) SHI H.
XX PA (YEH/) YEH C.
XX PA (YEOC/) YEH C.
XX PA (YAOY/) KAO Y.
XX PA (PANC/) PAN C.
XX PA (CHAN/) CHAN P.
XX
XX PI Lin C, Lin R, You C, Yan C, Lee B, Lee H, Lin Y, Fan C, Hsu H;
XX PI Shih C, Yeh C, Kao Y, Pan C, Chan P;
XX
XX DR WPI; 2005-553735/56.
XX
XX PT Detector for detecting and simultaneously diagnosing subtype of human
XX PT papilloma viruses (HPV) e.g. HPV 6, HPV 11 or HPV 16, has carrier,
XX PT several micro-dots immobilized on carrier and oligonucleotide sequences
XX PT contained in each micro-dot.
XX
XX PS Claim 15; SEQ ID NO 419; 105pp; English.
XX
XX CC The invention relates to a detector (I) for detecting and simultaneously
XX CC diagnosing one or more subtypes of human papilloma viruses (HPV)
XX CC contained in a biological sample. (I) is useful for detecting and
XX CC simultaneously diagnosing one or more subtypes of HPV contained in a
XX CC biological sample. (I) enables rapid and reliable detection of HPV
XX CC subtype in a biological sample. The present sequence represents a human
XX CC papilloma virus subtype probe.
XX
XX SQ Sequence 16 BP; 3 A; 2 C; 4 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 13.4; DB 1; Length 16;
XX Best Local Similarity 93.3%; Pred. No. 2.7e+02;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 601 TACATGGCCATCATTA 615
XX |||||
XX DB 16 TACAGGCCATCATTA 2
XX
XX RESULT 455
XX ABF73244/c
XX ID ABF73244 standard; DNA; 13 BP.
XX
XX AC ABF73244;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 173241 for detecting SNP TSC0043153.
XX
XX KM SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KM central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.

```

PD 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 173241; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 6 A; 0 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1603 ATTCTCCCTATC 1615
Db 13 ATTCTCCCTATC 1

RESULT 456
ABH37834/C
ID ABH37834 standard; DNA; 13 BP.
XX
XX ABH37834;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 237811 for detecting SNP TSC0058003.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is

PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 237811; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 0 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1593 AAAAATCTCAATT 1605
Db 13 AAAAATCTCAATT 1

RESULT 457
ABC89691
ID ABC89691 standard; DNA; 13 BP.
XX
XX ABC89691;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 89708 for detecting SNP TSC0022491.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 89708; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 8 A; 2 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1592 AAAAAATCTCAAT 1604
1 AAAAAATCTCAAT 13

RESULT 458
ABH06065
ID ABH06065 standard; DNA; 13 BP.

AC ABH06065;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 206042 for detecting SNP TSC0007438.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB000713.

PR 07-APR-2000; 2000DE-01019173.

PA (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 206042; 29pp + Sequence listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 8 A; 3 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1591 CAAAAATCTCAA 1603
1 CAAAAATCTCAA 13

Db 1 CAAAAATCTCAA 13

RESULT 459
ABF59772
ID ABF59772 standard; DNA; 13 BP.

AC ABF59772;

DT 21-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 159769 for detecting SNP TSC0040218.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB000713.

PR 07-APR-2000; 2000DE-01019173.

PA (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 159769; 29pp + Sequence listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 6 A; 0 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 781 ATTATGAGAAAG 793
1 ATTATGAGAAAG 13

RESULT 460

ABF29162/c
ID ABF29162 standard; DNA; 13 BP.

AC ABF29162;

DT 21-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 129159 for detecting SNP TSC0032336.

XX

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
PS Claim 1; SEQ ID NO 129159; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 13 BP; 3 A; 0 C; 6 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 608 CCATCATATCATCC 620
Db 13 CCATCATATCATCC 1
|||||
|||||
RESULT 461
ABC98834/C
ID ABC98834 standard; DNA; 13 BP.
XX ABC98834;
AC ABC98834;
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 98851 for detecting SNP TSC0024561.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX OS
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX PR

XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
PS Claim 1; SEQ ID NO 98852; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 13 BP; 2 A; 0 C; 5 G; 6 T; 0 U; 0 Other;
SQ
Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1639 CTCACCAACCAATC 1651
Db 13 CTCACCAACCAATC 1
|||||
|||||
RESULT 462
ABC98835
ID ABC98835 standard; DNA; 13 BP.
XX ABC98835;
AC ABC98835;
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 98852 for detecting SNP TSC0024561.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX OS
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
PS Claim 1; SEQ ID NO 98852; 29pp + Sequence Listing; German.
XX

CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 6 A; 5 C; 0 G; 2 T; 0 U; 0 Other;

XX Query Match 0.7%; Score 13; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+02;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1639 CTCAACCAATC 1651
Db 1 CTCAACCAATC 13

RESULT 463
ABC77569
ID ABC77569 standard; DNA; 13 BP.
XX ABC77569;
XX
XX 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 77586 for detecting SNP TSC0019760.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIC-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 77586; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 13 BP; 5 A; 6 C; 0 G; 2 T; 0 U; 0 Other;

XX Query Match 0.7%; Score 13; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+02;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 CCNAACATCTCCA 259
Db 1 CCNAACATCTCCA 13

RESULT 464
ABF98357/C
ID ABF98357 standard; DNA; 13 BP.
XX ABF98357;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 198354 for detecting SNP TSC0004656.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIC-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 198354; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 4 A; 3 C; 0 G; 6 T; 0 U; 0 Other;

XX Query Match 0.7%; Score 13; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+02;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 780 GATTATGAGAA 792
Db 13 GATTATGAGAA 1

RESULT 465
ABC9690/C

ID ABC89690 standard; DNA; 13 BP.
XX ABC89690;
AC
XX
XX
DT 21-FEB-2002 (first entry)
XX
XX
DE Oligonucleotide SEQ ID NO 89707 for detecting SNP TSC0022491.
XX
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KM central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIC-) EPIDENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
PI WPI; 2001-657177/75.
XX
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 89707; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 3 A; 0 C; 2 G; 8 T; 0 U; 0 Other;
SQ
Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1592 AAAAATCTCAAT 1604
DB 13 AAAAATCTCAAT 1
RESULT 466
ABC77568/c
ID ABC77568 standard; DNA; 13 BP.
XX ABC77568;
AC
XX
XX 21-FEB-2002 (first entry)
XX
XX
XX Oligonucleotide SEQ ID NO 77585 for detecting SNP TSC0019760.
XX
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KM central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX

XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIC-) EPIDENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
PI WPI; 2001-657177/75.
XX
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 77585; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 2 A; 0 C; 6 G; 5 T; 0 U; 0 Other;
SQ
Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 247 CCAACATCTCCA 259
DB 13 CCAACATCTCCA 1
RESULT 467
ABC10989/c
ID ABC10989 standard; DNA; 13 BP.
XX ABC10989;
AC
XX
XX 20-FEB-2002 (first entry)
XX
XX
XX Oligonucleotide SEQ ID NO 10980 for detecting SNP TSC0002720.
XX
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KM central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIC-) EPIDENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX

DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 10980; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 3 C; 1 G; 5 T; 0 U; 0 Other;
XX
Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 38 AGAAGCGTTTATA 50
Db 13 AGAAGCGTTTATA 1
XX
RESULT 468
ABH06064/C
ID ABH06064 standard; DNA; 13 BP.
XX
AC ABH06064;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 206041 for detecting SNP TSC0007438.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 206041; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 2 A; 0 C; 3 G; 8 T; 0 U; 0 Other;
XX
Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1591 CAAAAATCTCAA 1603
Db 13 CAAAAATCTCAA 1
XX
RESULT 469
ABF99773/C
ID ABF99773 standard; DNA; 13 BP.
XX
AC ABF99773;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 159770 for detecting SNP TSC0040218.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 159770; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 3 C; 0 G; 6 T; 0 U; 0 Other;
XX
Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 781 ATTTATGGAAG 793
 DB 13 ATTTATGGAAG 1
 RESULT 470
 ABH37835
 ID ABH37835 standard; DNA, 13 BP.
 AC ABH37835;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 237812 for detecting SNP TSC0058003.
 XX
 KM SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KM central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 237812; 29bp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 7 A; 2 C; 0 G; 4 T; 0 U; 0 Other;
 Query Match 0.7%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1593 AAAATCTCAATT 1605
 DB 1 AAAATCTCAATT 13
 RESULT 471
 ABC34325
 ID ABC34325 standard; DNA, 13 BP.
 AC ABC34325;
 XX
 DT 20-FEB-2002 (first entry)

XX
 DE Oligonucleotide SEQ ID NO 34342 for detecting SNP TSC0010966.
 XX
 KM SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KM central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 34342; 29bp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 6 A; 3 C; 0 G; 4 T; 0 U; 0 Other;
 Query Match 0.7%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1594 AAAATCTCAATTC 1606
 DB 1 AAAATCTCAATTC 13
 RESULT 472
 ABC10988
 ID ABC10988 standard; DNA, 13 BP.
 AC ABC10988;
 XX
 DT 20-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 10979 for detecting SNP TSC0002720.
 XX
 KM SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KM central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPiG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 10979; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 5 A; 1 C; 3 G; 4 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 AGAAGCGTTTATA 50
Db 1 AGAAGCGTTTATA 13
RESULT 473
ABF29163
ID ABF29163 standard; DNA; 13 BP.
XX
XX ABF29163;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 129160 for detecting SNP TSC0032336.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPiG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX
XX Claim 1; SEQ ID NO 129160; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 4 A; 6 C; 0 G; 3 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 608 CCATCATACATCC 620
Db 1 CCATCATACATCC 13
RESULT 474
ABF98356
ID ABF98356 standard; DNA; 13 BP.
XX
XX ABF98356;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 198353 for detecting SNP TSC0004656.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPiG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 198353; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but

CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 SQ Sequence 13 BP; 6 A; 0 C; 3 G; 4 T; 0 U; 0 Other;
 Query Match 0.7%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 780 GATTATGAGAAA 792
 1 GATTATGAGAAA 13
 DB
 RESULT 475
 ABC34324/c
 ID ABC34324 standard; DNA; 13 BP.
 AC ABC34324;
 XX
 DT 20-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 34341 for detecting SNP TSC0010966.
 XX
 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KM central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 34341; 29pp + Sequence Listing; German.
 XX
 This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 4 A; 0 C; 3 G; 6 T; 0 U; 0 Other;
 Query Match 0.7%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1594 AAAATCTCAATTC 1606
 13 AAAATCTCAATTC 1
 DB

RESULT 476
 ABF73245
 ID ABF73245 standard; DNA; 13 BP.
 XX
 AC ABF73245;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 173242 for detecting SNP TSC0043153.
 XX
 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KM central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 173242; 29pp + Sequence Listing; German.
 XX
 This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 2 A; 5 C; 0 G; 6 T; 0 U; 0 Other;
 Query Match 0.7%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1603 ATCTTCCTATC 1615
 1 ATCTTCCTATC 13
 DB
 RESULT 477
 AAT33386
 ID AAT33386 standard; cDNA; 15 BP.
 XX
 AC AAT33386;
 XX
 DT 16-MAY-1997 (first entry)
 XX
 DE Human vascular endothelial growth factor antisense oligonucleotide.
 XX
 KM Antisense; VEGF; vascular endothelial growth factor; hypoxia;
 KM neovascularisation; angiogenesis; metastasis; retinopathy; macular;

KW degeneration; expression inhibitor; ss.
 XX Synthetic.
 OS
 XX WO627006-A2.
 PN
 XX
 PD 06-SEP-1996.
 XX
 PF 29-FEB-1996; 96WO-US002840.
 XX
 PR 02-MAR-1995; 95US-00398945.
 PR 08-DEC-1995; 95US-00569926.
 XX
 PA (HYBR-) HYBRIDON INC.
 XX
 PI Robinson GS;
 XX
 DR WPI; 1996-412773/41.
 XX
 PT Human vascular endothelial growth factor anti:sense oligo:nucleotide -
 PT inhibits the expression of VEGF, useful in treatment of hypoxia induced
 PT neovascularisation and angiogenesis associated disease states.
 PT
 PS Claim 17; Page 51; 92pp; English.
 XX
 XX AAT33371-T33431 are antisense oligonucleotides used to inhibit the
 CC expression of human vascular endothelial growth factor (VEGF). The
 CC synthetic oligonucleotides contain phosphorothioate linkages and
 CC essentially consist of 2'-O-alkylated ribonucleotides. Inhibiting the
 CC expression of VEGF is useful in the treatment of hypoxia induced
 CC neovascularisation and angiogenesis associated disease states,
 CC retinopathy of prematurity, diabetic retinopathy and age related macular
 CC degeneration
 CC
 SQ Sequence 15 BP; 0 A; 8 C; 3 G; 4 T; 0 U; 0 Other;
 XX
 QY Query Match 0.7%; Score 13; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1011 CTTCTCTCTGCCC 1023
 1 CTTCTCTCTGCCC 13
 QY
 DB
 RESULT 478
 AAT48401
 ID AAT48401 standard; DNA; 15 BP.
 XX
 AC AAT48401;
 XX
 DT 11-MAR-1997 (first entry)
 XX
 DE Oligonucleotide H-8A specific for human VEGF nucleic acid.
 XX
 KW Vascular endothelial growth factor; inhibition; decrease; antisense;
 KW neovascularisation; retinopathy; age-related macular degeneration;
 KW diabetes; ss.
 XX
 XX Synthetic.
 OS
 XX WO623065-A2.
 PN
 XX 01-AUG-1996.
 PD
 XX 26-JAN-1996; 96WO-US001189.
 PF
 XX 26-JAN-1995; 95US-00378860.
 PR
 XX (HYBR-) HYBRIDON INC.
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 PI Robinson GS, Smith LEH;

XX
 DR WPI; 1996-362689/36.
 XX
 XX Inhibiting neovascularisation using VEGF-specific oligo:nucleotide(s) -
 PT for treatment of retinopathies and age-related macular degeneration.
 PT
 PS Disclosure; Page 12; 66pp; English.
 XX
 XX Neovascularisation can be reduced by blocking vascular endothelial growth
 CC factor (VEGF) expression using a synthetic oligonucleotide specific for
 CC VEGF. Inhibiting neovascularisation is useful for treatment of
 CC retinopathy of prematurity, diabetic retinopathy and age-related macular
 CC degeneration. The present sequence is an example of a suitable
 CC oligonucleotide specific for human VEGF
 CC
 SQ Sequence 15 BP; 0 A; 8 C; 3 G; 4 T; 0 U; 0 Other;
 XX
 QY Query Match 0.7%; Score 13; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1011 CTTCTCTCTGCCC 1023
 1 CTTCTCTCTGCCC 13
 QY
 DB
 RESULT 479
 AAX33621/C
 ID AAX33621 standard; DNA; 15 BP.
 XX
 AC AAX33621;
 XX
 DT 25-JUN-1999 (first entry)
 XX
 DE Thrombin inhibitor SEQ ID NO. 9.
 XX
 KW Thrombin inhibitor; molecular design; exon shuffling; DNA library;
 KW function improvement; high functional fit evolution; ss.
 XX
 XX Synthetic.
 OS
 XX WO9911818-A1.
 PN
 XX 11-MAR-1999.
 PD
 XX 28-AUG-1998; 98WO-JP003854.
 PF
 XX 28-AUG-1997; 97JP-00249679.
 PR
 XX (KARU/) KARUBE I.
 PA
 XX Karube I, Okabe Y, Sumikura K;
 PI
 XX WPI; 1999-228983/19.
 DR
 XX
 PT Molecular design by exon shuffling within a library of DNA sequences.
 PT
 PS Example 2; Page 15; 42pp; Japanese.
 XX
 XX This sequence represents a thrombin inhibitor that was used in an example
 CC of the process of the invention. The process is for molecular design, and
 CC is carried out by shuffling exons within a library of similar DNA
 CC sequences, followed by ranking of the products of reshuffling by their
 CC fit to the desired functionality, and repeating the shuffling and ranking
 CC until a product of the desired functionality is obtained. A similar
 CC process may be carried out using polypeptide sequences. The technique can
 CC be used for the improvement of function, and devising of new functions,
 CC of polypeptides and nucleic acids, for a broad range of uses such as
 CC drugs and foodstuffs. Evolution of high functional fit is rapid compared
 CC to the use of conventional genetic evolution algorithms
 CC
 SQ Sequence 15 BP; 3 A; 1 C; 10 G; 1 T; 0 U; 0 Other;

Query Match 0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1014 CCTCTGCCCCCTAC 1026
14 CCTCTGCCCCCTAC 2

Db

RESULT 480
ID ABRK5500/c
XX ABRK5500 standard; DNA; 15 BP.
AC ABRK5500;
XX
XX 18-JUN-2002 (first entry)
XX
XX Selectin L Lymphocyte Adhesion Molecule 1 (SELL) oligonucleotide #36.
DE
XX
XX Human; Selectin L Lymphocyte Adhesion Molecule 1; SELL;
KM neonatal pertussis; whooping cough; haplotyping; primer;
KM allele-specific oligonucleotide; ss.
XX
XX Homo sapiens.
OS
XX
XX MO200216654-A1.
PN
XX
XX 28-FEB-2002.
PD
XX
XX 27-AUG-2001; 2001WO-US026675.
PF
XX
XX 25-AUG-2000; 2000US-0228262P.
PR
XX
XX (GENA-) GENAISSANCE PHARM INC.
PA
XX
XX Anastasio AB, Bieglecki KM, Klieem SE, Koshy B, Kumar AM;
PI WPI; 2002-292071/33.
XX
XX
XX Novel genetic variants of selectin L lymphocyte adhesion molecule 1
PT (SELL) gene useful for therapeutic purposes and for expressing SELL
PT protein useful in identifying drugs to treat whooping cough.
XX
XX
XX Claim 17; Page 14; 137pp; English.

The invention relates to an isolated polynucleotide (I) comprising a nucleotide sequence which is a polymorphic variant of a reference sequence for Selectin L Lymphocyte Adhesion Molecule 1 (SELL) gene. SELL polypeptide is useful for screening for drugs targeting the polypeptide. Oligonucleotides derived from (I) are used to target SELL and a haplotype or haplotype pair of SELL gene. These are useful in developing diagnostic tests and therapeutic treatments for neonatal pertussis (whooping cough). (1) is useful for studying the expression and function of SELL and expressing SELL protein for use in screening for candidate drugs to treat diseases related to SELL activity. The polymorphism and haplotype data are useful for validating whether SELL is a suitable target for drugs to treat whooping cough, screening for such drugs and reducing bias in clinical trials of such drugs. Establishing the SELL haplotype or haplotype pair of an individual is useful for improving the efficiency and reliability of several steps in the discovery and development of drugs for treating diseases associated with SELL activity e.g. neonatal pertussis (whooping cough). The haplotyping method is useful to validate SELL as a candidate target for treating a specific condition or disease predicted to be associated with SELL activity. The method is also useful in screening for compounds targeting SELL to treat a specific condition or disease predicted to be associated with SELL activity, e.g. detecting which of the SELL haplotypes or haplotype pairs present in individual members of a population with the specific disease of interest enables one to screen for compounds that display the highest desired agonist or antagonist activity for each of the most frequent SELL isoforms present in the disease population. A polymorphic variant of SELL is useful in studying the effect of the variation on the biological activity of SELL, on the binding affinity of candidate drugs targeting SELL for the

CC treatment of neonatal pertussis (whooping cough) and in assays to measure
CC the binding affinities of one or more candidate drugs targeting the SELL
CC protein. ABRK5465-ABRK5559 represent SELL gene allele-specific
CC oligonucleotides of the invention
XX
XX Sequence 15 BP; 3 A; 1 C; 8 G; 2 T; 0 U; 1 Other;
S0

Query Match 0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.7e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
1278 CACCATCTCCCACT 1292
15 CACCATCTCCCACT 1

Db

RESULT 481
ID ABRK5827
XX ABRK5827 standard; DNA; 15 BP.
AC ABRK5827;
XX
XX 24-SEP-2002 (first entry)
XX
XX Solute Carrier Family 1 (SLC1A4) allele-specific oligonucleotide #67.
DE
XX
XX Solute carrier family 1; SLC1A4; haplotyping; human; cancer; primer;
KM glutamate/neutral amino acid transporter; neurological disease; PCR; ss;
KM amino acid transporter disorder; single nucleotide polymorphism; SNP.
XX
XX Homo sapiens.
OS
XX
XX WO200244198-A2.
PN
XX
XX 06-JUN-2002.
PD
XX
XX 29-NOV-2001; 2001WO-US044781.
PF
XX
XX 30-NOV-2000; 2000US-0250254P.
PR
XX
XX (GENA-) GENAISSANCE PHARM INC.
PA
XX
XX Bieglecki KM, Kazemi A, Russo DP, Sausker EA;
PI WPI; 2002-519580/55.
XX
XX
XX Novel genetic variants of Solute Carrier Family 1 (Glutamate/Neutral
PT Amino Acid Transporter), Member 4 isoforms, for improving efficiency and
PT reliability in drug development for treating cancers.
XX
XX
XX Claim 15; Page 16; 139pp; English.

The invention relates to an isolated polynucleotide (I) comprising a first nucleotide sequence which comprises solute carrier family 1 (glutamate/neutral amino acid transporter), member 4 (SLC1A4) isoforms (II) and an isolated polypeptide (III) comprising an amino acid sequence which is a polymorphic variant of a reference sequence for SLC1A4 protein. Also described are methods for: (1) haplotyping or genotyping SLC1A4 gene of an individual; (2) predicting a haplotype pair for SLC1A4 gene of an individual; (3) identifying an association between a trait and at least one haplotype or haplotype pair of SLC1A4 gene. (III) is useful in screening for drugs targeting (III) that are useful for treating cancer, neurological diseases and amino acid transporter disorders. The methods are useful for improving the efficiency and reliability of several steps in the discovery and development of drugs for treating diseases associated with SLC1A4 activity. The haplotyping method is also used by the pharmaceutical research scientist to validate SLC1A4 as a candidate target for treating a specific condition or disease predicted to be associated with SLC1A4 activity, e.g. cancer, neurological diseases and amino acid transporter disorders, and in the design of clinical trials for treating a specific condition of disease associated with SLC1A4 activity. The methods are also useful for screening compounds targeting SLC1A4. Anti-SLC1A4 antibody is useful in diagnostic.

CC prognostic and therapeutic methods. ABK95761-ABK95877 represent SLC1A4
 CC gene allele-specific oligonucleotides, primer extension oligonucleotides
 CC and related PCR primers used to identify single nucleotide polymorphisms
 CC (SNP) of the gene

XX Sequence 15 BP; 0 A; 7 C; 2 G; 5 T; 0 U; 1 Other;

Query Match 0.7%; Score 13; DB 1; Length 15;
 Best Local Similarity 86.7%; Pred. No. 2.7e+02;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 686 TCCTGCTGCGCTCC 700
 Db 1 TCCTGCTGCGCTTC 15

RESULT 482

ABK95804
 ID ABK95804 standard; DNA; 15 BP.

AC ABK95804;

DT 24-SEP-2002 (first entry)

DE Solute Carrier Family 1 (SLC1A4) allele-specific oligonucleotide #44.

XX Solute carrier family 1; SLC1A4; haplotyping; human; cancer; primer;
 KM glutamate/neutral amino acid transporter; neurological disease; PCR; ss;
 KM amino acid transporter disorder; single nucleotide polymorphism; SNP.

OS Homo sapiens.

PN WO200244198-A2.

PD 06-JUN-2002.

PF 29-NOV-2001; 2001WO-US044781.

PR 30-NOV-2000; 2000US-0250254P.

PA (GENA-) GENAISSANCE PHARM INC.

PI Bieglecki KM, Kazemi A, Russo DP, Sauker EA;

DR WPI; 2002-519580/55.

XX Novel genetic variants of Solute Carrier Family 1 (Glutamate/Neutral
 PT Amino Acid Transporter), Member 4 isogenes, for improving efficiency and
 PT reliability in drug development for treating cancers.

PS Claim 15; Page 15; 139pp; English.

XX The invention relates to an isolated polynucleotide (I) comprising a
 CC first nucleotide sequence which comprises solute carrier family 1
 CC (glutamate/neutral amino acid transporter), member 4 (SLC1A4) isogenes
 CC (II) and an isolated polypeptide (III) comprising an amino acid sequence
 CC which is a polymorphic variant of a reference sequence for SLC1A4
 CC protein. Also described are methods for: (1) haplotyping or genotyping
 CC SLC1A4 gene of an individual; (2) predicting a haplotype pair for SLC1A4
 CC gene of an individual; (3) identifying an association between a trait and
 CC at least one haplotype or haplotype pair of SLC1A4 gene. (III) is useful
 CC in screening for drugs targeting (III) that are useful for treating
 CC cancer, neurological diseases and amino acid transporter disorders. The
 CC methods are useful for improving the efficiency and reliability of
 CC several steps in the discovery and development of drugs for treating
 CC diseases associated with SLC1A4 activity. The haplotyping method is also
 CC used by the pharmaceutical research scientist to validate SLC1A4 as a
 CC candidate target for treating a specific condition or disease predicted
 CC to be associated with SLC1A4 activity, e.g. cancer, neurological diseases
 CC and amino acid transporter disorders, and in the design of clinical
 CC trials for treating a specific condition of disease associated with
 CC SLC1A4 activity. The methods are also useful for screening compounds
 CC targeting SLC1A4. Anti-SLC1A4 antibody is useful in diagnostic.

CC prognostic and therapeutic methods. ABK95761-ABK95877 represent SLC1A4
 CC gene allele-specific oligonucleotides, primer extension oligonucleotides
 CC and related PCR primers used to identify single nucleotide polymorphisms
 CC (SNP) of the gene

XX Sequence 15 BP; 1 A; 7 C; 3 G; 3 T; 0 U; 1 Other;

Query Match 0.7%; Score 13; DB 1; Length 15;
 Best Local Similarity 86.7%; Pred. No. 2.7e+02;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 428 ACCTG3CCTTCGCG 442
 Db 1 ACCTG6CCTTCCCG 15

RESULT 483

ABK16925
 ID ABK16925 standard; DNA; 15 BP.

AC ABK16925;

DT 26-MAR-2002 (first entry)

DE Pyridoxal (Pyridoxine, vitamin B6) Kinase (PDXK) probe #5.

KM Pyridoxal kinase; pyridoxine; vitamin B6;
 KM PDXK autoimmune polyglandular disease type 1; transgenic animal;
 KM gene therapy; allele specific oligonucleotide; ASO; probe; ss.

OS Homo sapiens.

PN WO200190125-A2.

PD 29-NOV-2001.

PF 24-MAY-2001; 2001WO-US016909.

PR 24-MAY-2000; 2000US-0206664P.

PA (GENA-) GENAISSANCE PHARM INC.

PI Chew A, Duda A, Koshy B;

DR WPI; 2002-106169/14.

XX Isolated human pyridoxal (pyridoxine, vitamin B6) kinase polynTs, useful
 PT for therapeutic purposes, for studying the expression and function of the
 PT polynT, and for expressing pyridoxal protein.

PS Claim 17; Page 13; 135pp; English.

XX The invention describes an isolated human pyridoxal (pyridoxine, vitamin
 CC B6) kinase, (PDXK) polynucleotide. The polynucleotide is useful in
 CC studying the expression and function of PDXK, and in expressing PDXK
 CC protein for use in screening for candidate drugs to treat PDXK related
 CC diseases and for therapeutic purposes. A transgenic animal is useful for
 CC studying expression of the PDXK isogenes in vivo, for in vivo screening the
 CC efficacy of therapeutic agents and compounds for autoimmune polyglandular
 CC disease type 1. The polypeptide is useful for studying the effect of the
 CC variation on the biological activity of PDXK and the binding affinity of the
 CC candidate drugs targeting PDXK for the treatment of autoimmune
 CC polyglandular disease type 1. Genotyping and haplotyping is useful for
 CC improving the efficacy and reliability of several steps in the discovery
 CC and development of drugs for treating diseases associated with PDXK
 CC activity, e.g., autoimmune polyglandular disease type 1, to validate PDXK
 CC as a candidate agent for treating a specific condition or disease
 CC predicted to be associated with PDXK activity, and in the design of
 CC clinical trials of candidate drugs. This sequence is one of 20 (see
 CC ABK16921-ABK16940) allele specific oligonucleotide (ASO) probe used for
 CC detecting PDXK gene polymorphisms, described in the method of the
 CC invention

XX
SQ Sequence 15 BP; 0 A; 7 C; 1 G; 6 T; 0 U; 1 Other;
Query Match 0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.7e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 106 CCTCTGCTGCTTT 120
DB 1 CCTCTGCTGCTTT 15
RESULT 484
ABN80579
ID ABN80579 standard; DNA, 15 BP.
AC ABN80579;
XX
XX 19-JUL-2002 (first entry)
DE Human P450(cytochrome) oxidoreductase allele specific PCR primer #19.
KW Human; P450(cytochrome) oxidoreductase; POR; cancer; haplotype; SNP;
KM single nucleotide polymorphism; flavoprotein; enzyme; PCR; primer; ss.
XX Homo sapiens.
XX WO200226768-A2.
XX
XX 04-APR-2002.
XX
XX 01-OCT-2001; 2001WO-US030877.
XX
XX 29-SEP-2000; 2000US-0236449P.
XX
XX (GENA-) GENAISSANCE PHARM INC.
XX
XX Kazemi A, Klem SE, Lanz EM, Messer C, Tanguay DA;
PI WPI; 2002-394236/42.
XX
XX New genetic variants comprising haplotypes of the P450 (cytochrome)
PT oxidoreductase (POR) isoenzyme, useful in improving the efficiency of drug
PT screening protocols for compounds targeting POR.
XX
XX Claim 14; Page 14; 14pp; English.
XX
XX The present invention provides the protein, gene and cDNA sequences of
CC human P450(cytochrome) oxidoreductase POR, and single nucleotide
CC polymorphisms (SNPs) identified therein. The sequences can be used to
CC haplotype the POR gene of an individual, and to establish whether POR is
CC a suitable target for drugs to treat cancer and disorders associated with
CC impaired protein synthesis in cells. The present sequence is an allele
CC specific primer for the coding sequences of the invention
XX
SQ Sequence 15 BP; 5 A; 3 C; 5 G; 1 T; 0 U; 1 Other;
Query Match 0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.7e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 30 GTGCATCCAGAGCG 44
DB 1 GTGCATCCAGAGSG 15
RESULT 485
ABK92616/C
ID ABK92616 standard; DNA, 15 BP.
XX
XX ABK92616;
XX
XX 20-AUG-2002 (first entry)
DT

XX
DE ASO primer #14 to detect human ADORA3 gene polymorphisms.
XX
XX Human; single nucleotide polymorphism; SNP; ADORA3; haplotyping;
KW chromosome 1p21-p13; adenosine A3 receptor; genotyping;
KW pathophysiological heart condition; myocardial ischaemia;
KW chronic heart failure; allele-specific oligonucleotide; ASO; primer; ss.
XX
XX Homo sapiens.
XX
XX WO200236610-A2.
XX
XX 10-MAY-2002.
XX
XX 31-OCT-2001; 2001WO-US045718.
XX
XX 31-OCT-2000; 2000US-0244626P.
XX
XX (GENA-) GENAISSANCE PHARM INC.
XX
XX Gilson CR, Kazemi A, Koshy B, Monroe G;
XX WPI; 2002-489998/52.
XX
XX Novel genetic variants of the adenosine A3 receptor, useful
PT therapeutically and in screening for drugs to treat diseases related to
PT ADORA3 activity e.g., myocardial ischemia and chronic heart failure.
XX
XX Claim 15; Page 14; 82pp; English.
XX
XX The present invention relates to novel single nucleotide polymorphisms
CC (SNPs) in the human adenosine A3 receptor (ADORA3) gene located on
CC chromosome 1p21-p13, and methods for haplotyping and/or genotyping the
CC ADORA3 gene. The methods of the invention make use of allele-specific
CC oligonucleotides (ASOs) as probes and primers and/or primer-extension
CC oligonucleotides for detecting the ADORA3 gene polymorphisms. The
CC polymorphisms and screened compounds are useful for the treatment of
CC diseases associated with ADORA3 activity, such as pathophysiological
CC conditions of the heart e.g. myocardial ischaemia and chronic heart
CC failure. ABK92603-ABK92628 represent ASO primers for detecting human
CC ADORA3 gene polymorphisms
XX
SQ Sequence 15 BP; 2 A; 7 C; 1 G; 4 T; 0 U; 1 Other;
Query Match 0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.7e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1205 AGGGCTGGAATGA 1219
DB 15 AGGGCTGGAATGA 1
RESULT 486
ABL52021/C
ID ABL52021 standard; DNA, 15 BP.
XX
XX ABL52021;
XX
XX 11-JUL-2002 (first entry)
XX
DE Human SLC18A2 allele specific oligonucleotide primer SEQ ID NO:69.
XX
XX Human; solute carrier family 18 member 2; SLC18A2; vesicular monoamine;
KW vesicular monoamine transporter; VMAT2; polymorphic site; SNP;
KW single nucleotide polymorphism; antiinflammatory; neuroleptic;
KW haplotyping; genotyping; respiratory inflammatory disease;
KW neuropsychiatric disorder; monoaminergic brain system; primer; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH misc_feature 14
FT

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FT      /*ag= a
TN      /note= "polymorphic site indicated by an ambiguity base"
XX
XX      WO200222652-A2.
XX
XX      21-MAR-2002.
XX
XX      17-SEP-2001; 2001WO-US042217.
XX
XX      15-SEP-2000; 2000US-0232895P.
XX
XX      (GENA-) GENAISSANCE PHARM INC.
XX
XX      Anastasio AE, Han J, Klem SE, Sausker EA;
XX
XX      WPI; 2002-393942/42.
XX
XX      Novel genetic variants of soluble carrier family 18 (vesicular
XX      monoamine), member 2 gene useful for screening drugs to treat diseases
XX      e.g. neuropsychiatric disorders involving monoaminergic brain systems.
XX
XX      Claim 17; Page 15; 183pp; English.
XX
XX      The present invention describes an isolated polynucleotide (I) having a
XX      sequence (S1) comprising soluble carrier family 18 (vesicular monoamine),
XX      member 2 (SLC18A2) isogene selected from 49 isogenes with regions of a
XX      sequence (SS) of 40023 bp (see ABU51954), and defined by a corresponding
XX      set of polymorphisms whose locations and identities are given in the
XX      specification; or a sequence (S2) complementary to (S1). (1) has
XX      antiinflammatory and neuroleptic activities, and can be used in gene
XX      therapy. Methods from the present invention can be used for haplotyping
XX      and genotyping the SLC18A2 gene in an individual. SLC18A2 is also known
XX      as the vesicular monoamine transporter (VMAT2). (1) is useful in studying
XX      the expression and function of SLC18A2, and in expressing the SLC18A2
XX      protein for use in screening for candidate drugs to treat diseases
XX      related to SLC18A2 activity and in studying the effect of the variation
XX      on the biological activity of SLC18A2 as well as on the binding affinity
XX      of candidate drugs targeting SLC18A2 for the treatment of respiratory
XX      inflammatory diseases such as neuropsychiatric disorders involving
XX      monoaminergic brain systems. The present sequence represents an allele
XX      specific oligonucleotide (ASO) primer for human SLC18A2, which is given
XX      in the present invention
XX
XX      Sequence 15 BP; 4 A; 3 C; 2 G; 5 T; 0 U; 1 Other;
XX
XX      Query Match      0.7%; Score 13; DB 1; Length 15;
XX      Best Local Similarity 86.7%; Pred. No. 2.7e+02;
XX      Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0.
XX
XX      207 CGAATGATGATACGT 221
XX      | : |||||
XX      15 CRTAATGATTAACGT 1
XX
XX      RESULT 487
XX      ID AAS97335 AAS97335 standard; DNA; 15 BP.
XX
XX      AC AAS97335;
XX
XX      DT 12-MAR-2002 (first entry)
XX
XX      DE Human CRYBB1 gene ASO PCR primer #18.
XX
XX      Human, crystallin beta B1, CRYBB1; chromosome 22q12.1; ophthalmological;
XX      cataract; allele specific oligonucleotide; ASO; ss; haplotype;
XX      genotyping; transgenic animal; PCR primer.
XX
XX      Homo sapiens.
XX
XX      WO200185998-A1.
XX
XX      15-NOV-2001.

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PF	07-MAY-2001; 2001WO-US014715.
XX	
XX	05-MAY-2000; 2000US-0202253P.
XX	
PA	(GENA-) GENNAISSANCE PHARM INC.
PI	
XX	Choi JY, Kazemi A, Klieem SE, Koshy B, Rounds E;
XX	
DR	WPI; 2002-062253/08.
XX	
PT	Novel polymorphic variants of crystallin, beta B1 useful in studying
PT	expression and function of the protein, useful for screening candidate
XX	drugs to treat diseases e.g. cataract.
PS	
XX	Claim 15; Page 12; 94p; English.
CC	
CC	The invention relates to an isolated polynucleotide comprising a sequence
CC	which is a polymorphic variant of a reference sequence for crystallin,
CC	beta B1 (CRYBB1, located on chromosome 22q12.1) gene or their fragment,
CC	where the polymorphic variant comprises a CRYBB1 isogene defined by a
CC	haplotype from haplotypes 1-16 as given in the specification. Also
CC	included are a transgenic non-human animal transformed or transfected
CC	with the polymorphic variant, a computer system for storing and analysing
CC	polymorphism data for CRYBB1 gene, a genome anthology for the CRYBB1 gene
CC	which comprises the defined CRYBB1 isogenes, methods of determining the
CC	individuals haplotype or genotype with a disease or trait and a
CC	association of a particular haplotype with a disease or trait and a
CC	composition comprising at least one genotyping oligonucleotide
CC	(especially allele-specific oligonucleotides (ASO)) for detecting a
CC	polymorphism in the CRYBB1. The isogenes or haplotypes are useful for
CC	improving the efficiency and reliability of several steps in the
CC	discovery and development of drugs for treating diseases associated with
CC	CRYBB1 activity, e.g. cataract. and can also be used by the
CC	pharmaceutical research scientist to validate CRYBB1 as a candidate
CC	target for, and in design of clinical trials of candidate drugs for,
CC	treating a specific condition drugs or disease predicted to be associated
CC	with CRYBB1 activity. The ASOs are useful as probes and primers, and for
CC	assaying a polymorphism in the target region. The present sequence is an
CC	ASO PCR primer for CRYBB1
XX	
SQ	Sequence 15 BP; 2 A; 8 C; 3 G; 1 T; 0 U; 1 Other;
	Query Match 0.7%; Score 13; DB 1; Length 15;
	Best Local Similarity 86.7%; Pred. 2.7e+02;
	Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0
Qy	622 CTCACGCCCCGCGCTG 636
Db	1 CTCACGCCCCACGCTG 15
RESULT 488	
AAAS16726/c	
ID	AAAS16726 standard; DNA; 15 BP.
XX	
AC	AAAS16726;
XX	
DT	14-FEB-2002 (first entry)
XX	
DE	Human APOA4 allele specific oligonucleotide, ASO, probe #9.
XX	
XX	Human; ss; APOA4; apolipoprotein A-IV; antiatherosclerotic; cardiant;
KW	haplotype; chromosome 11q23-qter; coronary heart disease; obesity;
KW	atherosclerosis; probe.
XX	
OS	Homo sapiens.
XX	
PN	WO200177124-A2.
XX	
PD	18-OCT-2001.
XX	
PF	03-APR-2001; 2001WO-US010670.

XX 05-APR-2000; 2000US-0194362P.
PR (GENA-) GENAISSANCE PHARM INC.
XX
XX Bentivegna SC, Choi JY, Kliem SE, Koshy B;
PI WPI; 2002-041281/05.
XX
XX New haplotypes of the human apolipoprotein A-IV gene, useful to diagnose
PT and treat disorders associated with its abnormal expression or function
XX such as coronary artery disease.
XX
PS Claim 16; Page 15; 71pp; English.
XX
XX The invention relates to haplotyping the human apolipoprotein A-IV
CC (APOA4) gene of an individual, comprising determining if the individual
CC has one of the APOA4 haplotypes or haplotype pairs fully defined in the
CC specification. Also disclosed are genotyping oligonucleotides (or allele
CC specific oligonucleotides, ASO) as well as methods for correlating a
CC particular haplotype pair with a trait e.g. obesity, in a population. The
CC APOA4 gene is located on chromosome 11q23-qter. The methods of the
CC invention are useful to diagnose and develop treatment for disorders
CC associated with abnormal APOA4 expression or function, for example
CC coronary heart disease and atherosclerosis. The APOA4 isogenes and
CC screened compounds are useful for the treatment of disorders associated
CC with abnormal APOA4 expression or function such as coronary artery
CC disease. The present sequence is an APOA4 allele specific
CC oligonucleotide, ASO, probe used to detect an APOA4 polymorphism
XX
SQ Sequence 15 BP; 4 A; 3 C; 6 G; 1 T; 0 U; 1 Other;

Query Match 0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.7e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 828 CCTCCCTGCTGCT 842
Db 15 CCTCCACTGCTGCT 1

RESULT 489
ID ABA81517 standard; DNA; 15 BP.
XX
AC ABA81517;
XX
DT 13-AUG-2002 (first entry)
XX
DE Human CASP5 gene allele-specific oligonucleotide sequencing primer #38.
XX
KW Human; caspase 5; apoptosis-related cysteine protease; CASP5; primer; ss;
KW haplotyping; haplotype pair; cancer; single nucleotide polymorphism;
KW hereditary nonpolypoid colorectal cancer; gastrointestinal tumour;
KW endometrial tumour; chromosome 11q22.2-q22.3; sequencing.
XX
OS Homo sapiens.
XX
PN WO200226769-A2.
XX
PD 04-APR-2002.
XX
PF 01-OCT-2001; 2001WO-US030878.
XX
PR 29-SEP-2000; 2000US-0236568P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Choi JY, Kliem SE, Russo DP;
XX
XX WPI; 2002-435191/46.
XX
PT Novel caspase 5 apoptosis-related cysteine protease, useful

PT therapeutically and in screening for drugs targeting protease
PT polypeptide.
XX
XX Claim 14; Page 15; 115pp; English.
XX
XX The invention relates to single nucleotide polymorphisms in the gene
CC encoding the human caspase 5, apoptosis-related cysteine protease (CASP5)
CC polypeptide. A method for haplotyping the CASP5 gene in an individual
CC comprises identifying the nucleotide at one or more polymorphic sites and
CC determining whether one of the copies of the gene is defined by one of
CC the CASP5 haplotypes given in the specification or whether both copies
CC are defined by a haplotype pair. This method is useful in genotyping,
CC whereby all possible haplotype pairs can be assigned to specific
CC genotypes. An association between a trait and a haplotype or haplotype
CC pair of the CASP5 gene can be identified by comparing the frequency of
CC the haplotype or haplotype pair in a population exhibiting the trait with
CC the frequency of the haplotype or haplotype pair in a reference
CC population, where a higher haplotype frequency in the trait population
CC indicates the trait is associated with the haplotype or haplotype pair.
CC CASP5 and its corresponding DNA are used for studying the expression and
CC function of CASP5, for use in screening for candidate drugs to treat
CC diseases related to CASP5 activity, such as cancer (e.g. hereditary
CC nonpolypoid colorectal cancer, gastrointestinal tumours and endometrial
CC tumours). Sequences ABA81480-ABA81519 represent allele-specific
CC oligonucleotide sequencing primers used to detect CASP5 gene
CC polymorphisms
XX
SQ Sequence 15 BP; 4 A; 5 C; 2 G; 3 T; 0 U; 1 Other;

Query Match 0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.7e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 467 CAGTGTGTAAGTTC 481
Db 15 CAGTGTGTAAGTTC 1

RESULT 490
ID ABA97329 standard; DNA; 15 BP.
XX
AC ABA97329;
XX
DT 18-JUN-2002 (first entry)
XX
DE CCR5 allele-specific primer for detecting polymorphisms SEQ ID 13.
XX
KW Human chemokine C-C motif receptor 5; CCR5; haplotype pair; isogene;
KW single nucleotide polymorphism; SNP; human immunodeficiency virus 1;
KW HIV-1 infection; acquired immunodeficiency syndrome; AIDS; antiviral;
KW genotype; polymorphic variant; transgenic; drug screening; gene therapy;
KW allele specific oligonucleotide; ASO; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200177125-A2.
XX
PD 18-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US010708.
XX
PR 05-APR-2000; 2000US-0194361P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Choi JY, Kliem SE, Koshy B;
XX
XX WPI; 2002-041282/05.
XX
XX New haplotypes of the human chemokine (C-C motif) receptor 5 gene, useful
PT to diagnose and treat diseases associated with its abnormal expression or
PT function, including human immunodeficiency virus-1 infection.

XX Claim 16; Page 13; 61pp; English.
PS
XX
CC The present sequence is that of an allele-specific primer used to assay a
CC polymorphism in the human chemokine (C-C motif) receptor 5 (CCR5) gene of
CC the invention. The specification describes haplotyping the CCR5 gene of
CC an individual by determining if the individual has one of the CCR5
CC haplotypes or haplotype pairs fully defined in the specification. The
CC specification also describes an isolated polynucleotide comprising a
CC nucleotide sequence which is a polymorphic variant of the reference CCR5
CC gene sequence (see AB497318) and comprises an isogene defined by a
CC haplotype described in the specification and its encoded polypeptide. The
CC methods of the invention are useful to diagnose and develop treatment for
CC diseases associated with abnormal expression or function of the gene. The
CC CCR5 isogenes and the screened compounds are useful for treating human
CC immunodeficiency virus (HIV)-1 infection and the progression to acquired
CC immunodeficiency syndrome (AIDS). The invention has antiviral
CC applications. The specification describes genotyping the CCR5 gene of an
CC individual; predicting a haplotype pair for the CCR5 gene of an
CC individual; identifying an association between a trait and a haplotype or
CC haplotype pair of the CCR5 gene. The specification describes a
CC composition comprising a genotyping oligonucleotide for detecting a CCR5
CC polymorphism; a recombinant non-human organism transformed with CCR5
CC polynucleotide expressing a CCR5 protein encoded by the variant sequence;
CC an isolated antibody specific for the CCR5 polypeptide and a method for
CC screening drugs targeting the CCR5 polypeptide
XX
SQ Sequence 15 BP; 8 A; 2 C; 1 G; 3 T; 0 U; 1 Other;
Query Match 0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.7e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Gy 1666 AGCCGTAAATATA 1680
Db 1 AGCCTATAAATARA 15
RESULT 491
ABL36318
ID ABL36318 standard; DNA; 15 BP.
XX
AC ABL36318;
XX
DT 22-APR-2002 (first entry)
XX
DE Human lysosomal acid phosphatase 2 (ACP2) allele-specific probe 20.
XX
KW Human; ss; lysosomal acid phosphatase 2; ACP2; gene; chromosome 11;
KW lysosome-specific enzyme; orthophosphoric monoester hydrolasts;
KW Hodgkin's disease; HD; acid phosphatase deficiency;
KW novel polymorphic site; ACP2 haplotype; ACP2 genotype; polymorphism;
KW transgenic animal; primer; probe; primer-extension oligonucleotide; SNP;
KW single nucleotide polymorphism.
XX
OS Homo sapiens.
XX
PN WO200194362-A2.
XX
PD 13-DEC-2001.
XX
PF 07-JUN-2001; 2001WO-US018457.
XX
PR 07-JUN-2000; 2000US-0210047P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Klien SE, Messer C, Tanguay DA;
XX
DR WPI; 2002-154563/20.
XX
PT Novel genetic variants of acid phosphatase 2, lysosomal polypeptide gene
PT useful in studying expression and function of the protein, and for

PT screening drugs to treat diseases e.g. Hodgkin's disease.
XX
PS Claim 17; Page 14; 109pp; English.
XX
XX The invention comprises the human lysosomal acid phosphatase 2 (ACP2)
CC nucleic acid and protein sequences. Specifically, the invention relates
CC to the discovery of 22 novel polymorphic sites within the ACP2 gene. The
CC invention also comprises methods for haplotyping and genotyping the ACP2
CC gene in an individual. The ACP2 gene (located on chromosome 11) encodes a
CC lysosomal-specific enzyme that catalyzes the hydrolysis of
CC orthophosphoric monoesters to alcohol and phosphate. The ACP2 gene and
CC protein are pharmaceutically important in the treatment of Hodgkin's
CC disease (HD) and acid phosphatase deficiency. The novel ACP2 gene
CC polymorphisms of the invention are useful in haplotyping the ACP2 gene.
CC ACP2 haplotyping is useful in validating ACP2 as a target (and designing
CC drugs) for treating an ACP2-related disease or condition (e.g. Hodgkin's
CC disease and acid phosphatase deficiency). The ACP2 gene polymorphisms are
CC useful for ACP2 genotyping, which can also be used to develop diagnostic
CC tests and therapeutic treatments. The ACP2 protein and nucleic acids of
CC the invention are useful in the production of a transgenic animal which
CC expresses ACP2 protein. The ACP2 nucleic acids of the invention are
CC useful in the production of allele-specific oligonucleotides designed to
CC genotype each of the ACP2 polymorphisms. Nucleic acids AB136299-AB136320
CC represent claimed ACP2 allele-specific probes. Nucleic acids AB136321-
CC AB136364 represent claimed ACP2 allele-specific PCR primers. Nucleic
CC acids AB136365-AB136408 represent claimed ACP2 primer-extension
CC oligonucleotides
XX
SQ Sequence 15 BP; 1 A; 8 C; 0 G; 5 T; 0 U; 1 Other;
Query Match 0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.7e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Gy 1005 CATTCTTCTCCTCT 1019
Db 1 CATTCTCTCTCCTCT 15
RESULT 492
AAL39772
ID AAL39772 standard; DNA; 15 BP.
XX
AC AAL39772;
XX
DT 05-SEP-2002 (first entry)
XX
DE SMOH polymorphism detecting primer SEQ ID No 87.
XX
KW Cytostatic; polymorphic variant; single nucleotide polymorphism; SMOH;
KW human smoothened Drosophila homologue; basal cell carcinoma; BCC;
KW gene therapy; antisense gene therapy; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200229004-A2.
XX
PD 11-APR-2002.
XX
PF 04-OCT-2001; 2001WO-US031304.
XX
PR 04-OCT-2000; 2000US-0237871P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Bentivegna SC, Choi JY, Koshy B, Lee HH, Sausker EA;
XX
DR WPI; 2002-519113/55.
XX
PT New genetic variants of smoothened Drosophila homolog (SMOH) gene useful
PT for therapeutic purposes and for expressing SMOH protein useful in
PT identifying drugs to treat basal cell carcinomas.
XX

PS Claim 15; Page 15; 179pp; English.
XX
CC The invention relates to an isolated polynucleotide comprising a sequence
CC which is a polymorphic variant of a reference sequence for the human
CC smoothened Drosophila homologue (SMOH) gene or its fragment, or a
CC polymorphic variant of a reference sequence for a SMOH cDNA or its
CC fragment. A new isolated polypeptide is useful for screening for drugs
CC targeting the polypeptide. A new method is useful for identifying an
CC association between a trait such as a clinical response to a drug
CC targeting SMOH and a haplotype or haplotype pair of SMOH gene. The
CC methods have applicability in developing diagnostic tests and therapeutic
CC treatments for basal cell carcinomas (BCCs). The isolated polynucleotide
CC is useful for studying the expression and function of SMOH and expressing
CC SMOH protein for use in screening for candidate drugs to treat diseases
CC related to SMOH activity. The polymorphism and haplotype data are useful
CC for validating whether SMOH is a suitable target for drugs to treat BCCs,
CC screening for the drugs and reducing bias in clinical trials of the
CC drugs. The isolated polynucleotide is useful for therapeutic purposes.
CC The new method, an oligonucleotide and kit of the invention are useful
CC for determining whether an individual has one of the haplotypes or the
CC haplotype pairs. The polynucleotides of the invention can be used to
CC treat disorders by gene therapy and antisense gene therapy. This
CC polynucleotide sequence represents a primer used for detecting human
CC smoothened Drosophila homologue gene polymorphisms of the invention
XX
SQ Sequence 15 BP; 3 A; 5 C; 4 G; 2 T; 0 U; 1 Other;

Query Match 0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.7e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 124 AGGACCTGAGCCCC 138
DB 1 AGGACCTGAGCTTC 15

RESULT 493
ADF74524/c
ID ADF74524 standard; DNA; 15 BP.
XX
AC ADF74524;
XX
DT 26-FEB-2004 (first entry)
XX
DE Allele-specific oligo probe for detecting CERP haplotypes (SeqID 5).
XX
KM ss; cholesterol ester transfer protein; CERP; ASO; haplotype;
KM statin-specific variation; high density lipoprotein cholesterol; HDLC;
KM cardiovascular disease; dyslipidaemia; hyperlipidaemia;
KM hypercholesterolaemia; allele specific oligonucleotide; probe; human.
XX
OS Homo sapiens.
XX
PN WO2003091698-A2.
XX
PD 06-NOV-2003.
XX
PF 28-APR-2003; 2003WO-US013346.
XX
PR 26-APR-2002; 2002US-0375791P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Brain CD, Dain BJ, Judson RS, Messer C, Reed CR;
XX
DR WPI; 2003-865625/80.
XX
PT New kit for determining whether an individual has a statin response
PT marker I or II comprising a set of oligonucleotides for identifying an
PT allele at a polymorphic site, useful in diagnosing or treating e.g.,
PT hypercholesterolemia.
XX
PS Disclosure; SEQ ID NO 5; 72pp; English.

XX
CC This invention relates to novel genetic markers and variants of the gene
CC encoding the cholesterol ester transfer protein (CERP) located on
CC chromosome 16q13. Specifically, it refers to a set of haplotypes in the
CC CERP gene that are associated with statin-specific variation in high
CC density lipoprotein cholesterol (HDL) response. The present invention
CC describes a kit for determining whether an individual has a statin
CC response marker I or II, which comprises a set of oligonucleotides
CC designed for identifying at least one of the alleles at each of the
CC polymorphic sites of CERP. Accordingly, the method of the invention can
CC be used in preparing a composition for diagnosing or treating
CC cardiovascular disease caused by elevated LDL or HDLC, and more
CC particularly for the treatment of dyslipidaemia, hyperlipidaemia or
CC hypercholesterolaemia. This oligonucleotide sequence is a human allele-
CC specific oligo (ASO) probe used for detecting the CERP haplotypes of the
XX
SQ Sequence 15 BP; 1 A; 1 C; 6 G; 6 T; 0 U; 1 Other;

Query Match 0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.7e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1520 CAGAAACACCTCAC 1534
DB 15 CAGAAACRCACTCAC 1

RESULT 494
ADN89026
ID ADN89026 standard; DNA; 15 BP.
XX
AC ADN89026;
XX
DT 15-JUL-2004 (first entry)
XX
DE Hyperlipidaemia treatment associated human ITGB3 haplotype probe #91.
XX
KM ss; probe; antilipemic; gene therapy; allele; polymorphic site;
KM integrin beta 3; ITGB3; statin response marker; hyperlipidaemia.
XX
OS Homo sapiens.
XX
PN WO2004033710-A2.
XX
PD 22-APR-2004.
XX
PF 09-OCT-2003; 2003WO-US032361.
XX
PR 09-OCT-2002; 2002US-0417743P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Bentivegna SC, Bieglecki KM, Brain CD, Dain BJ, Cappola G;
PI Judson RS, Lachowicz M, Lee HH, Litvin L, Messer C, Petersen N;
PI Reed CR, Rounds EM, Russo DP, Windemuth AK;
XX
DR WPI; 2004-340942/31.
XX
PT New kit comprising a set of oligonucleotides, useful for determining
PT whether an individual has a statin response marker I or II for preparing
PT a composition for treating hyperlipidaemia.
XX
PS Disclosure; SEQ ID NO 94; 202pp; English.
XX
XX A kit comprising a set of oligonucleotides designed for identifying at
CC least one of the alleles at each polymorphic site (PS) in a set of 129
CC polymorphic sites (PSs) given in the specification, is new. The kit
CC identifies at least one of the alleles at each polymorphic site (PS) in a
CC set of 129 polymorphic sites (PSs) given in the specification, for
CC example: PS1 and PS42; PS19 and PS42; PS3, PS12, and PS42; a set of
CC polymorphic sites comprising a linked haplotype to any one of haplotypes
CC 101-194, 201-463 or 501-515 given in the specification; or a set of

polymorphic sites comprising a substitute haplotype for any one of haplotypes 101-194, 201-463 or haplotypes 501-515 given in the specification; where the nucleotide position of each polymorphic site corresponds to the following nucleotide position in the 32577-bp sequence: 1118 (PS1), 1773 (PS3), 1875 (PS4), 1911 (PS5), 1957 (PS6), 2087 (PS10), 2157 (PS12), 13384 (PS15), 13405 (PS16), 16200 (PS19), 17194 (PS20), 17273 (PS21), 20035 (PS26), 20047 (PS28), 20615 (PS30), 21944 (PS33), 22155 (PS35), 25705 (PS37), 25921 (PS38), 27882 (PS39), and 30618 (PS42). INDEPENDENT CLAIMS are also included for: determining whether an individual has a statin response marker I or a statin response marker II; selecting a statin therapy to provide an optimal High Density Lipoprotein Cholesterol (HDL) response in an individual; predicting an individual's High Density Lipoprotein Cholesterol (HDL) response to treatment with a statin; predicting an individual's High Density Lipoprotein Cholesterol (HDL) response to treatment with a statin; manufacturing a drug product; seeking regulatory approval for marketing a pharmaceutical formulation for treating a disease or condition in a population partially or wholly defined by having a statin response marker I; marketing a drug product comprising a statin as at least one active ingredient for treating a disease or condition in a population partially or wholly defined by having a statin response marker I; an isolated polynucleotide comprising a first nucleotide sequence which comprises the integrin, beta 3 (ITGB3) isogene encoding a ITGB3 polypeptide, where the integrin isogene consisting of isogenes 1-38 and 40-98 defined by a correspondingly numbered 1000-2235, haplotype, where each of the isogenes comprises nucleotides 1000-2235, 4256-4716, 1317913723, 14235-14858, 16126-16619, 16930-17414, 19241-19644, 19748-20177, 2053721009, 21731-22412, 24385-24930, 25559-26029, 27822-28255, 30265-30754, and 31300-31718 of the 32577-bp sequence, 27822-28255, 30265-30754, and 31300-31718 of the 32577-bp sequence, except where substituted by the sequence of alleles for the except where substituted by the sequence of alleles for the except where substituted by the sequence of alleles for the polymorphic sites whose nucleotide positions in the 32577-bp sequence and a second nucleotide sequence which is complementary to the first nucleotide sequence; a recombinant nonhuman organism transformed or transfected with the isolated polynucleotide, where the organism expresses an ITGB3 polypeptide encoded by the selected ITGB3 isogene; an isolated fragment of an integrin, beta 3 (ITGB3) isogene, where the fragment comprises one or more polymorphisms consisting of thymine at PS 1, guanine at PS2, cytosine at PS3, thymine at PS4, cytosine at PS5, adenine at PS6, thymine at PS7, thymine at PS8, guanine at PS9, adenine at PS10, adenine at PS11, thymine at PS12, adenine at PS13, guanine at PS 16, adenine at PS 18, thymine at PS 19, guanine at PS21, guanine at PS22, cytosine at PS23, thymine at PS24, thymine at PS25, adenine at PS26, adenine at PS27, cytosine at PS29, adenine at PS30, cytosine at PS31, guanine at PS32, adenine at PS33, adenine at PS35, cytosine at PS37, thymine at PS38, cytosine at PS39, adenine at PS40, thymine at PS41, thymine at PS42, guanine at PS43 and guanine at PS44; a genome anthology for the integrin, beta 3 (ITGB3) gene which comprises two or more ITGB3 isogenes consisting of isogenes 1-98, where each of the selected isogenes is defined by a correspondingly numbered haplotype given in the specification, and where each of the isogenes comprises nucleotides 1000-2235, 4256-4716, 13179-13723, 14235-14858, 16126-16619, 16930-17414, 19241-19644, 19748-20177, 2053721009, 21731-22412, 24385-24930, 2555926029, 27822-28255, 30265-30754, and 31300-31718 of the 32577-bp sequence except where substituted by the sequence of alleles for the correspondingly numbered haplotype at each of the polymorphic sites; haplotyping the integrin, beta 3 (ITGB3) gene of an individual; assigning a haplotype pair for the integrin, beta 3 (ITGB3) gene to an individual; reducing the potential for bias in a clinical trial of a candidate drug for treating a disease or condition predicted to be associated with ITGB3 activity; an isolated polypeptide comprising a ITGB3 protein variant consisting of protein variants A, B, C, D, E, F and G and comprising 788-amino acid sequence, except where substituted by the corresponding sequence of amino acids whose positions and alleles are given in the specification; with the selected ITGB3 protein antibody specific for and immunoreactive with the selected ITGB3 protein variant comprising the isolated polypeptide; screening for drugs targeting the selected ITGB3 protein variant comprising the isolated polypeptide; an isolated fragment of an ITGB3 protein variant, where the fragment is at least 6 amino acids in length and comprises one or more variant amino acids consisting of methionine at a position corresponding to amino acid position 66, methionine at a position corresponding to amino acid position 445, and glutamine at a position corresponding to amino acid position 515 the 788-amino acid sequence; screening for drugs targeting

the selected ITGB3 protein variant comprising the isolated polypeptide; screening for compounds targeting the ITGB3 protein to treat a condition or disease predicted to be associated with ITGB3 activity; validating the ITGB3 protein as a candidate target for treating a medical condition predicted to be associated with ITGB3 activity; and an isolated oligonucleotide designed for detecting a polymorphism in the integrin, beta 3 (ITGB3) gene at a polymorphic site (PS) consisting of PS1-PS44, where the oligonucleotide contains or is located one to several nucleotides downstream of the selected PS, where the oligonucleotide has a length of about 15 to about 100 nucleotides. Preferred Kit: The kit further comprises a manual with instructions for performing one or more reactions on a human nucleic acid sample to identify the allele(s) present in the individual at each polymorphic site in the set of polymorphic sites and determining if the individual has a statin response marker I or a statin response marker II based on the identified allele(s). The set of oligonucleotides is designated for identifying both alleles at each polymorphic site of the selected set of polymorphic sites. The set of PSs comprises PS3, PS12 and PS42; PS 1, PS12 and PS42; PS3 and PS42; PS1 and PS42; PS1, PS3, PS12 and PS42; or PS39. The set of PS 18 PS3, PS12 or PS42. The individual is Caucasian. The linkage disequilibrium between the linked haplotype and any one of haplotypes 101-194, 201-463 or 501-515 has $r^2 \geq 0.2$ consisting of at least 0.75, at least 0.80, at least 0.85, at least 0.90, at least 0.95 or 1.0. At least one of the oligonucleotides in the set of oligonucleotides is an allele-specific oligonucleotide comprising a nucleotide sequence consisting of 10-15 bp. The set of polymorphic sites is PS3, PS12, and PS42 and the set of oligonucleotides comprises first, second and third allele-specific oligonucleotide (ASO) probes, where the first ASO probe comprises 15-bp sequence, or its complement, and S in the 15-bp sequence is guanine; the second ASO probe comprises 15-bp sequence, or its complement, and Y in the 15-bp sequence is cytosine; the third ASO probe comprises 15 bp, or its complement, and Y in the 15-bp sequence is cytosine. Preferred Article: The article of manufacture comprises a pharmaceutical formulation and at least one indicium identifying a population for whom the pharmaceutical formulation is indicated, where the pharmaceutical formulation comprises a statin as at least one active ingredient and the identified population is partially or wholly defined by having a statin response marker I, where a trial population to the pharmaceutical marker I exhibits a better HDLC response to the pharmaceutical formulation than to treatment with atorvastatin or a salt of atorvastatin acid. It also comprises packaging material, where the formulation contained within the packaging material, where the pharmaceutical formulation comprises a statin as at least one separate active ingredient, and the packaging material formulation is indicated for a which states that the pharmaceutical formulation is indicated for a population partly or wholly defined by having a statin response marker I, where a trial population having the statin response marker exhibits a better HDLC response to the pharmaceutical formulation than to treatment with atorvastatin or a salt of atorvastatin acid. Preferred Oligonucleotide: The isolated oligonucleotide is an allele-specific oligonucleotide that specifically hybridizes to an allele of the ITGB3 gene at a region containing the polymorphic site. The isolated oligonucleotide is a primer-extension oligonucleotide. The kit is for haplotyping the integrin, beta 3 (ITGB3) gene of all individual, comprises a set of oligonucleotides designed for identifying at least one of the alleles at each polymorphic site (PS) in a set of two or more polymorphic sites. Preferred Method: Determining whether an individual has a statin response marker I or a statin response marker II comprises determining the copy number in the individual of the haplotype, where if the selected haplotype is one of haplotypes given in the specification, then the individual has a statin response marker I if the individual has at least one copy of the selected haplotype and a statin response marker II if the individual has zero copy of the selected haplotype; and the individual has a statin response marker I if the individual has zero or one copy of the selected haplotype and a statin response marker II if the individual has two copies of the selected haplotype. The individual is a candidate for treatment with a statin. The determining step comprises genotyping each polymorphic site in a set of polymorphic sites comprising the selected haplotype and using the results of the genotyping step to identify, for the set of polymorphic sites the haplotype pair present in the individual. The determining step comprises consulting a data repository that provides information on the copy number present in the individual for the selected haplotype. The data repository is the

CC individual's medical records or a medical data card. Assigning an
CC individual to a first or second statin response marker group comprises
CC determining the copy number in the individual or a haplotype and
CC assigning the individual to the first statin response marker group if the
CC individual has at least one copy of the selected haplotype and to the
CC second statin response marker group if the individual has zero copy of
CC the selected haplotype; and assigning the individual to the first statin
CC response marker group if the individual has zero or one copy of the
CC selected haplotype and to the second statin response marker group if the
CC individual has two copies of the selected haplotype. The determining step
CC comprises genotyping each polymorphic site in a set of polymorphic sites

Query Match 0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.7e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1273 GAGACCACTATCTCC 1287
1 GAGACCACTATCTCC 15

RESULT 495
ADS88857
ID ADS88857 standard; DNA; 16 BP.

XX ADS88857;

DT 16-DEC-2004 (first entry)

DE Primer for second strand synthesis of a random 7 residue peptide DNA.

XX adeno-associated virus; AAV; capsid protein; VP1, VP2, VP3; gene therapy;
KM coronary artery endothelial cell; coronary heart disease;
KM cardiovascular disease; infectious disease; primer; ss.

XX Synthetic.

XX WO2004083441-A2.

XX 30-SEP-2004.

PF 19-MAR-2004; 2004WO-EP002923.

XX 19-MAR-2003; 2003US-0455594P.

PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

PA (UYRE-) UNIV FREIBURG ALBERT-LUDWIGS.

PI Kleinschmidt J, Mueller O, Trepel M, Kaul F, Leder C;

XX WPI; 2004-691059/67.

XX Producing a repertoire of random peptides on the surface of adeno-
PT associated virus (AAV) particles, useful for gene therapy, comprises
PT expressing in a recombinant host cell nucleic acids encoding a diverse
PT population of peptides.

XX Example 1; Page 18; 36pp; English.

XX The specification describes a method for producing a repertoire of random
CC peptides on the surface of adeno-associated virus (AAV) particles. The
CC method comprises expressing in a recombinant host cell nucleic acids
CC encoding a diverse population of peptides, where each peptide is
CC expressed as a fusion with an AAV capsid protein of an AAV particle which
CC displays at its surface the diverse population of peptides, and the AAV
CC particle have the ability to replicate provided by genetic information
CC packaged with it and a helper vector providing the adenovirus helper
CC functions. The capsid protein is VP1, VP2, or VP3 protein. The method is
CC useful for producing a repertoire of random peptides on the surface of
CC AAV particles. The method is useful in gene therapy, where the AAV
CC vectors obtained are useful for treating diseases associated with a
CC dysfunction of human coronary artery endothelial cells, e.g. coronary
CC heart disease or cardiovascular diseases. They are also useful for

CC treating infectious diseases. The present primer was used for second
CC strand synthesis of an oligonucleotide that encodes a random 7 residue
CC peptide insert at position 3967 in the AAV genome. It was used to
CC generate random peptide libraries in the plasmid level.

XX Sequence 16 BP; 1 A; 7 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1261 GTGACCGCCCTGG 1273
4 GTGACCGCCCTGG 16

RESULT 496
ADN12185
ID ADN12185 standard; DNA; 30 BP.

XX ADN12185;

DT 01-JUL-2004 (first entry)

DE Tachykinin receptor NK1 amplifying primer NK13' (nested).

XX Tachykinin; vascular disease; platelet aggregation; vulnery;
KM thrombolytic; neurokinin; thrombosis; wound healing; PCR; primer; NK1,
KM NK3; tachykinin receptor; ss.

XX Synthetic.

XX WO2004030695-A1.

XX 15-APR-2004.

PP 06-OCT-2003; 2003WO-GB004335.

PR 04-OCT-2002; 2002GB-00023077.

PA (UYRE-) UNIV READING.

PI Gibbins JM, Lowry PJ, Graham GJ, Page NM;

XX WPI; 2004-330076/30.

XX Use of tachykinin antagonist or agonist for treating diseases mediated by
PT binding of tachykinin ligand to its platelet associated receptor and
PT failure of platelet having tachykinin receptor to aggregate normally in
PT presence of tachykinin.

XX Disclosure; Page 21; 46pp; English.

XX The invention relates to the use of a tachykinin antagonist in the
CC manufacture of a medicament for treating e.g. a disease mediated by
CC binding of a tachykinin ligand to its platelet associated receptor. A
CC method of identifying an antagonist or agonist of tachykinin having a
CC platelet associated tachykinin receptor involves contacting a compound to
CC be evaluated with platelets expressing the tachykinin receptor in the
CC presence of the tachykinin and monitoring for an increase or decrease of
CC platelet aggregation. The agonist is useful in the manufacture of a
CC medicament in bulk quantities for treating a disease or conditions
CC mediated by binding of a tachykinin ligand to its platelet-associated
CC receptor (e.g. thrombosis), and by a failure of or a reduced ability of
CC platelet having a tachykinin receptor to aggregate normally in the
CC presence of the tachykinin; antagonizing or stimulating the effect of
CC tachykinin on platelet associated tachykinin receptor; and stimulating
CC platelet aggregation (e.g. wound healing). Sequences ADN12182-ADN12193
CC represent PCR primers for amplifying tachykinin receptors NK1, NK2 and
CC NK3.

XX Sequence 30 BP; 7 A; 8 C; 14 G; 1 T; 0 U; 0 Other;

Query Match 0.7%; Score 13; DB 1; Length 30;
 Best Local Similarity 65.5%; Pred. No. 6.8e+02;
 Matches 19; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 11 CACCGCGGAGCGGCGGAGTGATCCAG 39
 1 CCTCGGGGAGGCGCAGCAGAGAGCCAG 29

Db

RESULT 497
 AAT76484/c
 ID AAT76484 standard; DNA; 16 BP.
 AC AAT76484;
 XX
 DT 16-SEP-1997 (first entry)
 XX
 DE Endothelial nitric oxide antisense oligonucleotide.
 XX
 XX Asthma; airway epithelium; adenosine free; cystic fibrosis;
 KW chronic obstructive pulmonary disease; bronchitis; ss.
 XX
 OS Synthetic.
 XX
 PN WO9640162-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 06-JUN-1996; 96WO-US009306.
 XX
 PR 07-JUN-1995; 95US-00474497.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 PI Nyce JW, Metzger WJ;
 XX
 DR WPI; 1997-051871/05.
 XX
 PT Treatment of airway diseases such as asthma - by topically applying
 PT adenosine-free antisense oligo:nucleotide to airway epithelium of
 PT subject.
 XX
 PS Example 5; Page 42; 71pp; English.
 XX
 CC A method for treating airway disease in a subject has been produced.
 CC which involves the topical administration of an essentially adenosine
 CC free antisense oligonucleotide (ON) to the airway epithelium of the
 CC subject. The present sequence is an antisense oligonucleotide specific
 CC for endothelial nitric oxide. The method can be used to treat airway
 CC diseases such as cystic fibrosis, asthma, chronic obstructive pulmonary
 CC disease, bronchitis and other airway diseases characterised by an
 CC inflammatory response. By eliminating adenosine from the antisense ON,
 CC its liberation upon antisense degradation is prevented, thereby
 CC preventing adenosine-induced bronchoconstriction in patients with hyper-
 CC reactive airways
 CC
 SQ Sequence 16 BP; 0 A; 5 C; 7 G; 4 T; 0 U; 0 Other;

QY 636 GTGAGCCAGCCAGCC 651
 16 GGCGCCAGCCAGCC 1

Db

Query Match 0.7%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 498
 AAV70488/c
 ID AAV70488 standard; DNA; 16 BP.
 AC AAV70488;
 XX
 DT

DT 08-APR-1999 (first entry)
 XX
 XX Control probe hybridising to HCV variants.
 DE
 XX Nucleic acid detection; nucleic acid characterisation; hybridisation;
 KW infection; disease; cancer; forensic; paternity; multiplexing; probe;
 KW bridging oligonucleotide; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1
 FT /*tag= a
 FT /note= "labeled with fluorescein"
 FT
 XX
 PN WO9850403-A1.
 XX
 PD 12-NOV-1998.
 XX
 PF 05-MAY-1998; 98WO-US003194.
 XX
 PR 05-MAY-1997; 97US-00851588.
 PR 19-SEP-1997; 97US-00934097.
 PR 03-MAR-1998; 98US-00034205.
 XX
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
 XX
 PI Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;
 PI Anderson TA, Dahlberg JE;
 XX
 DR WPI; 1998-610317/51.
 XX
 PT Detection and characterisation of nucleic acid sequences - by mixing a
 PT folded target and one or more probes to form a probe/folded target
 PT complex and detecting and characterising the complexes.
 XX
 PS Example 8; Page 129; 279pp; English.
 XX
 CC The invention relates to methods and compositions of detection and
 CC characterisation of nucleic acid sequences and sequence changes. One
 CC method of detection and characterisation comprises: (a) providing: (i) a
 CC folded target having a DNA sequence comprising at least 1 double stranded
 CC region and at least 1 single stranded region; and (ii) at least 1 probe
 CC complementary to at least a portion of the folded target; and (b) mixing
 CC the target and probes so that the probe hybridises to form a probe
 CC /folded target complex. Also provided are methods for determination of
 CC structure formation in nucleic acid targets; for analysing folded nucleic
 CC acids targets; and for analysis and characterisation of nucleic acid
 CC sequences to detect the presence of pathogenic nucleic acid sequences
 CC indicative of an infection, the presence of variants or alleles of
 CC mammalian genes associated with disease and cancers, and the
 CC identification of the source of nucleic acids found in forensic samples,
 CC as well as in paternity determinations. The methods allow simultaneous
 CC analysis of both strands (e.g. the sense and antisense strands) and are
 CC ideal for high-level multiplexing. The products produced are amenable to
 CC qualitative, quantitative and positional analysis. The methods may be
 CC performed in solution or in the solid phase (e.g. on a solid support).
 CC The methods are powerful in that they allow for analysis of longer
 CC fragments of nucleic acid than current methodologies. The present
 CC sequence represents a control probe that can hybridise to all HCV
 CC variants
 CC
 SQ Sequence 16 BP; 3 A; 3 C; 7 G; 3 T; 0 U; 0 Other;

QY 1436 CCACAGGCGCTTTGGC 1451
 16 CCACAGGCGCTTTGGC 1

Db

Query Match 0.7%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 499
AAZ09807/c
ID AAZ09807 standard; DNA; 16 BP.
XX
AC AAZ09807;
XX
DT 26-NOV-1999 (first entry)
XX
DE p53 exon 8 PCR primer 1.
XX
KW Primer extension; primer; preamplification; 3'-5' exonuclease activity;
KW PEP-PCR; mutation analysis; microsatellite analysis; DNA polymerase; p53;
KW ss.
XX
OS Synthetic.
XX
PN DE19813317-A1.
XX
PD 30-SEP-1999.
XX
PP 26-MAR-1998; 98DE-01013317.
XX
PR 26-MAR-1998; 98DE-01013317.
XX
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
XX
PI Rueschoff J, Dietmaier W;
XX
DR WPI; 1999-541759/46.
XX
PT Nucleic acid amplification involving primer extension preamplification,
XX especially for whole genome amplification.
XX
PS Example 6; Page 7; 24pp; German.
XX
CC This invention describes a novel method for the amplification of nucleic
CC acid fragments from a sample in two or three thermal cycling reactions
CC using random primers in the first reaction and specific primers in the
CC second reaction is new and comprises using a mixture of at least two DNA
CC polymerases, at least one of which has 3'-5' exonuclease activity. The
CC process is useful for whole genome amplification by primer extension
CC preamplification polymerase chain reaction (PEP-PCR). DNA amplified by
CC the process can be used for mutation analysis, as a template for
CC sequencing reactions, or for microsatellite analysis. The use of a
CC mixture of DNA polymerases, including at least one with proofreading
CC ability, results in increased sensitivity, such that cell-specific
CC amplification products can be generated with a probability of more than
CC 90% from samples containing no more than 100 cells, preferably no more
CC than 5-10 cells. AAZ09799-209815 represent PCR primers used in the method
CC of the invention
XX
SQ Sequence 16 BP; 5 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
XX
Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1061 AGCAGGTCTACTGCG 1076
Db 16 ATCAGGTCTACTGTC 1
XX
RESULT 500
AAZ54320
ID AAZ54320 standard; DNA; 16 BP.
XX
AC AAZ54320;
XX
DT 05-JUL-1999 (first entry)
XX
DE Inducible nitric oxide synthase antisense oligonucleotide.
XX

KW Antisense oligonucleotide; multiple target; antisense treatment;
KW impaired respiration; inflammation; lung disease;
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW acute asthma; allergy; asthma; impeded respiration;
KW respiratory distress syndrome; pain; cystic fibrosis;
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW prostate cancer; ss.
XX
OS Synthetic.
XX
PN WO9913886-A1.
XX
PD 25-MAR-1999.
XX
PP 17-SEP-1998; 98WO-US019419.
XX
PR 17-SEP-1997; 97US-0059160P.
XX
PR 09-JUN-1998; 98US-00093972.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 1999-229400/19.
XX
PT New antisense oligonucleotides used in treatment of, e.g. pulmonary
XX vasoconstriction.
XX
PS Disclosure; Page 62; 120pp; English.
XX
CC The specification describes antisense oligonucleotides (AAZ52869-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target genes, gene initiation
CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-
CC end and the juxta-section between coding and non-coding regions and all
CC segments of RNAs encoding proteins associated with one or more diseases,
CC conditions or mixtures. The antisense oligonucleotides may be derived
CC from sequences AAZ5272-74. These multiple target oligonucleotides
CC (specifically AAZ5180-271) can be used for the antisense treatment of
CC diseases and conditions. Typical diseases and conditions are those
CC associated with impaired respiration and inflammation, including lung
CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
CC acute asthma, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
CC colon cancer, breast cancer, lung cancer, pancreatic cancer, e.g.
CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
CC well as all types of cancers which may metastasize or have metastasized
CC to the lungs, including breast and prostate cancer
XX
SQ Sequence 16 BP; 0 A; 8 C; 1 G; 7 T; 0 U; 0 Other;
XX
Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 537 CTTCTTCCCATGCC 552
Db 1 CTTCTTCCCATGCC 16
XX
RESULT 501
AAZ54275/c
ID AAZ54275 standard; DNA; 16 BP.
XX
AC AAZ54275;
XX
DT 05-JUL-1999 (first entry)
XX
DE

DE Endothelial nitric oxide synthase antisense oligonucleotide.
XX
XX Antisense oligonucleotide; multiple target; antisense treatment;
XX impaired respiration; inflammation; lung disease;
XX pulmonary vasoconstriction; inflammation; allergic rhinitis;
XX acute asthma; allergy; asthma; impeded respiration;
XX respiratory distress syndrome; pain; cystic fibrosis;
XX pulmonary hypertension; pulmonary vasoconstriction; emphysema;
XX chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
XX colon cancer; breast cancer; lung cancer; pancreatic cancer;
XX hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
XX prostate cancer; ss.
XX
XX Synthetic.
OS
XX WO9913886-A1.
XX
XX 25-MAR-1999.
XX
XX 17-SEP-1998; 98WO-US019419.
XX
XX 17-SEP-1997; 97US-0059160P.
XX 09-JUN-1998; 98US-00093972.
XX
XX (UYEC-) UNIV EAST CAROLINA.
XX
XX Nyce JW;
XX
XX WPI; 1999-229400/19.
XX
XX New antisense oligonucleotides used in treatment of, e.g. pulmonary
XX vasoconstriction.
XX
XX Disclosure; Page 61; 120pp; English.
XX
XX The specification describes antisense oligonucleotides (AAx52869-X55271)
XX directed against at least 2 mRNAs selected from target genes, coding and
XX non-coding regions of RNAs corresponding to target genes, gene initiation
XX codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-
XX end and the juxta-section between coding and non-coding regions and all
XX segments of RNAs encoding proteins associated with one or more diseases,
XX conditions or mixtures. The antisense oligonucleotides may be derived
XX from sequences AAx55272-74. These multiple target oligonucleotides
XX (specifically AAx5180-271) can be used for the antisense treatment of
XX diseases and conditions. Typical diseases and conditions are those
XX associated with impaired respiration and inflammation, including lung
XX diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
XX acute asthma, allergies, asthma, impeded respiration, respiratory
XX distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
XX pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
XX disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
XX colon cancer, breast cancer, lung cancer, pancreatic cancer,
XX hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
XX well as all types of cancers which may metastasize or have metastasized
XX to the lungs, including breast and prostate cancer
XX
XX Sequence 16 BP; 0 A; 5 C; 7 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 636 GTCTGCGCAGCCAGCC 651
DB 16 GGCAGCCAGCCAGCC 1
RESULT 502
AAx54321
ID AAx54321 standard; DNA; 16 BP.
XX
XX AAx54321;
XX

DT 05-JUL-1999 (first entry)
XX
XX Inducible nitric oxide synthase antisense oligonucleotide.
DE
XX Antisense oligonucleotide; multiple target; antisense treatment;
XX impaired respiration; inflammation; lung disease;
XX pulmonary vasoconstriction; inflammation; allergic rhinitis;
XX acute asthma; allergy; asthma; impeded respiration;
XX respiratory distress syndrome; pain; cystic fibrosis;
XX pulmonary hypertension; pulmonary vasoconstriction; emphysema;
XX chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
XX colon cancer; breast cancer; lung cancer; pancreatic cancer;
XX hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
XX prostate cancer; ss.
XX
XX Synthetic.
OS
XX WO9913886-A1.
XX
XX 25-MAR-1999.
XX
XX 17-SEP-1998; 98WO-US019419.
XX
XX 17-SEP-1997; 97US-0059160P.
XX 09-JUN-1998; 98US-00093972.
XX
XX (UYEC-) UNIV EAST CAROLINA.
XX
XX Nyce JW;
XX
XX WPI; 1999-229400/19.
XX
XX New antisense oligonucleotides used in treatment of, e.g. pulmonary
XX vasoconstriction.
XX
XX Disclosure; Page 62; 120pp; English.
XX
XX The specification describes antisense oligonucleotides (AAx52869-X55271)
XX directed against at least 2 mRNAs selected from target genes, coding and
XX non-coding regions of RNAs corresponding to target genes, gene initiation
XX codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-
XX end and the juxta-section between coding and non-coding regions and all
XX segments of RNAs encoding proteins associated with one or more diseases,
XX conditions or mixtures. The antisense oligonucleotides may be derived
XX from sequences AAx55272-74. These multiple target oligonucleotides
XX (specifically AAx5180-271) can be used for the antisense treatment of
XX diseases and conditions. Typical diseases and conditions are those
XX associated with impaired respiration and inflammation, including lung
XX diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
XX acute asthma, allergies, asthma, impeded respiration, respiratory
XX distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
XX pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
XX disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
XX colon cancer, breast cancer, lung cancer, pancreatic cancer,
XX hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
XX well as all types of cancers which may metastasize or have metastasized
XX to the lungs, including breast and prostate cancer
XX
XX Sequence 16 BP; 0 A; 8 C; 1 G; 7 T; 0 U; 0 Other;
SQ
Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 537 CTTCTTCCCATCGCC 552
DB 1 CTTCTTCCCATCGCC 16
RESULT 503
AAx3719/c
ID AAx3719 standard; DNA; 16 BP.
XX
XX AAx3719;
XX

AC AAA3719;
XX
XX 28-JUL-2000 (first entry)
XX
XX Low adenosine antisense oligonucleotide SEQ ID NO:1408.
XX
XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
XX phosphorothioate; impaired respiration; inflammation; allergy;
XX allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
XX antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
XX lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
XX respiratory distress syndrome; pain; cystic fibrosis; emphysema;
XX pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
XX cancer; leukemia; lymphoma; carcinoma; metastasis; ss.
XX
XX Homo sapiens.
XX
XX MO20009525-A2.
XX
XX 24-FEB-2000.
XX
XX 03-AUG-1999; 99WO-US017712.
XX
XX 03-AUG-1998; 98US-0095212P.
XX
XX (UYEC-) UNIV EAST CAROLINA.
XX
XX NYce JW;
XX
XX WPI; 2000-205971/18.
XX
XX New antisense oligonucleotides useful for treating e.g. pulmonary
XX vasoconstriction, inflammation, allergies, asthma, hypertension,
XX bronchitis, emphysema, respiratory distress syndrome, ischemia or
XX cancers.
XX
XX Claim 18; Page 440; 1343pp; English.
XX
XX The present invention describes a new composition comprising an antisense
XX oligonucleotide (ON) with low adenosine (up to 15%), which targets
XX nucleic acids involved in bronchoconstriction, allergies, and/or
XX inflammation. The ON can have antiinflammatory, antiallergic,
XX antiasthmatic, cytostatic and analgesic activities. The compositions are
XX useful for the treatment of diseases associated with inflammation,
XX impaired airways, including lung disease and diseases whose secondary
XX effects afflict the lungs of a subject. They can be used for treating
XX e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
XX impaired respiration, respiratory distress syndrome, pain, cystic
XX fibrosis, pulmonary hypertension, emphysema, chronic obstructive
XX pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
XX carcinomas, and cancers which may metastasise to the lungs, including
XX breast and prostate cancer. The reduction of the adenosine content of the
XX ONs reduces side effects. The A-containing ONs break down with the
XX release of deoxyadenosine which activates adenosine receptors causing
XX bronchoconstriction and inflammation. AAA3313 to AAA3512 represent the
XX nucleotide sequences given in the sequence listing from the present
XX invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
XX sequences are also called SEQ ID NO:1 to 185, but the sequences differ
XX from the previously named sequences. SEQ ID NO:11 to 1680 (AAA2323 to
XX AAA3392) are specifically claimed ONs from the present invention. N.B.
XX Sequences given in the disclosure of the present invention do not match
XX up with their corresponding SEQ ID NO: sequences given in the sequence
XX listing
XX
XX Sequence 16 BP; 0 A; 5 C; 7 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 504
AAA3764
ID AAA3764 standard; DNA; 16 BP.
XX
XX AAA3764;
XX
XX 28-JUL-2000 (first entry)
XX
XX Low adenosine antisense oligonucleotide SEQ ID NO:1453.
XX
XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
XX phosphorothioate; impaired respiration; inflammation; allergy;
XX allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
XX antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
XX lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
XX respiratory distress syndrome; pain; cystic fibrosis; emphysema;
XX pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
XX cancer; leukemia; lymphoma; carcinoma; metastasis; ss.
XX
XX Homo sapiens.
XX
XX MO20009525-A2.
XX
XX 24-FEB-2000.
XX
XX 03-AUG-1999; 99WO-US017712.
XX
XX 03-AUG-1998; 98US-0095212P.
XX
XX (UYEC-) UNIV EAST CAROLINA.
XX
XX NYce JW;
XX
XX WPI; 2000-205971/18.
XX
XX New antisense oligonucleotides useful for treating e.g. pulmonary
XX vasoconstriction, inflammation, allergies, asthma, hypertension,
XX bronchitis, emphysema, respiratory distress syndrome, ischemia or
XX cancers.
XX
XX Claim 18; Page 446; 1343pp; English.
XX
XX The present invention describes a new composition comprising an antisense
XX oligonucleotide (ON) with low adenosine (up to 15%), which targets
XX nucleic acids involved in bronchoconstriction, allergies, and/or
XX inflammation. The ON can have antiinflammatory, antiallergic,
XX antiasthmatic, cytostatic and analgesic activities. The compositions are
XX useful for the treatment of diseases associated with inflammation,
XX impaired airways, including lung disease and diseases whose secondary
XX effects afflict the lungs of a subject. They can be used for treating
XX e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
XX impaired respiration, respiratory distress syndrome, pain, cystic
XX fibrosis, pulmonary hypertension, emphysema, chronic obstructive
XX pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
XX carcinomas, and cancers which may metastasise to the lungs, including
XX breast and prostate cancer. The reduction of the adenosine content of the
XX ONs reduces side effects. The A-containing ONs break down with the
XX release of deoxyadenosine which activates adenosine receptors causing
XX bronchoconstriction and inflammation. AAA2313 to AAA3512 represent the
XX nucleotide sequences given in the sequence listing from the present
XX invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
XX sequences are also called SEQ ID NO:1 to 185, but the sequences differ
XX from the previously named sequences. SEQ ID NO:11 to 1680 (AAA2323 to
XX AAA3392) are specifically claimed ONs from the present invention. N.B.
XX Sequences given in the disclosure of the present invention do not match
XX up with their corresponding SEQ ID NO: sequences given in the sequence
XX listing
XX
XX Sequence 16 BP; 0 A; 8 C; 1 G; 7 T; 0 U; 0 Other;
SQ
Query Match 0.7%; Score 12.8; DB 1; Length 16;

Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 537 CTTCTTCCCATCGCC 552
|||||
Db 1 CTTCTTCCCATCGCTCC 16

RESULT 505

AAA33765
ID AAA33765 standard; DNA; 16 BP.

AC AAA33765;

DT 28-JUN-2000 (first entry)

DE Low adenosine antisense oligonucleotide SEQ ID NO:1454.

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
XX phosphorohioate; impaired respiration; inflammation; allergy;
XX allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
XX antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
XX lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
XX respiratory distress syndrome; pain; cystic fibrosis; emphysema;
XX pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
XX cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

OS Homo sapiens.

PN WO200009525-A2.

PD 24-FEB-2000.

PF 03-AUG-1999; 99WO-US017712.

PR 03-AUG-1998; 98US-0095212P.

XX (UYEC-) UNIV EAST CAROLINA.

PA NYCE JW;

DR WPI; 2000-205971/18.

XX New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischaemia or
PT cancers.

PS Claim 18; Page 446; 1343pp; English.

XX The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impaired respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA3313 to AAA3512 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:11 to 1660 (AAA3233 to
CC AAA33992) are specifically claimed ONs from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match

CC up with their corresponding SEQ ID NO: sequences given in the sequence
CC listing
XX Sequence 16 BP; 0 A; 8 C; 1 G; 7 T; 0 U; 0 Other;

QY Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 537 CTTCTTCCCATCGCC 552
|||||
Db 1 CTTCTTCCCATCGCTCC 16

RESULT 506

AAZ97920/C
ID AAZ97920 standard; DNA; 16 BP.

AC AAZ97920;

DT 15-SEP-2003 (revised)

DT 26-APR-2000 (first entry)

DE HIV-1 protease gene probe SEQ ID NO:410.

XX Human immunodeficiency virus; HIV; protease; probe; detection;
XX drug selected mutation; hybridisation; genotyping; infection;
XX drug resistance; ss.

OS Human immunodeficiency virus 1.

PN WO9967428-A2.

PD 29-DEC-1999.

PF 22-JUN-1999; 99WO-EP004317.

PR 24-JUN-1998; 98EP-00870143.

XX (INNO-) INNOGENETICS NV.

PA Stuyver I;

DR WPI; 2000-147219/13.

XX Detection of drug-selected mutations in the HIV protease gene used to
PT treat HIV infections.

PS Claim 3; Page 43; 76pp; English.

XX The present invention describes the detection of drug-selected mutations
CC in the HIV protease gene. The method of detection allows the simultaneous
CC characterisation of a range of codons involved in drug resistance using
CC sets of probes optimised to function together in a reverse-hybridisation
CC assay. AAZ97517 to AAZ97997 represent specifically claimed probes for use
CC in the assay, and AAZ97479 to AAZ97501 represent specifically claimed HIV
CC protease gene polymorphic nucleotide sequences. AAZ97502 to AAZ97515, and
CC AAZ98004 to AAZ98007, represent PCR primers for the HIV protease gene.
CC and AAZ97516 represents an HIV protease probe used in an example from the
CC present invention. The method, probes and primers can be used for the
CC detection of drug-selected mutations in the HIV protease gene. The method
CC allows the simultaneous characterisation of a range of codons involved in
CC drug resistance. The method may also be used for HIV protease genotyping
CC assays. The probes are able to discriminate between wild type and mutated
CC protease sequences. The method allows rapid and reliable detection of
CC drug-selected mutation in HIV. (Updated on 15-SEP-2003 to standardise OS
CC field)

XX Sequence 16 BP; 5 A; 2 C; 3 G; 6 T; 0 U; 0 Other;

QY Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1586 TGAGTCAAAAATCTC 1601
|||||
DB 16 TGAGTCACCAAAATTC 1

RESULT 507
AAFI9886
ID AAFI9886 standard; DNA, 16 BP.
XX
AC AAFI9886;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human inducible nitric oxide synthase polynucleotide fragment #1453.
XX
XX Low adenosine antisenase oligonucleotide; phosphorothioate; allergy;
KM human; airway disorder; bronchoconstriction; lung inflammation;
KM surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KM immunosuppressive; antiaesthetic; analgesic; hypotensive; cytostatic;
KM respiratory obstruction; pulmonary obstruction; impeded respiration;
KM surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KM pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KM cancer; ss.

XX Homo sapiens.
OS
XX WO200062736-A2.
XX
XX 26-OCT-2000.
XX
XX 24-MAR-2000; 2000WO-US008020.
XX
XX 06-APR-1999; 99US-0127958P.
XX
XX (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
XX NYce JW;
XX
XX WPI; 2000-679539/66.
XX
XX Low adenosine (A) content antisenase oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.
XX
XX
XX Claim 14; Page 256; 1592pp; English.

XX The present invention describes low adenosine (A) content antisenase
CC oligonucleotides and compositions (I) comprising them. In the antisenase
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiaesthetic, hypotensive and cyostatic activities.
CC The antisenase oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisenase oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome

CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAFI8434 to AAF21543 represent human polynucleotide
CC fragments and antisenase oligonucleotides used in the exemplification of
CC the present invention
XX
XX Sequence 16 BP; 0 A; 8 C; 1 G; 7 T; 0 U; 0 Other;
SQ

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 537 CTTCTTCCCATGCC 552
|||||
DB 1 CTTCTTCCCATGCC 16

RESULT 508
AAFI9887
ID AAFI9887 standard; DNA, 16 BP.
XX
AC AAFI9887;
XX
XX 14-MAR-2001 (first entry)
XX
XX Human inducible nitric oxide synthase polynucleotide fragment #1454.
DE
XX
XX Low adenosine antisenase oligonucleotide; phosphorothioate; allergy;
KM human; airway disorder; bronchoconstriction; lung inflammation;
KM surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KM immunosuppressive; antiaesthetic; analgesic; hypotensive; cytostatic;
KM respiratory obstruction; pulmonary obstruction; impeded respiration;
KM surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KM pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KM cancer; ss.

XX Homo sapiens.
OS
XX WO200062736-A2.
XX
XX 26-OCT-2000.
XX
XX 24-MAR-2000; 2000WO-US008020.
XX
XX 06-APR-1999; 99US-0127958P.
XX
XX (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
XX NYce JW;
XX
XX WPI; 2000-679539/66.
XX
XX Low adenosine (A) content antisenase oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.
XX
XX
XX Claim 14; Page 256; 1592pp; English.

XX The present invention describes low adenosine (A) content antisenase
CC oligonucleotides and compositions (I) comprising them. In the antisenase
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiaesthetic, hypotensive and cytostatic activities.
CC The antisenase oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,

XX	27-SEP-1999;	99US-0156326P.
PR	27-SEP-1999;	99US-0156467P.
PR	08-NOV-1999;	99US-00436430.
PR	06-DEC-1999;	99US-0169100P.
PR	29-DEC-1999;	99US-00474432.
PR	29-DEC-1999;	99US-0173612P.
PR	30-DEC-1999;	99US-00476387.
PR	04-FEB-2000;	2000US-00498824.
PR	20-MAR-2000;	2000US-00531025.
PR	14-APR-2000;	2000US-0197769P.
PR	23-MAY-2000;	2000US-00578823.
PR	09-AUG-2000;	2000US-00636385.
XX		
PA	(RIBO-) RIBOZYME PHARM INC.	
XX		
PI	McWiggen J, Ueman N, Blact L, Beigelman L, Burgin A;	
PI	Kapel'sky A, Metulic-adamic J, Swedler D, Draper K, Chowrira B;	
PI	Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;	
XX		
XX	WPI; 2001-244406/25.	
DR		
PT	Enzymatic nucleic acid molecules able to cleave separate RNA molecules	
PT	are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,	
PT	obesity and heart disease.	
XX		
XX	Example 1; Page 306; 7179P; English.	

The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine aminopeptidase (MeAP-2), human telomerase (hTERT), protein kinase C alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor receptor-2 (HER2/c-erbB/neu), phospholamban (PLN), premenin-1 (ps-1), premenin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, zinczyme, and/or DNAzyme motifs. The methods of the invention are useful for treating cancer, in particular breast cancer. Alzheimer's disease, diabetes, obesity, cardiac diseases e.g. heart disease, age-related diseases, hepatitis B infections, and hepatitis and hepatocellular carcinoma. The enzymatic nucleic acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased cells and to detect the presence of specific RNA in a cell. The present sequence represents a substrate/target sequence for a ribozyme used in the examples of the present invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have different sequences associated with them.

Sequence 16 BP; 3 A; 5 C; 6 G; 0 T; 2 U; 0 Other;

Query Match	0.7%;	Score 12.8;	DB 1;	Length 16;
Best Local Similarity	87.5%;	Pred. No. 3.3e+02;		

QY	1086	GCTGGCCATGAGCTCC	1101
Db	16	GCTGGCGATGACCTCC	1

RESULT 511

ID ADU94732 standard; RNA; 16 BP.

AC ADU94732;

DT 10-FEB-2005 (first entry)

DE Human TERT G-cleaver ribozyme substrate sequence #154

KM Enzymatic nucleic acid molecule; gene expression; down regulation;
KM protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase;
KM MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha

KM beta-secretase; BACE; human epidermal growth factor receptor-2; HHR2;
KM c-erbB; neu; phospholamban; PLM; preenilin-1; ps-1; preenilin-2; ps-2;
KM hepatitis B virus; HBV; hammetthead; HH; halpin; NCH; inozyme; G-cleaver
KM amyryzyme; zinyzyme; DNAzyme; cancer; breast cancer; Alzheimer's disease;
KM diabetes; obesity; cardiac disease; heart disease; age-related disease;
KM hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
KM 89.

OS	Homo sapiens.
XX	
PN	W0200116312-A2.

08-MAR-2001 PD

PF 30-AUG-2000; 2000WO-US023998.

PR 31-AUG-1999; 99US-0151713P.

PR 27-SEP-1999; 99US-0156236P

PR 08-NOV-1999; 99US-00436430.

PR 29-DEC-1999; 99US-00474432.

PR 30-DEC-1999; 99US-00476387

PR 20-MAR-2000; 2000US-00531025.

PR 23-MAY-2000; 2000US-00578223
DD 00 MAY 2000 2000US-00578223

XX
PA (PUBO-) PIVOUYE BHAPM TNC

XX	McSwiggan J	Heman N	Blatt
PI			

PI Karpelsky A, Matulic-Adamic J, Sweedler D, Draper K, Chowhira B,
PI Stinchcomb D, Baudry A, Zinnen S, Iuriga J, Siroat BS.

XX
DB WPT: 2001-244406/25.

Enzymatic nucleic acid

PT are used for creating cancer, Alzheimer's disease, diabetes, obesity and heart disease.

Example 1: Page 304; 717pp; English.

CC The present invention relates to the use of enzymatic nucleic acid

CC also methods for their use to down regulate or inhibit the expression of

CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C

receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),

CC nucleic acid molecules used to inhibit the expression of the said genes

CC zinczyme, and/or DNazyme motifs. The methods of the invention are useful

CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related

CC carcinoma. The enzymatic nucleic acid molecules can also be used as

CC cells and to detect the presence of specific RNA in a cell. The present

CC the examples of the present invention. Note: Some SEQ ID Nos are repeated
CC and are in the specification but there have different meanings

CC associated with them.

Sequence 16 BP; 2 A; 6 C; 8 G; 0 T; 0 U; 0 Other;

Query Match	0.7%	Score 12.8;	DB 1;	Length 16;
Best Local Similarity	87.5%;	Pred. No. 3.3e+02;		
Matches 14; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0

1296 CGGGGGCCACGAGAG 1311
 |||||
 1 GGGGGCCCCGAGAG 16

RESULT 512
 ID ADU94557
 ADU94557 standard; RNA; 16 BP.

AC ADU94557;
 XX
 DT 10-FEB-2005 (first entry)
 XX
 DE Human TERT G-cleaver ribozyme substrate sequence #72.

Enzymatic nucleic acid molecule; gene expression; down regulation;
 KM protein-tyrosine-phosphatase-1b; PTP-1B; methionine aminopeptidase;
 KM MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
 KM beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
 KM c-erbB2; neu; phospholamban; PLN; presentin-1; ps-1; presentin-2; ps-2;
 KM hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
 KM amberzyme; zinzyme; DNAzyme; cancer; breast cancer; Alzheimer's disease;
 KM diabetes; obesity; cardiac disease; heart disease; age-related disease;
 KM hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
 KM ss.

OS Homo sapiens.
 XX
 PN WO200116312-A2.
 XX
 PD 08-MAR-2001.
 XX
 PF 30-AUG-2000; 2000WO-US023998.
 XX
 PR 31-AUG-1999; 99US-0151713P.
 PR 27-SEP-1999; 99US-00406643.
 PR 27-SEP-1999; 99US-0156236P.
 PR 27-SEP-1999; 99US-0156447P.
 PR 08-NOV-1999; 99US-00436430.
 PR 06-DEC-1999; 99US-0169100P.
 PR 29-DEC-1999; 99US-00474432.
 PR 29-DEC-1999; 99US-0173612P.
 PR 30-DEC-1999; 99US-00476387.
 PR 04-FEB-2000; 2000US-00498824.
 PR 20-MAR-2000; 2000US-00531025.
 PR 14-APR-2000; 2000US-0197769P.
 PR 23-MAY-2000; 2000US-00578223.
 PR 09-AUG-2000; 2000US-00636385.

(RIBO-) RIBOZYME PHARM INC.
 PA
 PI Mcswigen J, Usman N, Blatt L, Beigelman L, Burgin A;
 PI Karpetsky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
 PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;
 XX
 DR WPI; 2001-244406/25.

Enzymatic nucleic acid molecules able to cleave separate RNA molecules
 PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
 PT obesity and heart disease.
 XX
 PS Example 1; Page 301; 717P; English.

The present invention relates to the use of enzymatic nucleic acid
 CC molecules (e.g. ribozymes) to modulate gene expression. The invention
 CC also methods for their use to down regulate or inhibit the expression of
 CC genes encoding protein-tyrosine-phosphatase-1b (PTP-1B), methionine
 CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
 CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
 CC receptor-2 (HER2/c-erbB2/neu), phospholamban (PLN), presentin-1 (ps-1),
 CC presentin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
 CC nucleic acid molecules used to inhibit the expression of the said genes
 CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,

zincyme, and/or DNAzyme motifs. The methods of the invention are useful for treating cancer, in particular breast cancer; Alzheimer's disease, diabetes, obesity, cardiac diseases e.g. heart disease, age-related diseases, hepatitis B infections, and hepatitis and hepatocellular carcinoma. The enzymatic nucleic acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased cells and to detect the presence of specific RNA in a cell. The present sequence represents a substrate/target sequence for a ribozyme used in the examples of the present invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have different sequences associated with them.

XX CC Sequence 16 BP; 1 A; 5 C; 5 G; 0 T; 5 U; 0 Other;
SQ

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 62.5%; Pred. No. 3.3e+02;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 680 TTGGCTCCTGCTGC 695
 :||:|:||:||||
Db 1 UGUUCACUUGCGC 16

RESULT 513
ABL4609/C
ID ABL46099 standard; DNA; 16 BP.
XX AC ABL46099;
XX DT 26-APR-2002 (first entry)
XX DE Control probe SEQ ID NO:66.
XX XS Nucleic acid accessible hybridisation site; detection; hybridisation;
KM characteristic; identification; nucleic acid structure; diagnosis;
KW PCR primer; probe; ss.
OS Synthetic.
XS MO200198537-A2.
PN
XX PD 27-DEC-2001.
XX PF 15-JUN-2001; 2001MO-US019401.
XX PR 17-JUN-2000; 2000US-0212308P.
XX PR 15-JUN-2001; 2001US-00212308.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX PA
XX PYamichev V, Alawi H, Dong F, Nerl BP, Vener IT;
PI
DR WPI; 2002-049698/06.
XX PT
PT Identifying oligonucleotides hybridizing to nucleic acids containing
PT secondary structure, useful in clinical diagnosis, comprises identifying
PT primers that interact with the target to form an extension product under
PT amplification conditions.
XX PS
PS Example 8; Page 158; 409pp; English.
XX
XX The present invention describes a method for identifying oligonucleotides
CC with desired hybridisation properties to nucleic acid targets containing
CC secondary structure. The method comprises amplifying a target nucleic
CC acid having at least one accessible and one inaccessible site. Primers
CC that form an extension product are identified as the oligonucleotides
CC which can interact with the folded target nucleic acid. Oligonucleotides
CC from the present invention can be used in novel detection methods for
CC clinical diagnostic purposes, including the detection and identification
CC of pathogenic organisms (e.g. HIV). The method allows the ability to
CC rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent
XX sequences used in the exemplification of the present invention

SQ Sequence 16 BP; 3 A; 3 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1436 CCACAGGCGCTTGGC 1451
 16 CCACAGGCGCTTGGC 1

RESULT 514
 ABS97178/c
 ID ABS97178 standard; DNA; 16 BP.
 AC ABS97178;
 XX
 DT 23-DEC-2002 (first entry)
 DE Human CYP4501A2 Exon 7 sequencing primer #2.

XX Human; 8a; primer; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;
 KM cytochrome P450 A2; CYP4501A2; cytochrome P450 02b; CYP45002E1; LTF;
 KM adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR112;
 KM aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
 KM cyclooxgenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
 KM epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
 KM glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
 KM HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NMNT;
 KM NADPH quinone oxidoreductase 2; NQO2; sulfoxidoreductase thermolabile; STM;
 KM UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
 UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
 KM multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
 KM multidrug resistance associated protein 3; cancer; prostate;
 KM acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
 KM altered drug metabolism; cardiovascular function; colorectal tumour;
 KM central nervous system; pulmonary; immunological; sequencing.

XX Homo sapiens.
 OS
 XX
 PN W0200257410-A2.
 XX
 PD 25-JUL-2002.
 XX
 PF 28-NOV-2001; 2001WO-US044838.
 XX
 PR 28-NOV-2000; 2000US-00724389.
 XX
 PA (DNAS-) DNA SCI LAB INC.
 XX
 PI Guida M, Hall J;
 XX
 DR WPI; 2002-698522/75.
 XX
 PT Isolated nucleic acid molecules having polymorphisms in known human genes
 PT e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
 PT for locating, identifying and characterizing the genes responsible for
 PT disorder-related traits.
 XX
 PS Example 2; Page 101, 714pp; English.
 XX
 CC This invention relates to the sequence of an isolated nucleic acid
 CC molecule comprising at least one base variation from that of a known
 CC human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
 CC cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADRB1),
 CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
 CC (ARNT), cathepsin S (CTSS), cyclooxgenase 2 (COX2), diazepam binding
 CC inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating
 CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
 CC transferase (HNMT), (kallikrein 2) KLK2, nicotinamide -N-methyl
 CC transferase (NMNT), NADPH quinone oxidoreductase 2 (NQO2),
 CC sulfoxidoreductase thermolabile (STM), UDP-glucuronosyl transferase 2B4
 CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl

CC transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1
 CC (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
 CC (MRP3), orphan nuclear receptor (NR112), or acetylcholine muscarinic
 CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
 CC The polymorphisms in the human genes cited in the invention are useful as
 CC genetic linkage markers for locating and characterizing the genes that
 CC are responsible for specific traits within the genome and eventually
 CC identifying the genes responsible for a variety of disorder-related
 CC traits as a result of their e.g., overexpression, constitutive
 CC expression, mutation or underexpression, which may be used in diagnosing
 CC and/or treating the disorders. The nucleic acid molecules comprising the
 CC polymorphic sequences contained in CYP4501A1, CYP4501A2, CYP4502E1,
 CC ARNT, EPHX2, GST12, NMNT, NQO2, NR112, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
 CC MDR1 and/or MDR3 are useful for screening individuals for altered drug
 CC metabolism. The polymorphic sequences contained in CYP4501A1, CYP4501A2,
 CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for
 CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
 CC used to screen for altered cardiovascular function, in COX2 for altered
 CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
 CC nervous system function, in FLAP and HNMT for altered pulmonary,
 CC immunological or haematological function, in KLK2 for altered serine
 CC protease activity in the prostate, in LTF for altered immunological or
 CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
 CC peripheral nervous system function. The present sequence represents a
 CC sequencing primer used to sequence the polymorphic genes of the invention

XX SQ Sequence 16 BP; 4 A; 4 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

374 GATCATCTTAGCCCA 389
 16 GATCATCTTAGCCCA 1

RESULT 515
 ABL31409
 ID ABL31409 standard; DNA; 16 BP.
 XX
 AC ABL31409;
 XX
 DT 21-MAR-2002 (first entry)
 DE Human HLA genotyping oligonucleotide SEQ ID NO 898.
 XX
 DE Human; human leukocyte antigen; HLA; genotype; polymorphism;
 KM human; human leukocyte antigen; HLA; genotype; polymorphism;
 KM immunogenetic; transplantation; genetic disease; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200192572-A1.
 XX
 PD 06-DEC-2001.
 XX
 PF 01-JUN-2001; 2001WO-JP004662.
 XX
 PR 01-JUN-2000; 2000JP-00164798.
 XX
 PA (NISN) NISSHINBO IND INC.
 XX
 PI Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;
 XX
 DR WPI; 2002-122074/16.
 XX
 PT Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of
 PT individuals e.g. by determining immunogenetic differences when
 PT transplanting between them.
 XX
 PS Claim 10; Page 263; 345pp; Japanese.
 XX

CC The invention relates to a typing kit for judging human leukocyte antigen
CC (HLA) genotype of a sample by hybridising a substrate on which 10-24 base
CC oligonucleotides (ABLJ0512-ABLJ1809) originating in the sequences of
CC genes e.g. belonging to HLA class I antigens on human genome and
CC containing gene polymorphisms as alloantigens have been immobilised as
CC primers for amplification of cleaved nucleic acids relating to gene
CC polymorphisms. The method is useful for judging HLA genotypes of
CC individuals by determining immunogenetic differences before transplanting
CC organ and tissue for transplantation e.g. of bone marrow, kidney, liver,
CC pancreas, langerhans islet in pancreas and cornea, susceptibility
CC diagnosis of genetic diseases and identifying individuals
CC
SQ Sequence 16 BP; 3 A; 0 C; 9 G; 4 T; 0 U; 0 Other;
Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
170 GGGGTTGCTACAGAT 185
Db 1 GGGGTTGCTACAGAT 16
RESULT 516
ABLJ1307
ID ABLJ1307 standard; DNA; 16 BP.
AC ABLJ1307;
XX
XX
XX 21-MAR-2002 (first entry)
XX
XX Human HLA genotyping oligonucleotide SEQ ID NO 796.
XX
XX Human; human leukocyte antigen; HLA; genotype; polymorphism;
XX immunogenetic; transplantation; genetic disease; ss.
XX
XX Homo sapiens.
XX
XX WO200192572-A1.
XX
XX 06-DEC-2001.
XX
XX 01-JUN-2001; 2001WO-IP004662.
XX
XX 01-JUN-2000; 2000JP-00164798.
XX
XX (NISR) NISSHINBO IND INC.
XX (SYST-) SYSTEM RES INC.
XX
XX Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;
XX WPI; 2002-122074/16.
XX
XX Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of
XX individuals e.g. by determining immunogenetic differences when
XX transplanting between them.
XX
XX Claim 10; Page 244; 345pp; Japanese.
XX
XX The invention relates to a typing kit for judging human leukocyte antigen
XX (HLA) genotype of a sample by hybridising a substrate on which 10-24 base
XX oligonucleotides (ABLJ0512-ABLJ1809) originating in the sequences of
XX genes e.g. belonging to HLA class I antigens on human genome and
XX containing gene polymorphisms as alloantigens have been immobilised as
XX primers for amplification of cleaved nucleic acids relating to gene
XX polymorphisms. The method is useful for judging HLA genotypes of
XX individuals by determining immunogenetic differences before transplanting
XX organ and tissue for transplantation e.g. of bone marrow, kidney, liver,
XX pancreas, langerhans islet in pancreas and cornea, susceptibility
XX diagnosis of genetic diseases and identifying individuals
XX

SQ Sequence 16 BP; 3 A; 0 C; 9 G; 4 T; 0 U; 0 Other;
Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
170 GGGGTTGCTACAGAT 185
Db 1 GGGGTTGCTACAGAT 16
RESULT 517
AAL56914
ID AAL56914 standard; DNA; 16 BP.
AC AAL56914;
XX
XX
XX 11-MAR-2004 (first entry)
XX
XX Human hypoxia-inducible factor-1 alpha antisense oligo #10.
XX
XX HIF-1alpha; hypoxia-inducible factor-1 alpha; human; antisense; cancer;
XX pre-eclampsia; cytosolic; gynaecological; antiinflammatory; nootropic;
XX neuroprotective; ss.
XX
XX Homo sapiens.
XX
XX WO2003085110-A2.
XX
XX 16-OCT-2003.
XX
XX 04-APR-2003; 2003WO-IB001758.
XX
XX 05-APR-2002; 2002US-0370126P.
XX
XX (CURE-) CUREON AS.
XX
XX Thru CA, Hog AM, Kristjansen PEG;
XX
XX WPI; 2003-812728/76.
XX
XX New oligonucleotide that modulates hypoxia-inducible factor-1alpha,
XX useful for treating e.g. cancer or Alzheimer's disease.
XX
XX Claim 1; Page 41; 0pp; English.
XX
XX The present invention relates to compounds capable of modulating hypoxia-
XX inducible factor-1alpha (HIF1a). The compounds are used to treat patients
XX with, or at risk of developing, cancer (e.g. of breast, prostate,
XX pancreas, lung), pre-eclampsia, inflammatory bowel disease or Alzheimer's
XX disease, for modulating angiogenesis, proliferation of erythrocytes and
XX other cells, iron, glucose and energy metabolism, pH regulation, tissue
XX invasion, apoptosis, multiple drug resistance, cellular stress responses,
XX and matrix metabolism, especially apoptosis where modulation is
XX sensitivity to an apoptotic stimulus, particularly a chemotherapeutic
XX agent and for inhibiting proliferation of cells (especially cancer cells)
XX in vitro. The present sequence is an antisense oligonucleotide against
XX HIF1alpha identified in the exemplification of the invention
XX
SQ Sequence 16 BP; 4 A; 4 C; 6 G; 2 T; 0 U; 0 Other;
Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
73 CAAAAAGAGTGTGCC 88
Db 1 CGAAGAGAGTGTGCC 16
RESULT 518
ABZ95580
ID ABZ95580 standard; DNA; 16 BP.

XX AC AB295580;
XX DT 17-OCT-2003 (first entry)
XX DE Human inducible nitric oxide synthase antisense fragment no.1444.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antiaesthetic; hypotensive; immunosuppressive; cyostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
XX OS
XX PN MO200285308-A2.
XX PD 31-OCT-2002.
XX PF 23-APR-2002; 2002WO-US013135.
XX PR 24-APR-2001; 2001US-0286137P.
XX PA (EPIC-) EPIGENESIS PHARM INC.
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX DR
XX PT Pharmaceutical composition for treating ailments associated with impaired
XX respiration, has oligo(s) antisense to specific gene(s) or its
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.
XX PS Disclosure; SEQ ID NO 10822; 872pp; English.
XX
XX CC The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiquinone. A composition of the invention
XX has antiinflammatory, antiallergic, antiaesthetic, hypotensive,
XX immunosuppressive, and cyostatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX preventing a respiratory, lung or malignant disease or condition, also
XX for enhancing the prophylactic or therapeutic respiratory effect of an
XX antiinflammatory steroid in a subject, for reducing or depleting levels
XX of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX receptor, producing bronchodilation, increasing levels of ubiquinone or
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX lung inflammation, lung allergies, or a respiratory disease or condition.
XX Note: The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 16 BP; 0 A; 8 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 537 CTTCTTCCATCGCC 552
| | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | |
Db 1 CTTCTTCCCGCTCC 16

RESULT 519
AB295535/C
ID AB295535 standard; DNA; 16 BP.

XX AC AB295535;
XX DT 17-OCT-2003 (first entry)
XX DE Human endothelial nitric oxide synthase antisense fragment no.1399.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antiaesthetic; hypotensive; immunosuppressive; cyostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
XX OS
XX PN MO200285308-A2.
XX PD 31-OCT-2002.
XX PF 23-APR-2002; 2002WO-US013135.
XX PR 24-APR-2001; 2001US-0286137P.
XX PA (EPIC-) EPIGENESIS PHARM INC.
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX DR
XX PT Pharmaceutical composition for treating ailments associated with impaired
XX respiration, has oligo(s) antisense to specific gene(s) or its
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.
XX PS Disclosure; SEQ ID NO 10777; 872pp; English.
XX
XX CC The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiquinone. A composition of the invention
XX has antiinflammatory, antiallergic, antiaesthetic, hypotensive,
XX immunosuppressive, and cyostatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX preventing a respiratory, lung or malignant disease or condition, also
XX for enhancing the prophylactic or therapeutic respiratory effect of an
XX antiinflammatory steroid in a subject, for reducing or depleting levels
XX of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX receptor, producing bronchodilation, increasing levels of ubiquinone or
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX lung inflammation, lung allergies, or a respiratory disease or condition.
XX Note: The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 16 BP; 0 A; 5 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 636 GTCAGCCAGCCACC 651
| | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | |
Db 16 GCGAGCCAGCCAGCC 1

RESULT 520
AB295581
ID AB295581 standard; DNA; 16 BP.

XX	ABZ95581;
AC	
XX	
DT	17-OCT-2003 (first entry)
XX	
DE	Human inducible nitric oxide synthase antisense fragment no.1445.
XX	
KW	Human; antisense; lung dysfunction; nasal airway dysfunction;
KM	antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KM	anticholinergic; hypotensive; immunosuppressive; cytotactic; gene therapy;
KW	adenosine gene therapy; respiratory; lung; adenosine sensitivity;
KX	adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX	lung inflammation; respiratory disease; de-
OS	Homo sapiens.
XX	
PN	WO200285308-A2.
XX	
PD	31-OCT-2002.
XX	
PF	23-APR-2002; 2002WO-US013135.
XX	
PR	24-APR-2001; 2001US-0286137P.
XX	
PA	(EPIG-) EPIGENESIS PHARM INC.
XX	
PI	Nyce JW, Li Y, Sandrasekara A, Katz E, Pabalan J, Aguilar D;
XX	Müller S, Tang L, Shahabuddin S;
XX	WPI, 2003-229219/22.
DR	
PT	Pharmaceutical composition for treating ailments associated with impaired
PT	respiration, has oligo(s) antisense to specific gene(s) or its
PT	corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT	ubiquinone.
XX	
PS	Disclosure, SEQ ID NO 10823; 872pp; English.
XX	
CC	The invention relates to a novel pharmaceutical composition, which has a
CC	first active agent comprising an oligonucleotide antisense to the
CC	initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC	5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC	junctions of genes encoding a polypeptide associated with lung and/or
CC	nasal airway dysfunction and a second active agent comprising an
CC	antiinflammatory steroid and ubiquinone. A composition of the invention
CC	has antiinflammatory, antiallergic, antisthmatic, hypotensive,
CC	immunosuppressive, and cytostatic activity. The composition may have a
CC	use in antisense gene therapy. The composition is useful for treating or
CC	preventing a respiratory, lung or malignant disease or condition, also
CC	for enhancing the prophylactic or therapeutic respiratory effect of an
CC	antiinflammatory steroid in a subject, for reducing or depleting levels
CC	of, or reducing sensitivity to adenosine, increasing levels of ubiquinone or
CC	receptor, producing bronchodilation, increasing levels of ubiquinone or
CC	lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC	lung inflammation, lung allergies, or a respiratory disease or condition.
CC	Note: The sequence data for this patent is not represented in the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences
CC	
CC	
XX	
SQ	Sequence 16 BP; 0 A; 8 C; 1 G; 7 T; 0 U; 0 Other;
	Query March 0 7%; Score 12.8; DB 1; Length 16;
	Best Local Similarity 87.5%; Pred. No. 3.3e+02;
	Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY	537 CTTCTTCCCATCGGC 552
DB	1 CTTCTTCCCATCGTC 16
	RESULT 521
	ABD19740
ID	ABD19740 standard; DNA; 16 BP.

XX ABD19740;
AC
XX
XX 29-JUL-2004 (first entry)
XX
XX
XX Human inducible nitric oxide synthase DNA fragment 1445.
XX
XX
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; anti-allergic; anti-inflammatory; antistatic;
KW analgesic; hypotensive; immunosuppressive; cytosolic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
XX pulmonary transplantation rejection; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200285309-A2.
XX
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013143.
XX
XX 24-APR-2001; 2001US-0286036P.
XX
XX (EPIC-) EPIGENESIS PHARM INC.
XX
XX Myce JW, Li Y, Sandraagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI, 2003-093058/08.
XX
XX
XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
XX
XX Claim 15; SEQ ID NO 10823; 763pp; English.
XX
XX
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antistatic,
CC analgesic, hypotensive, immunosuppressive and cytosolic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hyperextension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
XX Sequence 16 BP; 0 A; 8 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

537 CTTCTTCCCATGCC 552
1 CTTCTTCCCATGCC 16

RESULT 522
ABD19685/c
ID ABD19685 standard; DNA; 16 BP.
XX
XX ABD19685;
XX
XX 29-JUL-2004 (first entry)
XX
XX Human endothelial nitric oxide synthase fragment 1399.
XX
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;
XX surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
XX analgesic; hypotensive; immunosuppressive; cytosolic; cystic fibrosis;
XX beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
XX respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
XX emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
XX pulmonary transplantation rejection; ds.
XX
XX Homo sapiens.
XX
XX OS
XX PN WO200285309-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013143.
XX
XX 24-APR-2001; 2001US-0286036P.
XX
XX (EPIC-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX Miller S, Tang L, Shahabuddin S;
XX
XX WPI: 2003-093058/08.
XX
XX
XX This invention describes a novel composition (a) a first active agent,
XX comprising oligonucleotides, effective for alleviating
XX bronchoconstriction, respiratory tract inflammation, allergies and
XX reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
XX surfactant depletion or hyposecretion, when administered to a mammal. The
XX oligonucleotides are derived from a gene encoding or regulating
XX expression of a target polypeptide associated with lung airway or lung
XX dysfunction or cancer and can be anti-sense to the corresponding mRNA.
XX The invention also describes a kit, that comprises: (a) a delivery
XX device, in separate containers, (b) the oligonucleotides, (c)
XX instructions for adding a carrier and for use of the kit. The composition
XX of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
XX analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
XX beta-adrenergic agonist. The composition is useful for preventing or
XX treating a respiratory, lung or malignant disease. The administered
XX composition comprises oligo and is administered to reduce the production
XX or availability, or to increase the degradation of the target mRNA or to
XX reduce the amount of target polypeptide present in the lungs. The
XX pulmonary obstruction, and/or bronchoconstriction and/or lung
XX inflammation, allergies and/or surfactant hypoproduction are associated
XX with a disease or condition such as pulmonary vasoconstriction,

XX inflammation, allergies, asthma, impeded respiration, respiratory
XX distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
XX hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
XX transplantation rejection, pulmonary infections, bronchitis or cancer.
XX The reduced adenosine content of the anti-sense oligos corresponding to
XX thymidines present in the target RNA serves to prevent the breakdown of
XX the oligonucleotides into products that free adenosine into the system
XX e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
XX prevent any unwanted effects due to it
XX
XX Sequence 16 BP; 0 A; 5 C; 7 G; 4 T; 0 U; 0 Other;
XX

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

636 GTCAGCCAGCCACC 651
16 GGCAGCCAGCCAGCAC 1

RESULT 523
ABD19739
ID ABD19739 standard; DNA; 16 BP.
XX
XX ABD19739;
XX
XX 29-JUL-2004 (first entry)
XX
XX Human inducible nitric oxide synthase DNA fragment 1444.
XX
XX
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;
XX surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
XX analgesic; hypotensive; immunosuppressive; cytosolic; cystic fibrosis;
XX beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
XX respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
XX emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
XX pulmonary transplantation rejection; ds.
XX
XX Homo sapiens.
XX
XX OS
XX PN WO200285309-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013143.
XX
XX 24-APR-2001; 2001US-0286036P.
XX
XX (EPIC-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX Miller S, Tang L, Shahabuddin S;
XX
XX WPI: 2003-093058/08.
XX
XX
XX This invention describes a novel composition (a) a first active agent,
XX comprising oligonucleotides, effective for alleviating
XX bronchoconstriction, respiratory tract inflammation, allergies and
XX reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
XX surfactant depletion or hyposecretion, when administered to a mammal. The
XX oligonucleotides are derived from a gene encoding or regulating
XX expression of a target polypeptide associated with lung airway or lung
XX dysfunction or cancer and can be anti-sense to the corresponding mRNA.
XX The invention also describes a kit, that comprises: (a) a delivery

CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cyostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or surfactant hypoproduction are associated
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impaired respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it

XX SQ Sequence 16 BP; 0 A; 8 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 537 CTCTCTTCCGCGCC 552
Db 1 CTCTCTTCCGCGCTCC 16

RESULT 524
ADK82289/c
ID ADK82289 standard; DNA; 16 BP.

XX AC ADK82289;

XX DT 03-JUN-2004 (first entry)

XX DE Nucleic acid analysis method associated probe seqid 66.

XX KW nucleic acid analysis; hepatitis C virus;

XX KW non-contiguous single-stranded region; NCSR; cleavage structure;

XX KW clinical; diagnostic; microorganism detection;

XX KW microorganism identification; probe; ss.

XX OS Synthetic.

XX PN US6709815-B1.

XX PD 23-MAR-2004.

XX PF 18-JUL-2000; 2000US-00402618.

XX PR 05-MAY-1997; 97US-00851588.

XX PR 19-SEP-1997; 97US-00934097.

XX PR 03-MAR-1998; 98US-00034205.

XX PA (THIR-) THIRD WAVE TECHNOLOGIES INC.

XX PI Dong F, Lyamichev VI, Prudent JR, Fors L, Nerl BP, Brow MAD;

XX PI Anderson TA, Dahlberg JE;

XX DR WPI; 2004-256067/24.

XX PT Analyzing nucleic acids, comprises mixing target nucleic acid such as
XX PT hepatitis C virus nucleic acid, bridging oligonucleotide, second
XX PT oligonucleotide and cleavage agent to form cleavage structure.
XX PS Example 8; SEQ ID NO 66; 143bp; English.

CC The invention describes a method of analysing nucleic acids comprising
CC providing a target nucleic acid, e.g. hepatitis C virus nucleic acid
CC having non-contiguous single-stranded regions (NCSR) separated by an
CC intervening region, a bridging oligonucleotide capable of binding to the
CC first and second NCSR; a second oligonucleotide binding to a portion of
CC the first NCSR and a cleavage agent, and mixing the contents to form a
CC cleavage structure. The method is useful for analysing nucleic acids,
CC e.g. hepatitis C virus nucleic acid useful for clinical diagnostic
CC purposes and detection and identification of pathogenic microorganisms
CC such as hepatitis C virus. This sequence represents a probe associated
CC with the nucleic acid analysis method of the invention.

XX SQ Sequence 16 BP; 3 A; 3 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1436 CCACAGGCGCTTGGC 1451
Db 16 CCACAGGCGCTTGGC 1

RESULT 525
AD015394/c
ID AD015394 standard; DNA; 16 BP.

XX AC AD015394;

XX DT 01-JUL-2004 (first entry)

XX DE Glutathione S-transferase omega 2 (GSTO2) primer/probe #16.

XX KW Alzheimer's disease; Parkinson's disease; chromosome 10q24.32; D4S1652;
XX KW D10S1239; D10S1237; D1S2134; D8S1128; D8S373; D1S200; D5S1462; D5S1453;
XX KW D6S2439; D6S2427; D6S1017; D6S1007; D1S8800; D1S8103; D1S8877;
XX KW D20S851; D20S604; D2S6883; glutathione-S-transferase omega-1; GSTO1;
XX KW glutathione-S-transferase omega-2; GSTO2; Alzheimer's disease;
XX KW Parkinson's disease; primer; probe; ss.

XX OS Homo sapiens.

XX PN US2004014109-A1.

XX PD 22-JAN-2004.

XX PF 23-MAY-2003; 2003US-00444347.

XX PR 23-MAY-2002; 2002US-0382880P.

XX PR 16-JUL-2002; 2002US-0396223P.

XX PR 25-NOV-2002; 2002US-0428876P.

XX PA (PERI/) PERICAK-VANCE M A.

XX PA (VANC/) VANCE J M.

XX PA (HAIN/) HAINES J L.

XX PA (GILB/) GILBERT J.

XX PA (LIYY/) LI Y.

XX PI Perleak-Vance MA, Vance JM, Haines JL, Gilbert J, Li Y;

XX PI WPI; 2004-121564/12.

XX PT Screening or diagnosing a subject for Alzheimer's disease and/or
XX PT Parkinson's disease, comprises detecting the presence or absence of
XX PT markers, genes or enzymes linked to Alzheimer's disease and/or
XX PT Parkinson's disease.

XX PS Example; Page 12; 20pp; English.

XX CC The invention describes a method of screening or diagnosing a subject for
XX CC Alzheimer's disease and/or Parkinson's disease comprising detecting the
XX CC presence or absence of at least one or more markers, genes or enzymes
XX CC linked to Alzheimer's disease and/or Parkinson's disease. The marker,

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 685 CTCTGCTGCGCTTCC 700
|||||
1 CTCTGCTGCGCGCTTCC 16

RESULT 528

AD062809
ID AD062809 standard; DNA; 16 BP.

AC AD062809;

DT 07-OCT-2004 (first entry)

DE Aptamer-related DNA sequence #2.

KW aptamer; authentication; ss.

XX Synthetic.

OS JP2004196753-A.

XX 15-JUL-2004.

PD 20-DEC-2002; 2002JP-00370729.

XX 20-DEC-2002; 2002JP-00370729.

PR (KANF) KANEKA CORP.

XX WPI; 2004-503927/48.

DR Novel nucleic acid having a stable structure, useful for authentication

PT for conforming organisms, person or goods.

XX Example 2; SEQ ID NO 4; 9pp; Japanese.

CC The invention comprises an aptamer (e.g. DNA aptamer, peptide nucleic acid or Z type DNA). The aptamer of the invention is useful for authentication, for producing a plasmid that is transduced into a microorganism, or for recognising a compound (e.g. sulfo rhodamine B), which in turn is useful for authentication. The present DNA sequence was used in an example of the invention.

CC Sequence 16 BP; 0 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

QY Query Match 0.7%; Score 12.8; DB 1; Length 16;

Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 685 CTCTGCTGCGCTTCC 700
|||||
1 CTCTGCTGCGCGCTTCC 16

RESULT 529

AD090894/C
ID AD090894 standard; DNA; 16 BP.

AC AD090894;

DT 18-NOV-2004 (first entry)

DE Oligonucleotide of the invention SEQ ID NO:1910.

XX ss; cell proliferative disorder; breast; methylation; cyrostatic;
KW gene therapy; single nucleotide polymorphism; SNP.

XX Unidentified.

PN WO2004035803-A2.

XX 29-APR-2004.

PD 01-OCT-2003; 2003WO-EP010881.

XX 01-OCT-2002; 2002DE-01045779.

PR 07-JAN-2003; 2003DE-01000096.

PR 17-APR-2003; 2003DE-01017955.

XX (EPIG-) EPIGENOMICS AG.

PA Foekens J, Harbeck N, Koenig T, Maier S, Martens J, Model F,

PI Nimmrich I, Rujan T, Schmitt A, Schmitt M, Look MP, Marx A;

XX WPI; 2004-348468/32.

DR Predicting responsiveness of a subject with breast cell proliferative

PT disorder, useful for treating or differentiating breast cell

PT proliferative disorders comprises analyzing methylation pattern of a

PT genomic DNA from the subject.

XX Disclosure; SEQ ID NO 1910; 104pp; English.

CC The invention relates to a novel method for predicting the responsiveness of a subject with a cell proliferative disorder of the breast tissues to a therapy comprising analysing the methylation pattern of a target nucleic acid by contacting at least one of the target nucleic acids in a biological sample obtained from the subject prior to or during treatment. The method of the invention has cyrostatic activity, and may have a use in gene therapy. The set of oligonucleotides comprising at least two of the oligomers are useful for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) within the sequences. The methods, nucleic acid, oligonucleotide, and kit are useful for the treatment, characterisation, classification and/or differentiation, of breast cell proliferative disorders. The method is also useful for predicting the responsiveness of a subject with a cell proliferative disorder of the breast tissues to a therapy. The present sequence is used in the exemplification of the invention.

CC Sequence 16 BP; 7 A; 0 C; 7 G; 2 T; 0 U; 0 Other;

QY Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1001 TCCACATCTTCTCTT 1016
|||||
16 TCCACTTCTTCTCTCT 1

ADY03782/C
ID ADY03782 standard; DNA; 16 BP.

AC ADY03782;

DT 05-MAY-2005 (first entry)

DE Hepatitis C virus-specific antisense oligo - SEQ ID 44.

XX viral infections; virus; hepatitis B virus infection; hepatitis C virus infection;

XX gene silencing; antisense oligonucleotide; ss.

XX Hepatitis C virus.

PN WO2005013905-A2.

XX 17-FEB-2005.

PF 06-AUG-2004; 2004WO-US025401.

PR 07-AUG-2003; 2003US-0493990P.
XX (AVID-) AVI BIOPHARMA INC.
PA Iversen PL;
XX WPI; 2005-172937/18.
DR
XX New oligonucleotide analog, compound having a single-stranded, positive-
PT sense RNA genome, useful for inhibiting replication in mammalian host
PT cells of an RNA virus.
PS
XX Example 1; SEQ ID NO 44; 81bp; English.
XX The invention comprises oligonucleotides which are designed to inhibit
CC the replication of an RNA virus in a mammalian cell. The oligonucleotides
CC of the invention are useful for the treatment of Picornaviridae,
CC Caliciviridae, Togaviridae, Coronaviridae, Flaviviridae and Hepatitis B
CC virus infection. The present DNA sequence represents an oligonucleotide
CC of the invention which is designed to inhibit the replication of a virus.
XX
SQ Sequence 16 BP; 2 A; 7 C; 5 G; 2 T; 0 U; 0 Other;
Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1076 CCATCANGTGCTGCGC 1091
DB 16 CCATCAGGGGCTGCGC 1
RESULT 531
AEA50577
ID AEA50577 standard; DNA; 16 BP.
XX
AC AEA50577;
XX
DT 25-AUG-2005 (first entry)
XX
DE Human nucleic acid PCR primer #200.
XX
XX SNP detection: cardiovascular disease; myocardial infarction;
KM cerebrovascular ischemia; atherosclerosis; cerebrovascular disease;
KM unstable angina; coronary artery disease; congenital heart defect;
KM congestive heart failure; PCR; primer; ss; cardiovascular-gen.;
KM cerebroprotective; cardiac; vasotropic; antiarteriosclerotic;
KM antianginal.
XX
OS Homo sapiens.
XX
PN WO2005056837-A2.
XX
PD 23-JUN-2005.
XX
PF 24-NOV-2004; 2004WO-US039576.
XX
PR 26-NOV-2003; 2003US-0524882P.
PR 06-MAY-2004; 2004US-0568219P.
XX
PA (APPL-) APPLERA CORP.
PI Cargill M, Jakubova O, Devlin JJ, Tsuchihashi Z, Shaw P,
PI Ploughman LM, Zerba KE, Koustubh R, Kirchgessner T;
DR WPI; 2005-467032/47.
XX
PT Novel isolated nucleic acid molecule, useful for identifying individual
PT who has altered risk for developing cardiovascular disorder or altered
PT likelihood of responding to statin treatment.
XX
PS Claim 21; SEQ ID NO 85290; 200pp; English.
XX

CC The invention relates to an isolated nucleic acid molecule comprising 8
CC or more contiguous nucleotides, where one of the nucleotides is a single
CC nucleotide polymorphism (SNP). The invention also relates to a method of
CC identifying an individual who has an altered risk for developing a
CC cardiovascular disease or an altered likelihood of responding to statin
CC treatment, involving detecting a SNP in the individual's nucleic acids,
CC where the presence of the SNP is correlated with an altered risk for
CC developing a cardiovascular disease or responding to statin treatment,
CC and a method of treating a cardiovascular disease in an individual
CC involving administering to the individual an effective amount of statin
CC based on the individual's likelihood of responding to statin treatment as
CC predicted by the alleles present at one or more SNP sites. The nucleic
CC acids and the related polypeptides are useful for identifying an agent
CC useful for therapeutically or prophylactically treating cardiovascular
CC diseases which involves contacting a nucleic acid with a candidate agent
CC under conditions suitable to allow formation of a binding complex between
CC the nucleic acid and the candidate agent and detecting formation of the
CC binding complex, where the presence of the complex identifies the agent.
CC The cardiovascular disease is an acute coronary event chosen from
CC myocardial infarction, stroke, atherosclerosis, cerebrovascular disease,
CC unstable angina, coronary artery disease, congenital heart defect and
CC congestive heart failure. This sequence represents a PCR primer used in
CC genotyping of nucleic acid molecules of the invention.
XX
SQ Sequence 16 BP; 1 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 673 TGGGTCCTGGCTCTCC 688
DB 1 TGGTACTGCTCTCC 16
RESULT 532
AEB52878
ID AEB52878 standard; DNA; 16 BP.
XX
AC AEB52878;
XX
DT 22-SEP-2005 (first entry)
XX
DE Human leukocyte antigen-A DNA probe, SEQ ID 498.
XX
XX human leukocyte antigen; HLA; probe; transplant rejection; cancer;
KM cytostatic; diabetes; antidiabetic; multifactorial genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN JP2005185176-A.
XX
PD 14-JUL-2005.
XX
PF 25-DEC-2003; 2003JP-00430558.
XX
PR 25-DEC-2003; 2003JP-00430558.
XX
PA (CANO) CANON KK.
PI Tsukada M;
DR WPI; 2005-515775/53.
XX
PT Probe set for identifying human leukocyte antigen (HLA)-DP allele in
PT patients with organ transplant, cancer or diabetes enabling tailored
PT medical treatment.
XX
PS Claim 2; SEQ ID NO 498; 90pp; Japanese.
XX
XX The invention relates to a novel probe set for identifying a human
CC leukocyte antigen-A (HLA-A) allele in a test substance. The probe set
CC comprises several probes chosen from the fully defined nucleic acid

CC sequences (SEQ ID No: 251-431 and SEQ ID No: 455-631) as given in the
CC specification. The novel probe set can identify HLA-A alleles in patients
CC with organ transplants, cancer, diabetes and other multiple-factor
CC diseases, and enables tailored medical treatment to individual patients.
CC This oligo sequence represents a human leukocyte antigen-A DNA probe of
CC the invention.
CC
CC
SQ Sequence 16 BP; 3 A; 4 C; 8 G; 1 T; 0 U; 0 Other;
Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1299 GGGCCACGAGGAGGAG 1314
DB 1 GGGCCATGAGGCGAG 16
RESULT 533
ABF46499 standard; DNA; 13 BP.
XX
XX ABF46499;
AC
XX
XX 21-FEB-2002 (first entry)
DT
XX
XX Oligonucleotide SEQ ID NO 146496 for detecting SNP TSC0036939.
DE
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX MO200177384-A2.
PN
XX
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX
XX 07-APR-2000; 2000DE-01019173.
PR
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
PT
XX
XX Claim 1; SEQ ID NO 146496; 29bp + Sequence Listing; German.
PS
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI02073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
CC
SQ Sequence 13 BP; 3 A; 7 C; 0 G; 2 T; 0 U; 1 Other;
Query Match 0.7%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 2.2e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 238 GACCTCTCCCCA 250
DB 1 RACCTCTCCCCA 13
RESULT 534
ABH39848/c
ID ABH39848 standard; DNA; 13 BP.
XX
XX ABH39848;
AC
XX
XX 22-FEB-2002 (first entry)
DT
XX
XX Oligonucleotide SEQ ID NO 239825 for detecting SNP TSC0058496.
DE
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX
XX MO200177384-A2.
PN
XX
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX
XX 07-APR-2000; 2000DE-01019173.
PR
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
PT
XX
XX Claim 1; SEQ ID NO 239825; 29bp + Sequence Listing; German.
PS
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI02073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
CC
SQ Sequence 13 BP; 2 A; 0 C; 6 G; 4 T; 0 U; 1 Other;
Query Match 0.7%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 2.2e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1107 GTACACCCCATC 1119
DB 13 RTACACCCCATC 1
RESULT 535
ABH39849
ID ABH39849 standard; DNA; 13 BP.
XX
XX ABH39849;
AC
XX
XX 22-FEB-2002 (first entry)
DT
XX

DE Oligonucleotide SEQ ID NO 239826 for detecting SNP TSC0058496.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 239826; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABP99989, ABH00010-ABH99989 and ABH00010-ABH82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 4 A; 6 C; 0 G; 2 T; 0 U; 1 Other;
XX
XX Query Match 0.7%; Score 12.6; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 2.2e+02;
XX Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1107 GTACACCCCATC 1119
DB 1 RTACACCCCATC 13
RESULT 536
ABF46498/C
ID ABF46498 standard; DNA; 13 BP.
XX
XX ABR46498;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 146495 for detecting SNP TSC0036939.
DE
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX

XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 146495; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABP99989, ABH00010-ABH99989 and ABH00010-ABH82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 2 A; 0 C; 7 G; 3 T; 0 U; 1 Other;
XX
XX Query Match 0.7%; Score 12.6; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 2.2e+02;
XX Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 238 GACCTCTCCCAA 250
DB 13 RACCTCTCCCAA 1
RESULT 537
ABA98358
ID ABA98358 standard; DNA; 15 BP.
XX
XX ABA98358;
XX
XX 30-JUN-2002 (first entry)
XX
XX SCN2B gene polymorphisms ASO primer #2.
DE
XX
XX Human; sodium channel voltage gated type 2 beta polypeptide; SCN2B; ds;
XX gene therapy; neuroprotective; demyelinating disease.
XX
XX Homo sapiens.
XX
XX WO200179547-A1.
XX
XX 25-OCT-2001.
XX
XX 03-APR-2001; 2001WO-US010743.
XX
XX 13-APR-2000; 2000US-0196597P.
XX
XX (GENA-) GENAISSANCE PHARM INC.
XX
XX Chew A, Choi JY, Koshy B;
XX
XX WPI; 2002-075072/10.
XX
XX New polynucleotide containing polymorphisms in the human sodium channel
XX voltage gated type 2 beta polypeptide (SCN2B) gene, for developing drugs
XX for treating demyelinating diseases.
XX
XX Claim 15; Page 13; 63pp; English.
XX
XX

XX This invention relates to an isolated polynucleotide which is a
CC polymorphic variant of a reference sequence for sodium channel voltage
CC gated type 2 beta polypeptide (SCN2B) gene. The methods have
CC applicability in developing diagnostic tests and therapeutic treatments
CC for demyelinating diseases. The protein is useful for studying the
CC expression and function of SCN2B and expressing SCN2B protein for use in
CC screening for candidate drugs to treat diseases related to SCN2B
CC activity. The polymorphism and haplotype data are useful for validating
CC whether SCN2B is a suitable target for drugs to treat demyelinating
CC diseases, screening for such drugs and reducing bias in clinical trials.
CC The haplotyping method is useful to validate SCN2B as a candidate target
CC for treating a specific condition or disease predicted to be associated
CC with SCN2B activity. A recombinant non-human organism transformed or
CC transfected with the polypeptide is useful for studying expression of the
CC SCN2B isogenes in vivo, for in vivo screening and testing of drugs
CC against SCN2B protein and for testing the efficacy of therapeutic agents
CC and compounds for demyelinating diseases in a biological system. This
CC sequence is used during the detection of polymorphisms of the SCN2B gene

XX
SQ Sequence 15 BP; 2 A; 3 C; 8 G; 1 T; 0 U; 1 Other;

Query Match 0.7%; Score 12.6; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 3.1e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 17 GGGCAGCGCGGCA 29
|||||
DB 2 GGGCAGCGCGGCA 14

RESULT 538
ABK27519/C
ID ABK27519 standard; DNA; 15 BP.
AC ABK27519;
XX
XX 09-APR-2002 (first entry)
DT
XX
DE Human CTLA4 gene allele-specific oligonucleotide probe #2.
XX
XX Human; cytotoxic T-lymphocyte-associated protein 4; CTLA4; haplotyping;
KW haplotype pair; single nucleotide polymorphism; autoimmune disorder; ss;
KM genotyping; gene therapy; drug screening; antisense gene therapy; primer;
KW immunosuppressive; sequencing; PCR; probe.
XX
XX Homo sapiens.
OS
XX
XX WO200190122-A2.
PN
XX
XX 29-NOV-2001.
PD
XX
XX 23-MAY-2001; 2001WO-US016905.
PF
XX
XX 23-MAY-2000; 2000US-0206353P.
PR
XX
XX (GENA-) GENAISSANCE PHARM INC.
PA
XX
XX Chew A, Choi JY, Messer C;
PI
XX
XX WPI; 2002-089914/12.
DR
XX
XX New genetic variants of human cytotoxic T-lymphocyte-associated protein
PT 4, CTLA4 gene for studying expression, function of the gene and
PT expressing CTLA4 protein useful in identifying drugs to treat autoimmune
PT disorder.
XX
XX Claim 17; Page 12; 62pp; English.

XX The invention relates to single nucleotide polymorphisms in the gene
CC encoding the human cytotoxic T-lymphocyte-associated protein 4 or CTLA4
CC protein. A method for haplotyping the CTLA4 gene in an individual
CC comprises identifying the nucleotide at one or more polymorphic sites and

CC determining whether one of the copies of the gene is defined by one of
CC the CTLA4 haplotypes given in the specification or whether both copies
CC are defined by a haplotype pair. This method is useful in genotyping,
CC whereby all possible haplotype pairs can be assigned to specific
CC genotypes. An association between a trait and a haplotype or haplotype
CC pair of the CTLA4 gene can be identified by comparing the frequency of
CC the haplotype or haplotype pair in a population exhibiting the trait with
CC the frequency of the haplotype or haplotype pair in a reference
CC population, where a higher haplotype frequency in the trait population
CC indicates the trait is associated with the haplotype or haplotype pair.
CC CTLA4 and its corresponding DNA are used for studying the expression and
CC function of CTLA4, for use in screening for candidate drugs to treat
CC diseases related to CTLA4 activity, such as autoimmune disorders. The
CC sequences are also useful for studying the effect of variation on the
CC biological activity of CTLA4 as well as on the binding affinity of
CC candidate drugs targeting CTLA4. Sequences ABK27518-ABK27549 represent
CC allele-specific oligonucleotide probes, sequencing primers and PCR
CC primers used to detect CTLA4 gene polymorphisms

XX
SQ Sequence 15 BP; 4 A; 3 C; 5 G; 2 T; 0 U; 1 Other;

Query Match 0.7%; Score 12.6; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 3.1e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1464 CACTGCGTTTGAC 1476
|||||
DB 15 CACTGCGTTTGAC 3

RESULT 539
ABK70728
ID ABK70728 standard; DNA; 15 BP.
AC ABK70728;
XX
XX 15-JUL-2002 (first entry)
DT
XX
DE ASO primer #9 to detect human SCY8 gene polymorphisms.
XX
XX Human; single nucleotide polymorphism; SNP; monocyte chemotactic protein;
KW small inducible cytokine subfamily A member 8; SCY8; anti-HIV;
KM haplotyping; genotyping; inflammatory disease; HIV infection; ASO; ss;
KW human immunodeficiency virus; allele-specific oligonucleotide; primer.
XX
XX Homo sapiens.
OS
XX
XX WO200222888-A1.
PN
XX
XX 21-MAR-2002.
PD
XX
XX 17-SEP-2001; 2001WO-US029332.
PF
XX
XX 15-SEP-2000; 2000US-0232755P.
PR
XX
XX (GENA-) GENAISSANCE PHARM INC.
PA
XX
XX Anastasio AE, Chew A, Han J, Lee HH;
PI
XX
XX WPI; 2002-371973/40.
DR
XX
XX New genetic variants of Small Inducible Cytokine Subfamily A (Cys-Cys),
PT Member 8 (Monocyte Chemotactic protein) isogenes, useful for improving
PT efficiency and reliability in drug development for treating diseases.
XX
XX Claim 16; Page 13; 84pp; English.

XX The present invention relates to novel single nucleotide polymorphisms
CC (SNPs) in the human small inducible cytokine subfamily A (Cys-Cys),
CC member 8 (monocyte chemotactic protein) (SCY8) gene located on
CC chromosome 17, and methods for haplotyping and/or genotyping the SCY8
CC gene. The methods of the invention make use of allele-specific
CC oligonucleotides (ASOs) as probes and primers and/or primer-extension

CC oligonucleotides for detecting the SCY8 gene polymorphisms. The
CC polynucleotides and screened compounds are useful for the treatment of
CC diseases associated with SCY8A activity, such as inflammatory diseases
CC and human immunodeficiency virus (HIV) infection. ABK0720-ABK0743
CC represent ASO primers for detecting human SCY8A gene polymorphisms
XX

SO Sequence 15 BP; 3 A; 6 C; 3 G; 2 T; 0 U; 1 Other;

Query Match 0.7%; Score 12.6; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 3.1e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 726 GACCATGCCACG 738
Db 2 GACCATGCCACG 14

RESULT 540

AAH99963
ID AAH99963 standard; DNA; 15 BP.

AC AAH99963;

DT 18-JUN-2002 (first entry)

DE ASO primer for detecting CXCR4 polymorphisms # 5.

XX Human Chemokine receptor 4; CXCR4; human; ss; chromosome 2q21; HIV-1;

KM PCR primer.

XX Homo sapiens.

OS WO200179229-A2.

XX 25-OCT-2001.

XX 13-APR-2001; 2001WO-US012268.

XX 13-APR-2000; 2000US-0197025P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Bentivegna SC, Chew A, Choi JY, Koshy B;

XX WPI; 2002-075062/10.

XX Isolated human chemokine receptor 4 polynucleotide, useful for studying
PT expression and function of chemokine receptor 4 and for treating human
PT immunodeficiency virus-1.

XX Disclosure; Page 13; 54pp; English.

XX The invention relates to an isolated chemokine receptor 4 (CXCR4)

CC polynucleotide which is useful for studying expression and function of
CC chemokine receptor 4 and for the treatment of viruses, including HIV-1.

CC Methods associated with chemokine receptor 4 are useful for improving the
CC efficacy and reliability of several steps in the discovery and

CC development of drugs for treating diseases associated with CXCR4
CC activity, e.g., human immunodeficiency virus-1 infection. They can

CC validate CXCR4 as a candidate agent for treating a specific condition or
CC disease predicted to be associated with CXCR4 activity, and in the design

CC of clinical trials of candidate drugs for treating a specific condition
CC or disease predicted to be associated with CXCR4 activity. CXCR4

CC polynucleotides are useful for therapeutic purposes such as to treat HIV-
CC 1 infection and also are useful for studying expression of the CXCR4

CC isogenes in vivo. This sequence represents a ASO primer used to detect
CC CXCR4 gene polymorphisms

XX Sequence 15 BP; 2 A; 5 C; 4 G; 3 T; 0 U; 1 Other;

Query Match 0.7%; Score 12.6; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 3.1e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1068 CTACCTGCCATC 1080
Db 2 CTACCTGCCATC 14

RESULT 541

AAQ30786
ID AAQ30786 standard; DNA; 20 BP.

AC AAQ30786;

DT 25-MAR-2003 (revised)

DT 22-MAR-1993 (first entry)

DE PCR primer hsp15a2 to amplify human NK1R 5' N-terminal region.

XX Neurokinin-1 receptor short form; arthritis; Substance P;

KM polymerase chain reaction; rat NK1R; ss.

XX Synthetic.

XX EP514207-A2.

XX 19-NOV-1992.

XX 15-MAY-1992; 92EP-00304432.

XX 17-MAY-1991; 91US-00701930.

XX 17-MAY-1991; 91US-00701935.

XX 17-MAY-1991; 91US-00701937.

XX (MERI) MERCK & CO INC.

XX Strader CD, Fong TM;

XX WPI; 1992-384034/47.

XX Example 1; Page 8; 36pp; English.

XX The core region of human NK1R 5' was isolated by PCR and sequenced (see

CC AAQ30774-Q30778). The antisense primers hsp15a2, hsp15a1, hsp15a2,

CC hsp16a1 and hsp16a2 (AAQ30784-Q30788) were synthesised based on the human

CC core sequence. Human glioblastoma mRNA and each of these primers were

CC used in first strand cDNA synthesis to produce the template for a primary

CC PCR amplification. Primer hsp15a5 was used with 2 rat sense primers hsp1n

CC and hsp1n (AAQ30779 and AAQ30780) for the primary amplification. The PCR

CC product was then used as template for secondary PCR with the same rat

CC primers and the human antisense primer hsp13a4 (AAQ30783). The secondary

CC PCR product was the template for tertiary PCR amplification, again using

CC the same rat sense primers but with human antisense primer hsp13a1

CC (AAQ30782). The amplified DNA fragment hybridised to hsp13a2 (AAQ30781),

CC indicating it is not a non-specific by-product. The DNA was sequenced and

CC found to encode the human NK1R 5' N-terminal region and also contains a

XX 5' UTR. (Updated on 25-MAR-2003 to correct PN field.)

SO Sequence 20 BP; 5 A; 6 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 5.5e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 861 CGTAGTGGAATCAGACTA 879
Db 1 CATAGTGGAATTCAGACTA 19

RESULT 542

AAQ29675

ID	AAQ29675	standard; DNA; 20 BP.
XX		
AC	AAQ29675;	
DT	25-MAR-2003	(revised)
DT	15-MAR-1993	(first entry)
XX		
DB	hpr5a2 primer	793-774.
XX		
XX	Human; neurokinin-1 receptor; NK1R; membrane receptor; substance P;	
KW	neurotransmitter; polymerase chain reaction; PCR; rat NK1R; primer;	
KW	amplify; probe; ss.	
OS	Homo sapiens.	
XX		
XX	EP510878-A1.	
PN		
PD	28-OCT-1992.	
XX		
XX	16-APR-1992;	92EP-00303457.
PF		
XX	25-APR-1991;	91US-00691197.
PR	25-APR-1991;	91US-00691198.
PR	25-APR-1991;	91US-00691200.
XX		
XX	(MERI) MERCK & CO INC.	
PA		
PI	Fong TM, Strader CD;	
XX		
XX	WPI, 1992-359073/44.	
DR		
XX		
PT	New recombinant human neurokinin-1 receptor - used to detect and evaluate	
PT	substances that bind to substance P receptor, and to determine substance	
PT	P in body fluid of arthritis patients.	
XX		
PS	Disclosure; Page 8; 35pp; English.	
XX		
XX	The sequences given in AAQ29670-82, AAQ29783 and AAQ29746-48 are primers	
CC	which were used in the isolation of fragments of the human neurokinin-1	
CC	receptor (NK1R) cDNA. Human NK1R is a membrane receptor for the	
CC	neurotransmitter substance P. The primers were designed using regions of	
CC	the human NK1R cDNA and also regions of the rat NK1R which were thought	
CC	to be similar to human regions. Part of the human cDNA sequence was	
CC	derived by amplification using these primers. The remaining part of human	
CC	NK1R cDNA was obtained from a human cDNA library utilising portions of	
CC	PCR generated fragments as probes. See also AAQ29749. (Updated on 25-MAR-	
CC	2003 to correct PN field.)	
XX		
XX	Sequence 20 BP; 5 A; 6 C; 3 G; 6 T; 0 U; 0 Other;	
SO		
	Query Match	0.7%; Score 12.6; DB 1; Length 20;
	Best Local Similarity	78.9%; Pred. No. 5.5e+02;
	Matches 15; Conservative	0; Mismatches 4; Indels 0; Gaps 0
QY	861 CGTAGTGGATCACTA 879	
DB	1 CATAGTGTGATTCCTACTA 19	
	RESULT 543	
	ABK63893/C	
ID	ABK63893	standard; DNA; 20 BP.
AC		
XX	ABK63893;	
DE		
XX	18-JUN-2002	(first entry)
XX		
XX	Neurokinin 1 receptor (NK-1) antisense oligonucleotide #38.	
XX		
KW	Human; neurokinin receptor-1; NK-1; dermatological disorder;	
KW	immune disorder; autoimmune disorder; cardiovascular disorder;	
KW	vascular disorder; airway disorder; neuropathic disorder; pain;	
KW	psychiatric disorder; central nervous system disorder; inflammation;	

KM	respiratory condition; ophthalmic condition; intestinal condition;
KW	demyelinating disease; small cell lung cancer; depression;
KW	hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
KM	neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
OS	neuro-pathological disorder; stress; antisense; primer; ss.
XX	Homo sapiens.
XX	MO2002J3799-A2.
PN	
PD	21-FEB-2002.
PF	17-AUG-2001; 2001WO-IB001510.
PR	18-AUG-2000; 2000US-0226086P.
XX	(UNMC-) UNIV MCGILL.
PA	
P1	Henry JL, Cahill CM, Yashpal K;
DR	WPI, 2002-241835/29.
XX	
PT	Treating pathological condition involving neurokinin receptor-1, e.g.
PT	pain or inflammation, by administering oligonucleotide or a non-
PT	nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
PT	pathway.
XX	
XX	Example 18; Page 65; 100bp; English.
XX	The invention relates to a method of treating a pathological condition
CC	characterised partially by involvement of neurokinin receptor-1 (NK-1)
CC	receptor, especially treating, attenuating or preventing pain or
CC	inflammatory condition. The method comprises administering to a mammal,
CC	a compound chosen from an oligonucleotide, its analogue, and a disruptor
CC	which interferes with function or production of NK-1 receptors. The
CC	method is useful for treating a pathological condition characterised by
CC	involvement of NK-1 receptor such as dermatological, immune, autoimmune,
CC	cardiovascular, vascular disorders (e.g. migraine), allergy, neuropathic,
CC	psychiatric and central nervous system disorders (e.g. anxiety,
CC	peripheral aspects of chronic or acute pain, and for treating
CC	peripheral aspects of chronic or acute pain, and for treating
CC	attenuating or preventing pain or inflammation, neuropathic pain, inflammation or
CC	chronic, acute pain or inflammation, and central nervous system
CC	pain relating to psychiatric disorders and central nervous system
CC	disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
CC	in a mammal, in particular human. NK-1 receptor related disorders,
CC	diseases, or pathological conditions treatable by this method include
CC	respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
CC	conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
CC	(allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and
CC	Crohn's disease), cardiovascular conditions (stroke), chronic
CC	gastrointestinal tract inflammation, and inflammatory diseases such as
CC	inflammatory bowel diseases. Other disorders and diseases include
CC	cardiovascular pathologies including stroke, chronic inflammatory
CC	diseases such as rheumatoid arthritis, demyelinating diseases such as
CC	multiple sclerosis, small cell lung cancer, depression, hypersensitivity
CC	disorders such as allergies and poison ivy, vasospastic diseases such as
CC	angina, addiction disorders such as alcoholism, neurodegenerative
CC	diseases such as Alzheimer's disease, and other neuro-pathological
CC	dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
CC	diseases such as peripheral neuropathy, oedema, stress related and
CC	somatic disorders, and osteoarthritis. Antisense oligonucleotides
CC	effectively treat chronic conditions and other pathological states
CC	without the co-administration of substance P, and reduce the number of
CC	activated receptors while not reducing the number of quiescent NK-1
CC	receptors. Receptors not chronically stimulated are less affected,
CC	reducing side effects of treatment. ABK63834-ABK63906 represent NK-1
XX	receptor coding sequences and oligonucleotides of the invention
XX	
SQ	Sequence 20 BP; 6 A; 3 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.6; DB 1; Length 20;

Best Local Similarity 78.9%; Pred. NO. 5.5e+02;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 861 CGTAGTGGAGATCCACTA 879
| | | | | | | | | | | | | | |
Db 20 CATAGTGTGATCCCACTA 2

RESULT 544
ABK63874/c
ID ABK63874 standard; DNA; 20 BP.
XX
XX ABK63874;
XX
XX 18-JUN-2002 (first entry)
XX
XX Neurokinin 1 receptor (NK-1) antisense oligonucleotide #19.
XX
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;
KM immune disorder; autoimmune disorder; cardiovascular disorder;
KM vascular disorder; airway disorder; neuropathic disorder; pain;
KM psychiatric disorder; central nervous system disorder; inflammation;
KM respiratory condition; ophthalmic condition; intestinal condition;
KM demyelinating disease; small cell lung cancer; depression;
KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
KM neuro-pathological disorder; stress; antisense; primer; ss.
XX
XX Homo sapiens.
OS
XX WO200213799-A2.
XX
XX 21-FEB-2002.
XX
XX 17-AUG-2001; 2001WO-IB001510.
XX
XX 18-AUG-2000; 2000US-0226086P.
XX
XX (UYMC-) UNIV MCGILL.
XX
XX Henry JL, Cahill CM, Yaeshpal K;
PI
XX WPI; 2002-241835/29.
XX
XX
XX Treating pathological condition involving neurokinin receptor-1, e.g.
PT pain or inflammation, by administering oligonucleotide or a non-
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
PT pathway.
XX
XX Claim 24; Page 65; 100pp; English.

The invention relates to a method of treating a pathological condition characterised partially by involvement of neurokinin receptor-1 (NK-1) receptor, especially treating, attenuating or preventing pain or inflammatory condition. The method comprises administering to a mammal, a compound chosen from an oligonucleotide, its analogue, and a disruptor which interferes with function or production of NK-1 receptors. The method is useful for treating a pathological condition characterised by involvement of NK-1 receptor such as dermatological, immune, autoimmune, cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic, psychiatric and central nervous system disorders (e.g. anxiety, psychosis, schizophrenia), gut inflammation, arthritis, and central or peripheral aspects of chronic or acute pain, and for treating, attenuating or preventing pain or inflammation such as peripheral, chronic, acute pain or inflammation, neuropathic pain, inflammation or pain relating to psychiatric disorders and central nervous system disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia in a mammal, in particular human. NK-1 receptor related disorders, diseases, or pathological conditions treatable by this method include respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic conditions (e.g. conjunctivitis), cutaneous/dermatological conditions (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and Crohn's disease), cardiovascular conditions (stroke), chronic gastrointestinal tract inflammation, and inflammatory diseases such as

CC inflammatory bowel diseases. Other disorders and diseases include
CC cardiovascular pathologies including stroke, chronic inflammatory
CC diseases such as rheumatoid arthritis, demyelinating diseases such as
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity
CC disorders such as allergies and poison ivy, vasospastic diseases such as
CC angina, addiction disorders such as alcoholism, neurodegenerative
CC disorders such as acquired immune deficiency syndrome (AIDS) related
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
CC disorders such as peripheral neuropathy, oedema, stress related and
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides
CC effectively treat chronic conditions and other pathological states
CC without the co-administration of substance P, and reduce the number of
CC activated receptors while not reducing the number of quiescent NK-1
CC receptors. Receptors not chronically stimulated are less affected,
CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1
CC receptor coding sequences and oligonucleotides of the invention
XX
XX Sequence 20 BP; 6 A; 3 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 5.5e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 861 CGTAGTGGAGATCCACTA 879
| | | | | | | | | | | | | | |
Db 20 CATAGTGTGATCCCACTA 2

RESULT 545
ABK63855
ID ABK63855 standard; DNA; 20 BP.
XX
XX ABK63855;
XX
XX 18-JUN-2002 (first entry)
XX
XX Neurokinin 1 receptor (NK-1) sense oligonucleotide #6.
XX
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;
KM immune disorder; autoimmune disorder; cardiovascular disorder;
KM vascular disorder; airway disorder; neuropathic disorder; pain;
KM psychiatric disorder; central nervous system disorder; inflammation;
KM respiratory condition; ophthalmic condition; intestinal condition;
KM demyelinating disease; small cell lung cancer; depression;
KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
KM neuro-pathological disorder; stress; antisense; primer; ss.
XX
XX Homo sapiens.
OS
XX WO200213799-A2.
XX
XX 21-FEB-2002.
XX
XX 17-AUG-2001; 2001WO-IB001510.
XX
XX 18-AUG-2000; 2000US-0226086P.
XX
XX (UYMC-) UNIV MCGILL.
XX
XX Henry JL, Cahill CM, Yaeshpal K;
PI
XX WPI; 2002-241835/29.
XX
XX
XX Treating pathological condition involving neurokinin receptor-1, e.g.
PT pain or inflammation, by administering oligonucleotide or a non-
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
PT pathway.
XX
XX Claim 24; Page 20; 100pp; English.

The invention relates to a method of treating a pathological condition characterised partially by involvement of neurokinin receptor-1 (NK-1)

receptor, especially treating, attenuating or preventing pain or inflammatory condition. The method comprises administering to a mammal, a compound chosen from an oligonucleotide, its analogue, and a disruptor which interferes with function or production of NK-1 receptors. The method is useful for treating a pathological condition characterised by involvement of NK-1 receptor such as dermatological, immune, autoimmune, cardiovascular, vascular disorders (e.g. migraine), allergy, neuropathic, psychiatric and central nervous system disorders (e.g. anxiety, psychosis, schizophrenia), gut inflammation, arthritis, and central or peripheral aspects of chronic or acute pain, and for treating, attenuating or preventing pain or inflammation such as peripheral, chronic, acute pain or inflammation, neuropathic pain, inflammation or pain relating to psychiatric disorders and central nervous system disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia in a mammal, in particular human. NK-1 receptor related disorders, diseases, or pathological conditions treatable by this method include respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic conditions (e.g. conjunctivitis), cutaneous/dermatological conditions (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and Crohn's disease), cardiovascular conditions (stroke), chronic gastrointestinal tract inflammation, and inflammatory diseases such as inflammatory bowel diseases. Other disorders and diseases include cardiovascular pathologies including stroke, chronic inflammatory diseases such as rheumatoid arthritis, demyelinating diseases such as multiple sclerosis, small cell lung cancer, depression, hypersensitivity disorders such as allergies and poison ivy, vasospastic diseases such as angina, addition disorders such as alcoholism, neurodegenerative disorders such as acquired immune deficiency syndrome (AIDS) related dementia, epilepsy, Alzheimer's disease, and other neuro-pathological disorders such as peripheral neuropathy, edema, stress related and somatic disorders, and osteoarthritis. Antisense oligonucleotides effectively treat chronic conditions and other pathological states without the co-administration of substance P, and reduce the number of activated receptors while not reducing the number of quiescent NK-1 receptors. Receptors not chronically stimulated are less affected, reducing side effects of treatment. ABK63834-ABK63906 represent NK-1 receptor coding sequences and oligonucleotides of the invention

Query Match 0.7%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 5.5e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

861 CGTAGTGGGATCAGACTA 879
1 CATAGTGTGATCCACACTA 19

RESULT 546
AEE77702/C
ID AEE77702 standard; DNA; 20 BP.
AC AEE77702;
DT 09-FEB-2006 (first entry)
XX Human dopamine receptor D2 (DRD2) DNA oligonucleotide SEQ ID NO:1323.
DE Human dopamine receptor D2 (DRD2) DNA oligonucleotide; psychiatric disorder;
XX neuropsychologic disorder; dopamine receptor D2; DRD2; ss.
XX Homo sapiens.
OS Homo sapiens.
XX WO2005118843-A1.
XX 15-DEC-2005.
PD 01-JUN-2005; 2005WO-AU000775.
PF 01-JUN-2004; 2004AU-00902919.
PR 01-JUN-2004; 2004AU-00902919.
XX (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
PA

Morris CP, Van Daal A, Swagell CD, Lawford BR, Young RM; WPI; 2006-047555/05.

Identifying genetic profile associated with a neurological, psychiatric, or psychological condition, comprises screening individuals for a polymorphism in a genetic locus comprising the dopamine receptor D2 (DRD2) gene.

Claim 31; SEQ ID NO 1323; 634bp; English.

The invention relates to a method of identifying a genetic profile associated with a neurological, psychiatric or psychological condition, phenotype or state including a sub-threshold neurological, psychiatric or psychological condition, phenotype or state in an individual, comprising screening individuals for a polymorphism in a genetic locus comprising the dopamine receptor D2 (DRD2) gene. The invention also relates to a genetic mutation providing a genetic marker for a neurological, psychiatric, or psychological condition, state or phenotype in an individual, where the presence of a 957C polymorphism is indicative of a predisposition to developing a neurological, psychiatric or psychological condition, phenotype or state. The compositions and methods are useful for identifying a genetic profile associated with a neurological, psychiatric or psychological condition. The method enables clinicians to make a genetic-based diagnosis and can thereby implement treatment or preventative or symptom-ameliorating protocols to reduce the adverse consequences of the condition. This sequence represents a human dopamine receptor D2 (DRD2) DNA oligonucleotide used in the scope of the invention.

Query Match 0.7%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 5.5e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1047 GAAGAAGTTATCCAGCAG 1065
20 GAAGAAGGCGACCCAGCAG 2

RESULT 547
AEE77704/C
ID AEE77704 standard; DNA; 20 BP.
AC AEE77704;
DT 09-FEB-2006 (first entry)
XX Human dopamine receptor D2 (DRD2) DNA oligonucleotide SEQ ID NO:1325.
DE Human dopamine receptor D2 (DRD2) DNA oligonucleotide; psychiatric disorder;
XX neuropsychologic disorder; dopamine receptor D2; DRD2; ss.
XX Homo sapiens.
OS Homo sapiens.
XX WO2005118843-A1.
XX 15-DEC-2005.
PD 01-JUN-2005; 2005WO-AU000775.
PF 01-JUN-2004; 2004AU-00902919.
PR 01-JUN-2004; 2004AU-00902919.
XX (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
XX Morris CP, Van Daal A, Swagell CD, Lawford BR, Young RM;
XX WPI; 2006-047555/05.
XX Identifying genetic profile associated with a neurological, psychiatric,
PT

PT		or psychological condition, comprises screening individuals for a
PT		polymorphism in a genetic locus comprising the dopamine receptor D2
PT		(DRD2) gene.
P5		Claim 31; SEQ ID NO 1325; 634pp; English.
XX		
CC	The invention relates to a method of identifying a genetic profile	
CC	associated with a neurological, psychiatric or psychological condition,	
CC	phenotype or state including a sub-threshold neurological, psychiatric or	
CC	psychological condition, phenotype or state in an individual, comprising	
CC	screening individuals for a polymorphism in a genetic locus comprising	
CC	the dopamine receptor D2 (DRD2) gene. The invention also relates to a	
CC	genetic mutation providing a genetic marker for a neurological,	
CC	psychiatric, or psychological condition, state or phenotype in an	
CC	individual, where the presence of a 957C polymorphism is indicative of a	
CC	predisposition to developing a neurological, psychiatric or psychological	
CC	condition, phenotype or state. The compositions and methods are useful	
CC	for identifying a genetic profile associated with a neurological,	
CC	psychiatric or psychological condition. The method enables clinicians to	
CC	make a genetic-based diagnosis of a neurological, psychiatric or	
CC	psychological condition and can thereby implement treatment or	
CC	preventative or symptom-ameliorating protocols to reduce the adverse	
CC	consequences of the condition. This sequence represents a human dopamine	
CC	receptor D2 (DRD2) DNA oligonucleotide used in the scope of the	
CC	invention.	
SQ	Sequence 20 BP; 1 A; 7 C; 4 G; 8 T; 0 U; 0 Other;	
XX		
XX		
OY	Query Match 0.7%; Score 12.6; DB 1; Length 20;	
	Best Local Similarity 78.9%; Pred. No. 5.5e+02;	
Dd	Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
	1046 TGAAGAGTTTATCCAGCA 1064 19 TGAAGAGCGCACGCA 1	
RESULT 548		
ABZ58817		
ID	ABZ58817 standard; DNA; 14 BP.	
AC		
XX	ABZ58817;	
DT		
XX	28-APR-2003 (first entry)	
DE		
NX	Nucleotide sequence of oligonucleotide Sse83871-PvuII-Sse83871.	
KW	Gene delivery; adeno-associated virus; AAV; therapeutic protein; muscle;	
RW	acid alpha-glucosidase; type II glycogen storage disease; cytosstatic;	
XX	Pompe's disease; cardiomyopathy; ss.	
OS	Synthetic.	
NN		
PN	MO9726337-A1.	
XX		
PD	24-JUL-1997.	
XX		
PE	17-JAN-1997; 97WO-US000895.	
XX		
PR	18-JAN-1996; 96US-00588355.	
PR	16-JAN-1997; 97US-00784757.	
PA		
RA	(AVIDG-) AVIDGEN INC.	
XX	(UYJO) UNITV JOHNS HOPKINS.	
XX		
PI	Podsakoff GM, Kessler PD, Byrne BJ, Kurtzman GJ;	
XX		
DR	WPI, 1997-385340/35.	
PT		
PT	Delivering gene to muscle cell or tissue - using recombinant adeno-	
PT	associated viron encoding therapeutic gene, e.g for acid alpha-	
PT	glucosidase for treating glycogen storage disease type II.	
XX		

Disclousre; Page 35, 76pp; English.

The invention relates to production of a composition for delivering a gene (I) to muscle cell or tissue and involves mixing (a) recombinant adeno-associated virus (AAV) virion consisting of an AAV vector including (1) Linked to suitable control elements and (b) a vehicle. (I) is delivered to skeletal muscle (myoblasts or myocytes), smooth muscle or cardiac muscle (cardiomyocytes). It is under control of a muscle-specific or inducible promoter, e.g. the promoter of the myod gene or steroid-responsive elements. The virions are used to express therapeutic proteins in muscle, specifically acid alpha-glucosidase in cardiomyocytes (for treating type II glycogen storage disease (Pompe's disease), an inherited cardiomyopathy caused by deficiency of acid alpha-glucosidase), but also erythropoietin and more generally any protein capable of treating endocrine, metabolic, haematological and cardiovascular diseases, including e.g. AIDS, cancer and diabetes, including delivery of antigens for immunisation. The virions are injected directly into muscle or they are used to transduce cells in vitro for subsequent return to the patient. The present sequence represents an oligonucleotide used in the construction of a vector pJ909adhlaC2

Sequence 14 BP; 2 A; 5 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 315 GGACGCTGCCTACA 328
Db 1 GGACGCTGCCTGCA 14
|||||
|||

RESULT 549
AAT79147/C
ID AAT79147 standard; DNA; 14 BP.
XX
AC AAT79147;
XX
DT 08-OCT-1997 (first entry)
DE - Human VEGF cDNA antisense oligonucleotide A217N.
XX
KW Human; vascular endothelial growth factor; VEGF; antisense; preparation;
KM oligonucleotide; ss.
XX
OS Synthetic.
OS
PN JP09154579-A.
PN
PD 17-JUN-1997.
XX
PF 05-JUL-1996; 96JP-00195419.
XX
PR 03-OCT-1995; 95JP-00279752.
XX
PA (TOAG) TOA GOSEI CHEM IND LTD.
XX
WP1. 1997-375653/35.
XX
PT Method for preparing an anti-sense nucleic acid - useful for preventing
XX expression of a target gene.
PS Example; Page 18; 25pp; Japanese.
XX
CC The present sequence is an oligonucleotide antisense to human vascular
CC endothelial growth factor (hVEGF) cDNA. It was prepared by hybridising
CC several random nucleotide sequences to DNA or RNA encoding a target
CC protein, i.e. hVEGF cDNA, to obtain hybridising antisense
CC oligonucleotides, which preferably prevent the expression of the target
CC protein, and optionally lysing the hybridisation site with a nucleic acid
CC degrading substance
XX
SQ Sequence 14 BP; 4 A; 5 C; 1 G; 4 T; 0 U; 0 Other;
XX

Query Match	Similarity	92.9%	Score 12.4	DB 1	Length 14
Best Local	Similarity	92.9%	Pred. No. 2.8e+02		
Matches	13	Conservative	0	Mismatches	1
				Indels	0
				Gaps	0
QY	468 AGTGTGAACTTCA	481			
DQ	14 AGTGTGAACTTCA	1			
RESULT 550					
AAK54378	AAK54378 standard; DNA; 14 BP.				
XX	AAK54378;				
XX	05-JUL-1999 (first entry)				
DT					
DE	NK-KB antisense oligonucleotide fragment.				
KM	Antisense oligonucleotide; multiple target; antisense treatment;				
KM	impaird respiration; inflammation; lung disease;				
KM	pulmonary vasoconstriction; inflammation; allergic rhinitis;				
KM	acute asthma; allergy; asthma; impeded respiration;				
KM	respiratory distress syndrome; pain; cystic fibrosis;				
KM	pulmonary hypertension; pulmonary vasoconstriction; emphysema;				
KM	chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;				
KM	colorectal cancer; breast cancer; lung cancer; pancreatic cancer;				
KM	hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;				
XX	prostate cancer; ss.				
OS	Synthetic.				
PN	WO913086-A1.				
XX	25-MAR-1999.				
PD	17-SEP-1998; 98WC-US019419.				
PF	17-SEP-1997; 97US-0059160P.				
PR	09-JUN-1998; 98US-00093972.				
PA	(UYEC-) UNIV EAST CAROLINA.				
XX					
PI	Nyce JM;				
XX	WPI; 1999-229400/19.				
DR	New antisense oligonucleotides used in treatment of, e.g. pulmonary				
PT	vasoconstriction.				
PS	Disclosure; Page 63; 120pp; English.				
XX					
CC	The specification describes antisense oligonucleotides (AAK52869-X55271)				
CC	directed against at least 2 mRNAs selected from target genes, coding and				
CC	non-coding regions of RNAs corresponding to target genes, gene initiation				
CC	codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'				
CC	-end and the juxta-section between coding and non-coding regions and all				
CC	segments of RNAs encoding proteins associated with one or more diseases,				
CC	conditions or mixtures. The antisense oligonucleotides may be derived				
CC	from sequences AAK55272-74. These multiple target oligonucleotides				
CC	(specifically AAK55180-271) can be used for the antisense treatment of				
CC	diseases and conditions. Typical diseases and conditions are those				
CC	associated with impaired respiration and inflammation, including lung				
CC	diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,				
CC	acute asthma, allergies, asthma, impeded respiration, respiratory				
CC	distress syndrome, pain, cystic fibrosis, pulmonary hypertension,				
CC	pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary				
CC	cancer (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g				
CC	colon cancer, breast cancer, lung cancer, pancreatic cancer,				
CC	hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, at				
CC	well as all types of cancers which may metastasize or have metastasized				
CC	to the lungs, including breast and prostate cancer				

XX Sequence 14 BP; 0 A; 5 C; 5 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 344 CCTCTGTGTGGGCGC 357
|||||
Db 1 CCTCTGTGTGGGCGC 14
RESULT 551
AAA33822
ID AAA33822 standard; DNA; 14 BP.
XX
AC AAA33822;
XX
DT 28-JUL-2000 (first entry)
DE
Low adenosine antisense oligonucleotide SEQ ID NO:1511.
XX
XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
XX phosphorothioate; impaired respiration; inflammation; allergy;
XX allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
XX antiallergic; antiasthmatic; cyostatic; analgesic; impaired airway;
XX lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
XX respiratory distress syndrome; pain; cystic fibrosis; emphysema;
XX pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
XX cancer; leukaemia; lymphoma; carcinoma; metastasis; BS.
XX
OS Homo sapiens.
XX
XX WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US017712.
XX
PR 03-AUG-1998; 98US-0095212P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
XX New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers.
XX
XX Claim 18; Page 453; 1343pp; English.
PS
XX The present invention describes a new composition comprising an antisense
XX oligonucleotide (ON) with low adenosine (up to 15%), which targets
XX nucleic acids involved in bronchoconstriction, allergies, and/or
XX inflammation. The ON can have antiinflammatory, antiallergic,
XX antiasthmatic, cyostatic and analgesic activities. The compositions are
XX useful for the treatment of diseases associated with inflammation,
XX impaired airways, including lung disease and diseases whose secondary
XX effects afflict the lungs of a subject. They can be used for treating
XX e.g. ischemic conditions, pulmonary vasoconstriction, allergies, asthma,
XX impaired respiration, respiratory distress syndrome, pain, cystic
XX fibrosis, pulmonary hypertension, emphysema, chronic obstructive
XX pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
XX carcinomas, and cancers which may metastasise to the lungs, including
XX breast and prostate cancer. The reduction of the adenosine content of the
XX ONs reduces side effects. The A-containing ONs break down with the
XX release of deoxyadenosine which activates adenosine receptors causing
XX bronchoconstriction and inflammation. AAA33313 to AAA35312 represent the
XX nucleotide sequences given in the sequence listing from the present
XX invention, which correspond to SEQ ID NO:1 to 2815, and then the last 1653

CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1680 (AAA2323 to AAA3392) are specifically claimed ONS from the present invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence listing

CC XX Sequence 14 BP; 0 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 14;

Best Local Similarity 92.9%; Pred. No. 2.8e+02; Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 344 CCTCTGCTGGCGC 357

Db 1 CCTCTGCTGGCGC 14

RESULT 552

AAZ64750 standard; RNA; 14 BP.

XX AAZ64750;

DT 28-MAR-2000 (first entry)

XX Substrate for hairpin ribozyme which cleaves HCV at nt. 2740.

XX Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;

KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;

KW autoimmune disease; se.

XX Hepatitis C virus.

XX W0955847-A2.

PD 04-NOV-1999.

XX 26-APR-1999; 99WO-US009027.

XX 27-APR-1998; 98US-0083217P.

PR 18-SEP-1998; 98US-0100842P.

PR 25-FEB-1999; 99US-00257608.

PR 23-MAR-1999; 99US-00274553.

XX (RIBO-) RIBOZYME PHARM INC.

XX Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Macejak D;

XX WPI; 2000-062023/05.

XX Novel ribozymes for the treatment of diseases and conditions related to

XX hepatitis C infection.

XX Claim 2; Page 96; 123pp; English.

XX The present sequence represents the preferred target sequence of an

XX enzymatic nucleic acid, especially a hairpin ribozyme, which cleaves the

XX Hepatitis C virus (HCV) RNA sequence at the base position given in the

XX descriptor line. The HCV sequence was screened for optimal ribozyme

XX target sites using a computer folding algorithm and regions of the mRNA

XX which did not form secondary folding structures and contained potential

XX ribozyme cleavage sites were identified. Ribozymes were synthesized to

XX target these sites and their activities optimised by either varying the

XX length of the binding arms or by modification to prevent degradation by

XX nucleases. The ribozymes of the invention inhibit gene expression and/or

XX viral replication, and are used to treat diseases associated with

XX Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and

XX hepatocellular carcinoma. The ribozymes may be used in combination with

XX interferon to treat HCV infection, other infectious diseases, autoimmune

XX diseases, and cancer

XX Sequence 14 BP; 0 A; 5 C; 4 G; 0 T; 5 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 14;

Best Local Similarity 57.1%; Pred. No. 2.8e+02; Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 685 CTCCTGCTGGCGCTT 698

Db 1 CTCCTGCTGGCGCTT 14

RESULT 553

AAZ65593 standard; DNA; 14 BP.

XX AAZ65593;

DT 30-MAR-2000 (first entry)

XX Immunosuppressant inhibitor oligonucleotide VEGF-638.

XX Immunosuppressant inhibitor, transforming growth factor beta; TGF beta;

KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;

KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;

KW monocyte chemoattractant protein-1; MCP-1; ulcerative colitis; diabetes;

KW glomerulonephritis; acute respiratory distress syndrome; se;

XX atherosclerosis.

XX Unidentified.

XX W09963975-A2.

PD 16-DEC-1999.

XX 10-JUN-1999; 99WO-EP004013.

XX 10-JUN-1998; 98EP-00110709.

PR 25-JUL-1998; 98EP-00113974.

XX (BIOG-) BIOGNOSTIK GBS BIOMOLEKULARE DIAGNOSTIK.

XX Schlingensiepen K, Schlingensiepen R, Brysch W;

XX WPI; 2000-097470/08.

XX Composition containing immune stimulant and inhibitor of agent that

XX adversely affects the immune response, for treating cancers and

XX infections.

XX Claim 10; Fig 1; 30pp; English.

XX This sequence is an immunosuppressant inhibitor oligonucleotide, which is

XX used in the invention. The invention relates to a composition which

XX contains at least one inhibitor (less than 100 kb) of a substance (e.g.

XX transforming growth factor TGF-beta, vascular endothelial growth factor

XX VEGF, interleukin-10, IL-10, prostaglandin E2 PGE2, or their receptors)

XX that adversely affects the immune response. The composition also includes

XX at least one stimulant that positively affects the immune response. This

XX oligonucleotide is an example of an inhibitor that is used in the

XX composition. The composition is used as an immunostimulant for the

XX treatment of neoplasms and infections, particularly hyperproliferation;

XX leukemias; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,

XX colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,

XX breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,

XX malignant melanoma, brain tumours and sarcomas. The oligonucleotides,

XX most of which are directed against TGFbeta or VEGF, are inhibitors of

XX monocyte chemoattractant protein-1 (MCP-1) and are useful as anti-

XX inflammatory for treating e.g. asthma, Crohn's disease, ulcerative

XX colitis, diabetes, glomerulonephritis, acute respiratory distress

XX syndrome and the formation of atherosclerotic plaque

XX Sequence 14 BP; 0 A; 8 C; 1 G; 5 T; 0 U; 0 Other;

XX Query Match 0.7%; Score 12.4; DB 1; Length 14;

CC interferon alpha, beta or gamma or consensus interferon. The present
CC sequence represents a substrate for a HCV hairpin (HP) ribozyme. Note:
CC Some of the sequence data for this patent did not form part of the
CC printed specification. The complete sequence data for this patent was
CC obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/?seqDataEntry.html
XX
SQ Sequence 14 BP; 0 A; 5 C; 4 G; 0 T; 5 U; 0 Other;
Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 57.1%; Pred. No. 2.8e+02;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 685 CTCCTGCTGGCCTT 698
DB 1 CUCCUCUGGCGGU 14
RESULT 556
ABR76511
ID ABR76511 standard; RNA; 14 BP.
XX
AC ABR76511;
XX
DT 22-SEP-2005 (first entry)
XX
DE Hepatitis C virus hairpin ribozyme substrate sequence.
XX
KM ribozyme; enzymatic nucleic acid molecule; hepatitis C virus infection;
KM antiviral; gene therapy; substrate; ss.
XX
OS Hepatitis C virus.
XX
PN US002013458-A1.
XX
PD 31-JAN-2002.
XX
PF 15-FEB-2000; 2000US-00504231.
XX
PR 23-MAR-1999; 99US-00274553.
XX
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
PA (ROBE/) ROBERTS E.
PA (PAVO/) PAVO P A.
PA (MACE/) MACEJACK D.
XX
PI Blatt L, Mcswigen JA, Roberts E, Pavo PA, Macejack D;
XX
DR WPI; 2002-215899/27.
XX
PT New enzymatic nucleic acid molecule, which specifically cleaves minus
PT strand RNA derived from hepatitis C virus, useful for modulating the
PT expression and/or replication of hepatitis C virus.
XX
PS Example 1; Page 43; 65pp; English.
XX
PS The invention relates to an enzymatic nucleic acid molecule which
CC specifically cleaves minus strand RNA derived from hepatitis C virus
CC (HCV). The binding arms of the molecule comprise ribozyme sequences. The
CC molecule is selected from inozyme, G-cleaver, DNazyme, Amberzyme, and
CC zinczyme motifs. Also described: (1) a pharmaceutical composition
CC comprising the novel enzymatic nucleic acid; (2) a mammalian cell
CC including a nucleic acid sequence encoding at least one enzymatic
CC nucleic acid molecule, in a manner, which allows expression of that
CC molecule; (4) a mammalian cell including an expression vector of (3); (5)
CC methods for treating cirrhosis, liver failure or hepatocellular carcinoma
CC by administering to a patient the novel enzymatic nucleic acid or the
CC vector of (3); (6) a method of treating a patient having a condition
CC associated with HCV infection, by contacting cells of the patient with
CC the nucleic acid molecule, and further employing one or more drug
CC therapies; (7) a method for inhibiting HCV replication in a mammalian

CC cell by administering the novel enzymatic nucleic acid; and (8) a method
CC of cleaving a separate RNA molecule by contacting the novel enzymatic
CC nucleic acid with the separate RNA molecule. The enzymatic nucleic acid
CC is useful for modulating the expression and/or replication of hepatitis C
CC virus (HCV), and for inhibiting the expression of HCV minus strand. The
CC nucleic acid may also be used to treat or prevent the occurrence of a
CC disease state in a patient. The present sequence represents an HCV
CC hairpin ribozyme target substrate sequence which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 14 BP; 0 A; 5 C; 4 G; 0 T; 5 U; 0 Other;
Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 57.1%; Pred. No. 2.8e+02;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 685 CTCCTGCTGGCCTT 698
DB 1 CUCCUCUGGCGGU 14
RESULT 557
ABZ72766
ID ABZ72766 standard; RNA; 14 BP.
XX
AC ABZ72766;
XX
DT 09-APR-2003 (first entry)
XX
DE Rod opsin hairpin ribozyme target oligonucleotide SEQ ID NO:6.
XX
KM Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;
KM ophthalmological; gene therapy; eye; retinal dysfunction; AAV;
KM diabetic retinopathy; macular degeneration; autosomal dominant retinitis;
KM blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.
XX
OS Homo sapiens.
XX
PN WO200288320-A2.
XX
PD 07-NOV-2002.
XX
PF 01-MAY-2002; 2002MO-US013679.
XX
PR 01-MAY-2001; 2001US-00847601.
XX
PA (UYFL) UNIV FLORIDA.
XX
PI Lewin AS, Shaw LC, Grant MB;
XX
DR WPI; 2003-111880/10.
XX
PT A recombinant adeno-associated virus-vectorized ribozyme composition,
PT useful for treating a disease or dysfunction of the mammalian eye e.g.
PT retinal disease, e.g. diabetic retinopathy or age-related macular
PT degeneration.
XX
PS Claim 1; Page 61; 115pp; English.
XX
PS The present invention describes a recombinant adeno-associated virus
CC (AAV) vectorized ribozyme composition (I). (I) comprises: (a) at least a
CC first ribozyme that specifically cleaves an mRNA encoding a protein,
CC polypeptide, or peptide selected from the group of rod opsin, inos,
CC RGS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin
CC alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a
CC vector comprising a polynucleotide encoding the ribozyme, where the
CC polynucleotide operably positioned downstream of at least a first
CC promoter that directs expression of the polynucleotide in a selected
CC mammalian cell transformed with the vector; (c) a viral particle
CC comprising the ribozyme or the polynucleotide; (d) an AAV vector
CC comprising the ribozyme or the polynucleotide; or (e) a host cell
CC comprising the ribozyme or the polynucleotide. Also described is a method
CC for decreasing the amount of mRNA encoding a selected polypeptide in a

CC retinal cell of a mammalian eye, comprising providing to the eye the
CC composition described above, and for a time effective to specifically
CC cleave the mRNA in the cell. (I) has ophthalmological activity, and can
CC be used in gene therapy. (I) can be used for treating a disease or
CC dysfunction of the mammalian eye, such as a retinal disease or retinal
CC dysfunction, (diabetic) retinopathy, or (age-related) macular
CC degeneration. (I) is also useful for manufacturing a medicament for
CC treating the diseases mentioned above, including autosomal dominant
CC retinitis or a blood-retinal barrier dysfunction. (I) can also be useful
CC for treating, decreasing the severity, or ameliorating the symptoms of a
CC pathological condition, e.g. atrophic or pigmented lesions of the eye,
CC blindness, a reduction in central or peripheral vision, or a reduction in
CC total vision. AB2726763 to AB272953 represent sequences used in the
CC exemplification of the present invention
CC
CC
CC Sequence 14 BP; 0 A; 6 C; 3 G; 0 T; 5 U; 0 Other;
CC
CC

```

AS      Sequence 14 BP; 0 A; 6 C; 3 G; 0 T; 5 U; 0 Other;
SQ
Query Match          0.7%;    Score 12.4; DB 1; Length 14;
Best Local Similarity 64.3%;   Pred. No. 2.8e+02;
Matches    9; Conservative 4; Mismatches 1; Indels 0; Gaps 0.

```

```
QY      689 TGCTGGCCTTCCCC 702
          :||:| | :|||
Db      1  UGCGGUCUCCCC 14
```

RESULT 558
ABZ95638
ID ABZ95638 standard; DNA; 14 BP.

AC	ABZ95638;
XX	
DT	17-OCT-2003 (first entry)

Human NF-kappaB antisense fragment no.1502.

Human; antisense; lung dysfunction; nasal airway dysfunction;
antiflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
antislammatic; hypocensive; immunosuppressive; cytostatic; gene therapy;
antisense gene therapy; respiratory; lung; adenosine sensitivity;
adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
lung inflammation; respiratory disease; ds-

OS Homo sapiens.

PN WO200285308-A2.

PD 31-OCT-2002

PF 23-APR-2002; 2002WO-US013135

PR 24-APR-2001; 2001US-0286137P.

PA (EPIG-) EPIGENESIS PHARM INC.

PI	Nyce JW,	Li Y,	Sandrasagra A,	Katz E,	Pabalan J,	Aguilar D,
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DR WPI; 2003-229219/22.

AA Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ublquinone.

PS Disclosure; SEQ ID NO 10880; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has as first active agent comprising an oligonucleotide antisense to the CC initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of CC junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an

antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiaesthetic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antitense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine or receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIGO at [ftp.wigo.int/pub/published_pct_sequences](http://wigo.int/pub/published_pct_sequences)

Sequence	14 BP, 0 A, 5 C, 5 G, 4 T, 0 U, 0 Other;
Query Match	0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity	92.9%; Pred. NO. 2.8e+02;
Matches	13, Conservative 1, Indels 0, Gaps 0,

QY	344	CCTCTGTGGTGGGC	357
Db	1	CCTCTGTGGTGGGC	14

RESULT 559
ABD19802
ID ABD19802 standard; DNA; 14 BP.

AC ABD19802;

DT 29-JUL-2004 (first entry)

Human NF- κ B DNA fragment 1502

Human; antisense; bronchoconstriction; allergy; hyposecretion; pain; respiratory tract inflammation; adenosine sensitivity; lung; cancer; surfactant depletion; antiatheric; antiinflammatory; antiasthmatic; analgesic; hypotensive; immunosuppressive; cysteal; cystic fibrosis; beta-adrenergic agonist; respiratory disease; pulmonary vasculostic; respiratory distress syndrome; allergic rhinitis; pulmonary hypertension; emphysema; chronic obstructive pulmonary disease; cancer; bronchitis; pulmonary transplantation rejection; ds.

OS Homo sapiens

PN WO200285309-A2

PD 31-OCT-2002.

PF 23-APR-2002; 2002WO-US013143.

PR 24-APR-2001; 2001US-0286036P

PA (EPIG-) EPIGENESIS PHARM INC.

PI Nyce JW, Li Y, Sandrasagra A, Kacz E, Padarath O, Aguilar D,

DR WPI; 2003-093058/08

PT
PT
PT
PT
PT

Pharmaceutical composition for treating asthma, has antihense
oligonucleotide containing less percentage of adenosine, targeted to
nuclear acids associated with lung airway or lung dysfunction, and
bronchodilating agent.

Claim 15; SEQ ID NO 10880; 763pp; English

AA this invention describes a novel composition (a), a first active agent, CC comprising oligonucleotides, effective for alleviating allergies and CC comprising oligonucleotides, effective for alleviating allergies and CC bronchoconstriction, respiratory tract inflammation, allergies and CC bronchoconstriction, respiratory tract inflammation, allergies and CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors

CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it

XX
SQ Sequence 14 BP; 0 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 344 CCTCTGTGTGGGC 357
|||||
1 CCTCTGTGTGGGC 14

Db

RESULT 560
AD285160
ID AD285160 standard; DNA; 14 BP.
XX
AC AD285160;
XX
DT 28-JUL-2005 (first entry)
XX
DE MODY 3 diabetes-associated probe, SEQ ID 36.
XX
KM Analyte detection; microarray; probe; ss; diabetes.
XX
OS Unidentified.
XX
PN US2005112677-A1.
XX
PD 26-MAY-2005.
XX
PF 22-NOV-2004; 2004US-00994626.
XX
PR 22-NOV-2003; 2003KR-00083356.
XX
PA (SHIM/) SHIM J.
XX
PI Shim J;
XX
DR WPI; 2005-403357/41.
XX
PT Substrate for use in optically detecting target materials, comprises an
PT oxide layer having thickness that may vary to wavelength of excitation
PT light used.
XX
PS Example 1; SEQ ID NO 36; 20pp; English.
XX
CC The present invention relates to a novel substrate having an oxide layer.

CC which is useful in optically detecting a target material. The thickness
CC of the oxide layer may vary to the wavelength of excitation light used.
CC Also claimed is a method for detecting a target material, comprising
CC immobilizing a probe material on a substrate, reacting the immobilized
CC probe material and the target material, illuminating a reaction product
CC with excitation light, and measuring light emitted from the reaction
CC product by the excitation light. In an example from the invention,
CC microarrays were fabricated by forming fused silica (SiO2) layers on
CC silicon wafers, followed by linkage with a coupling agent and
CC immobilization of oligonucleotide probes. The microarrays were then
CC incubated with labeled oligonucleotide and exposed to excitation light,
CC and light emitted from the target oligonucleotides was measured, to
CC evaluate the intensity of detected signals with respect to the thickness
CC of the SiO2 layers. AD285128-AD285203, MODY 3 diabetes-associated probes
CC used with the target sequence of human glyceraldehyde-3-phosphate
CC dehydrogenase (GAPDH), were used to show that when a target
CC oligonucleotide is detected using a microarray including a substrate with
CC an oxide layer a good signal is obtained compared to that with no oxide
CC layers.

XX
SQ Sequence 14 BP; 5 A; 1 C; 8 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1307 AGGAGAGCCGAG 1320
|||||
1 AGGAGAGCCGAG 14

Db

RESULT 561
AEB01280
ID AEB01280 standard; DNA; 14 BP.
XX
AC AEB01280;
XX
DT 08-SEP-2005 (first entry)
XX
DE VEGF inhibition oligonucleotide SEQ ID NO 124.
XX
KM pharmaceutical; cell death; neoplasm; ss; Cytostatic; Apoptotic;
KM Immunostimulant; Antiarthritic; Antirheumatic; Antiproliferative;
KM TGF-beta antagonist; Vaccine.
XX
OS Synthetic.
XX
PN WO2005059133-A2.
XX
PD 30-JUN-2005.
XX
PF 20-DEC-2004; 2004WO-BP053604.
XX
PR 19-DEC-2003; 2003BP-00029367.
XX
PR 05-FEB-2004; 2004US-0541771P.
XX
PA (ANTISENSE PHARMA GMBH.
XX
PI Schlingensiepen K, Schlingensiepen R;
XX
DR WPI; 2005-479334/48.
XX
PT Pharmaceutical composition useful for treating neoplasm, comprises
PT stimulators stimulating function of immune system and/or immune cells and
PT substances inhibiting cell proliferation and/or inducing cell death.
XX
PS Claim 4; SEQ ID NO 124; 46pp; English.
XX
CC The invention relates to a pharmaceutical composition (PC) comprising one
CC or more stimulators that stimulate the function of immune system and/or
CC immune cells and one or more substances inhibiting cell proliferation
CC and/or inducing cell death. A pharmaceutical composition is useful for
CC treating neoplasms chosen from solid tumors; blood born tumors such as

CC leukemias, acute or chronic myeloid or lymphoblastic leukemia; tumor
 CC metastasis; benign tumors; or is chosen from bile duct carcinoma, bladder
 CC carcinoma, brain tumor, breast carcinoma, bronchogenic carcinoma,
 CC carcinoma of kidney, choriocarcinoma, cystadenocarcinoma, embryonal
 CC carcinoma, epithelial carcinoma, esophageal carcinoma, cervical
 CC carcinoma, colon carcinoma, colorectal carcinoma, endometrial carcinoma, liver
 CC gallbladder carcinoma, gastric carcinoma, head and neck carcinoma, liver
 CC carcinoma, lung carcinoma, medullary carcinoma, non-small cell
 CC bronchogenic/lung carcinoma, ovarian carcinoma, pancreas carcinoma, small
 CC papillary carcinoma, papillary adenocarcinoma, prostate carcinoma, skin
 CC intestine carcinoma, rectal carcinoma, renal cell carcinoma, skin
 CC carcinoma, small-cell bronchogenic/lung carcinoma, squamous cell
 CC carcinoma, sebaceous gland carcinoma, testicular carcinoma, uterine
 CC carcinoma, rheumatoid arthritis and psoriasis. The present sequence
 CC represents a VEGF inhibition oligonucleotide.

XX
 XX Sequence 14 BP; 0 A; 8 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 14;
 Best Local Similarity 92.9%; Pred. No. 2.8e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1008 CTTCTCTCTCTGC 1021
 1 CTCCTCTCTCTGC 14

Db

RESULT 562
 AEC63812
 ID AEC63812 standard; DNA; 14 BP.

AC AEC63812;
 XX 17-NOV-2005 (first entry)
 XX
 XX Novel microarray-related oligonucleotide probe SeqID49.
 DE
 XX DNA detection; DNA chip; DNA microarray; probe; ss.
 XX
 OS Unidentified.
 XX
 PN US2005202492-A1.
 XX
 PD 15-SEP-2005.
 XX
 PF 11-MAR-2005; 2005US-00078601.
 XX
 PR 12-MAR-2004; 2004KR-00017026.

PA (NAMT/) NAM Y.
 PA (HUHN/) HUH N.
 PA (SHIM/) SHIM H.
 PA (OHUJ/) OH J.
 XX
 XX Nam Y, Huh N, Shim H, Oh J;
 PI
 DR WPI; 2005-618101/63.

XX Polynucleotide microarray for photolithographic or spotting method,
 PT comprises probe polynucleotides spots capable of binding to same target
 PT polynucleotide immobilized on microarray.

XX Example; SEQ ID NO 49; 25pp; English.

XX This invention relates to a novel polynucleotide microarray comprising at
 CC least two probe polynucleotides capable of binding to the same target
 CC polynucleotide immobilized on the microarray. A spot region on a
 CC substrate of the polynucleotide microarray is segmented into blocks
 CC arranged in rows and columns adjacent to each other. The blocks are
 CC separated and a space is formed between the blocks. The microarray may be
 CC used for photolithographic or spotting methods and provides good
 CC analytical results of a target nucleic acid. The present sequence is that
 CC of an oligonucleotide probe which was used during the exemplification of

CC the novel microarrays of the invention.

XX
 XX Sequence 14 BP; 5 A; 1 C; 8 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 14;
 Best Local Similarity 92.9%; Pred. No. 2.8e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1307 AGGAGGAGCCAGAG 1320
 1 AGGAGGAGCCAGAG 14

Db

RESULT 563
 AAQ70347/c
 ID AAQ70347 standard; DNA; 15 BP.

AC AAQ70347;
 XX
 XX 25-MAR-2003 (revised)
 DT 15-FEB-1995 (first entry)
 XX
 XX Antisense oligonucleotide for mouse FGF.

DE
 XX Fibroblast growth factor; hybridisation; laser procedures;
 XX vascular smooth muscle cell; proliferation; SMC; vascular stenosis;
 XX post angioplasty restenosis; atherosclerosis; cardiac hypertrophy;
 XX organ transplant; ss.
 XX
 OS Synthetic.
 XX
 PN WO9415945-A1.
 XX
 PD 21-JUL-1994.
 XX
 PF 28-DEC-1993; 93WO-US012600.
 XX
 PR 31-DEC-1992; 92US-00999706.
 XX
 XX (TEXA-) TEXAS BIOTECHNOLOGY CORP.
 PA
 PI Denner LA, Rege AA, Dixon RA;
 XX
 DR WPI; 1994-249123/30.

XX New anti-sense polynucleotide(s) to fibroblast growth factor receptor -
 PT used for inhibiting vascular smooth muscle cell proliferation, partic.
 PT for treating restenosis.

XX Claim 3; Page 9; 53pp; English.

XX The sequence is an antisense molecule directed against position +1 to
 CC +15, relative to the start codon of the gene for mouse fibroblast growth
 CC factor 1. The polynucleotide can be used for inhibiting vascular smooth
 CC muscle cell proliferation and for treating a disease e.g. vascular
 CC stenosis, post angioplasty restenosis, atherosclerosis, arteriosclerosis,
 CC arterial venous shunt failure, cardiac hypertrophy, vascular surgery and
 CC organ transplant. See also AAQ70333-60. (Updated on 25-MAR-2003 to
 CC correct PN field.)

XX
 XX Sequence 15 BP; 3 A; 8 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 3.3e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1202 ATGAGGAGGCTGGA 1215
 15 ATGAGGAGGCTGGA 2

Db

RESULT 564
 AA66605

XX AAX66605 standard; RNA, 15 BP.
XX AAX66605;
XX 20-JUL-1999 (first entry)
XX
DE Human CD40 hammerhead ribozyme target SEQ ID NO:3237.
XX
XX Arthritic condition; graft tolerance; immune response; target; cleavage;
XX hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;
XX streptomycin; synovial membrane; joint; arthritis; osteoarthritis;
XX rheumatoid arthritis; autoimmune disease; allergy; inflammation;
XX diagnosis; ss.
XX Homo sapiens.
XX
XX MO9618736-A2.
XX
XX 20-JUN-1996.
XX
XX 22-NOV-1995; 95WO-US015516.
XX
XX 13-DEC-1994; 94US-00354920.
XX 23-DEC-1994; 94US-00363253.
XX 17-FEB-1995; 94US-00363254.
XX 20-APR-1995; 95US-00390850.
XX 02-MAY-1995; 95US-00426124.
XX 04-MAY-1995; 95US-00432874.
XX 07-JUL-1995; 95US-0000951P.
XX 07-JUL-1995; 95US-0000974P.
XX 07-AUG-1995; 95US-00512861.
XX 05-OCT-1995; 95US-00541365.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Beigelman L, Stinchcomb DT, Jarvis T, Draper K, Pavco P,
XX Mewissen J, Gustofson J, Usman N, Wincott F, Matulic-Adamic J,
XX Karpetsky A, Thompson JD, Modak A, Burgin A;
XX
XX WPI; 1996-300653/30.
XX
XX Enzymatic nucleic acid molecules having a hammer-head motif - used for
XX the treatment of arthritis, induction of graft tolerance or treatment of
XX auto-immune diseases.
XX
XX Claim 10; Page 204; 307pp; English.
XX
XX The present invention describes a novel enzymatic nucleic acid (ENA)
XX having a hammerhead motif (HM) comprising: (i) at least 5 ribose residues
XX ; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii) at least
XX ten 2'-O-methyl modifications; and (iv) a 3'-end modification. The ENA's
XX can inhibit collagenase and streptomycin production in the synovial
XX membrane of joints for the treatment or prevention of arthritis,
XX particularly osteoarthritis or rheumatoid arthritis. The ENA's can also
XX be used to treat antigen presenting cells of a donor to induce tolerance
XX in a recipient to an alloantigen of a donor. They can also be used for
XX enhancing graft tolerance or for treating autoimmune disease, and for
XX treating allergies and other inflammatory conditions. The ENA's can also
XX be used in diagnosis. Ribozyme therapy impacts on the expression of
XX streptomycin without introducing the non-specific effects upon gene
XX expression which accompany treatment with retinoids and dexamethasone.
XX The concentration of ribozyme required to affect a therapeutic treatment
XX is lower than that required of antisense molecules, and is highly
XX specific. The present sequence is used in the exemplification of the
XX present invention
XX
XX Sequence 15 BP; 2 A; 5 C; 2 G; 0 T; 6 U; 0 Other;
XX
XX Query Match 0.74; Score 12.4; DB 1; Length 15;
XX Best Local Similarity 57.1%; Pred. No. 3.3e+02;
XX Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

XX 1409 GCCTCTCTCCCAT 1422
XX
XX Db
XX 2 GCUCUCUCUCAU 15
XX
XX RESULT 565
XX
XX AAX66802
XX ID AAX66802 standard; RNA, 15 BP.
XX
XX AAX66802;
XX
XX 20-JUL-1999 (first entry)
XX
XX Mouse CD40 hammerhead ribozyme target SEQ ID NO:3434.
XX
XX Arthritic condition; graft tolerance; immune response; target; cleavage;
XX hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;
XX streptomycin; synovial membrane; joint; arthritis; osteoarthritis;
XX rheumatoid arthritis; autoimmune disease; allergy; inflammation;
XX diagnosis; ss.
XX
XX Mus sp.
XX
XX
XX MO9618736-A2.
XX
XX 20-JUN-1996.
XX
XX 22-NOV-1995; 95WO-US015516.
XX
XX 13-DEC-1994; 94US-00354920.
XX 23-DEC-1994; 94US-00363253.
XX 17-FEB-1995; 94US-00363254.
XX 20-APR-1995; 95US-00390850.
XX 02-MAY-1995; 95US-00426124.
XX 04-MAY-1995; 95US-00432874.
XX 07-JUL-1995; 95US-0000951P.
XX 07-JUL-1995; 95US-0000974P.
XX 07-AUG-1995; 95US-00512861.
XX 05-OCT-1995; 95US-00541365.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Beigelman L, Stinchcomb DT, Jarvis T, Draper K, Pavco P,
XX Mewissen J, Gustofson J, Usman N, Wincott F, Matulic-Adamic J,
XX Karpetsky A, Thompson JD, Modak A, Burgin A;
XX
XX WPI; 1996-300653/30.
XX
XX Enzymatic nucleic acid molecules having a hammer-head motif - used for
XX the treatment of arthritis, induction of graft tolerance or treatment of
XX auto-immune diseases.
XX
XX Claim 10; Page 209; 307pp; English.
XX
XX The present invention describes a novel enzymatic nucleic acid (ENA)
XX having a hammerhead motif (HM) comprising: (i) at least 5 ribose residues
XX ; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii) at least
XX ten 2'-O-methyl modifications; and (iv) a 3'-end modification. The ENA's
XX can inhibit collagenase and streptomycin production in the synovial
XX membrane of joints for the treatment or prevention of arthritis,
XX particularly osteoarthritis or rheumatoid arthritis. The ENA's can also
XX be used to treat antigen presenting cells of a donor to induce tolerance
XX in a recipient to an alloantigen of a donor. They can also be used for
XX enhancing graft tolerance or for treating autoimmune disease, and for
XX treating allergies and other inflammatory conditions. The ENA's can also
XX be used in diagnosis. Ribozyme therapy impacts on the expression of
XX streptomycin without introducing the non-specific effects upon gene
XX expression which accompany treatment with retinoids and dexamethasone.
XX The concentration of ribozyme required to affect a therapeutic treatment
XX is lower than that required of antisense molecules, and is highly
XX specific. The present sequence is used in the exemplification of the
XX present invention

XX SQ Sequence 15 BP; 2 A; 6 C; 1 G; 0 T; 6 U; 0 Other;
Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 57.1%; Pred. No. 3.3e+02;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 1409 GCTTCTCTCCCAT 1422
Db 1 GCUUCUUCUCCAU 14
RESULT 566
AAK65304/C
ID AAK65304 standard; RNA; 15 BP.
XX AC AAK65304;
XX DT 20-JUL-1999 (first entry)
XX DE Mouse B7-1 hammerhead ribozyme target SEQ ID NO:1936.
XX KW Arthritic condition; graft tolerance; immune response; target; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;
KW streptomycin; synovial membrane; joint; arthritis; osteoarthritis;
KW rheumatoid arthritis; autoimmune disease; allergy; inflammation;
KW diagnosis; ss.
XX OS Mus sp.
XX PN WO9618736-A2.
XX PD 20-JUN-1996.
XX PF 22-NOV-1995; 95WO-US015516.
XX PR 13-DEC-1994; 94US-00354920.
PR 23-DEC-1994; 94US-00363253.
PR 23-DEC-1994; 94US-00363254.
PR 17-FEB-1995; 95US-00390850.
PR 20-APR-1995; 95US-00426124.
PR 02-MAY-1995; 95US-00434509.
PR 04-MAY-1995; 95US-0000951P.
PR 07-JUL-1995; 95US-0000974P.
PR 07-JUL-1995; 95US-00512861.
PR 07-AUG-1995; 95US-00541365.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Beigelman L, Stinchcomb DT, Jarvis T, Draper K, Payco P;
PI Mcswiggen J, Gustofson J, Usman N, Wincott F, Matulic-Adamic J;
PI Karpelsky A, Thompson JD, Modak A, Burgin A;
XX DR WPI; 1996-300653/30.
XX PT Enzymatic nucleic acid molecules having a hammer-head motif - used for
PT the treatment of arthritis, induction of graft tolerance or treatment of
PT auto-immune diseases.
XX PS Claim 10; Page 179; 307pp; English.

CC be used in diagnosis. Ribozyme therapy impacts on the expression of
CC streptomycin without introducing the non-specific effects upon gene
CC expression which accompany treatment with retinoids and dexamethasone.
CC The concentration of ribozyme required to affect a therapeutic treatment
CC is lower than that required of antisense molecules, and is highly
CC specific. The present sequence is used in the exemplification of the
CC present invention
XX SQ Sequence 15 BP; 5 A; 4 C; 3 G; 0 T; 3 U; 0 Other;
Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 296 CCTGGCAATTGTC 309
Db 14 CCTGGCAATTGTC 1
RESULT 567
AAK66801
ID AAK66801 standard; RNA; 15 BP.
XX AC AAK66801;
XX DT 20-JUL-1999 (first entry)
XX DE Mouse CD40 hammerhead ribozyme target SEQ ID NO:3433.
XX KW Arthritic condition; graft tolerance; immune response; target; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;
KW streptomycin; synovial membrane; joint; arthritis; osteoarthritis;
KW rheumatoid arthritis; autoimmune disease; allergy; inflammation;
KW diagnosis; ss.
XX OS Mus sp.
XX PN WO9618736-A2.
XX PD 20-JUN-1996.
XX PF 22-NOV-1995; 95WO-US015516.
XX PR 13-DEC-1994; 94US-00354920.
PR 23-DEC-1994; 94US-00363253.
PR 23-DEC-1994; 94US-00363254.
PR 17-FEB-1995; 95US-00390850.
PR 20-APR-1995; 95US-00426124.
PR 02-MAY-1995; 95US-00434509.
PR 04-MAY-1995; 95US-0000951P.
PR 07-JUL-1995; 95US-0000974P.
PR 07-JUL-1995; 95US-00512861.
PR 07-AUG-1995; 95US-00541365.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Beigelman L, Stinchcomb DT, Jarvis T, Draper K, Payco P;
PI Mcswiggen J, Gustofson J, Usman N, Wincott F, Matulic-Adamic J;
PI Karpelsky A, Thompson JD, Modak A, Burgin A;
XX DR WPI; 1996-300653/30.
XX PT Enzymatic nucleic acid molecules having a hammer-head motif - used for
PT the treatment of arthritis, induction of graft tolerance or treatment of
PT auto-immune diseases.
XX PS Claim 10; Page 209; 307pp; English.

CC	can inhibit collagenase and stromelysin production in the synovial
CC	membrane of joints for the treatment or prevention of arthritis,
CC	particularly osteoarthritis or rheumatoid arthritis. The ENA's can also
CC	be used to treat antigen presenting cells of a donor to induce tolerance
CC	in a recipient to an alloantigen of a donor. They can also be used for
CC	enhancing graft tolerance or for treating autoimmune disease, and for
CC	treating allergies and other inflammatory conditions. The ENA's can also
CC	be used in diagnosis. Ribozyme therapy impacts on the expression of
CC	stromelysin without introducing the non-specific effects upon gene
CC	expression which accompany treatment with retinoids and dexamethasone.
CC	The concentration of ribozyme required to affect a therapeutic treatment
CC	is lower than that required of antisense molecules, and is highly
CC	specific. The present sequence is used in the exemplification of the
CC	present invention
CC	
SO	Sequence 15 BP; 2 A; 5 C; 2 G; 0 T; 6 U; 0 Other;
XX	
XX	
Qy	1409 GCCTCTCCTCCAAAT 1422
Db	: : :
	2 GCUCUCUCUCCAAU 15
RESULT 568	
AA65303/C	
ID	AA65303 standard; RNA; 15 BP.
XX	
AC	AA65303;
XX	
DT	20-JUL-1999 (first entry)
XX	
DE	Mouse B7-1 hammerhead ribozyme target SEQ ID NO:1935.
XX	
KW	Arthritic condition; graft tolerance; immune response; target; cleavage;
KW	hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;
KW	stromelysin; synovial membrane; joint; arthritis; osteoarthritis;
KW	rheumatoid arthritis; autoimmune disease; allergy; inflammation;
KW	diagnosis; ss.
XX	
OS	Mus sp.
XX	
PN	WO9618736-A2.
XX	
PD	20-JUN-1996.
XX	
PF	22-NOV-1995; 95MO-US015516.
XX	
PR	13-DEC-1994; 94US-00354920.
PR	23-DEC-1994; 94US-00363253.
PR	23-DEC-1994; 94US-00363254.
PR	17-FEB-1995; 95US-00390850.
PR	20-APR-1995; 95US-00426124.
PR	02-MAY-1995; 95US-00432874.
PR	04-MAY-1995; 95US-00434509.
PR	07-JUL-1995; 95US-0000951P.
PR	07-JUL-1995; 95US-0000974P.
PR	07-AUG-1995; 95US-00512861.
PR	05-OCT-1995; 95US-00541365.
XX	
PA	(RIBO-) RIBOZYME PHARM INC.
XX	
P1	Belgelman J, Scinchcomb DT, Jarvis T, Draper K, Payco P;
P1	McWeilgen J, Gustofson J, Usman N, Wincoft F, Matulic-Adamic J;
P1	Karpelesky A, Thompson JD, Modak A, Burgin A;
XX	
DR	WPI: 1996-300653/30.
XX	
PT	Enzymatic nucleic acid molecules having a hammer-head motif - used for
PT	the treatment of arthritis, induction of graft tolerance or treatment of
PT	auto-immune diseases.

[illegible]

CC ratio of intensity of the donor and acceptor fluorescence peaks is
CC measured to indicate the amount of interaction of the donor and acceptor
CC labels, which is a measure of the quantity of probes which are hybridised
CC to the completed RNA molecules. The process provides a highly sensitive
CC and simple method for monitoring the progress of RNA transcription in
CC vitro
XX
SQ Sequence 15 BP; 5 A; 2 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Gy 1155 CTTCAAGCATGCT 1168
Db 14 CTTCAAGCATGCT 1
RESULT 572
AAV48607/C
ID AAV48607 standard; DNA; 15 BP.
XX
AC AAV48607;
XX
XX 15-OCT-1998 (first entry)
DT
XX
DE jund gene antisense oligonucleotide Jund-24.
XX
XX jund; jund; antisense oligonucleotide; modulate; gene expression; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX EP856579-A1.
XX
PD 05-AUG-1998.
XX
XX 31-JAN-1997; 97EP-00101531.
XX
XX 31-JAN-1997; 97EP-00101531.
XX
PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
PI Schlingensiepen K, Brysch W;
XX
XX WPI; 1998-400910/35.
XX
XX Preparation of antisense oligo:nucleotide(s) which lack long runs of
XX consecutive guanosine or inosine - and have specific ratio of residues
XX able to form two or three hydrogen bonds, have greater activity and
XX reduced toxicity, used therapeutically or to modulate growth of cells in
XX culture.
XX
PS Claim 10; Fig 5a; 286pp; English.
XX
XX AAV48564-708 represent antisense oligonucleotides directed against the
XX jund and jund genes. Of these, only oligonucleotides AAV48565-614
XX resulted in effective downregulation of negative growth control by jund
XX or jund, while AAV48615-708 had little effect. The oligonucleotides
XX exemplify the invention. The specification describes oligonucleotides
XX that contain 8-30 nucleotides, which contain at most 8 nucleotides that
XX can each form three hydrogen bonds to cytosine; do not contain four
XX consecutive nucleotides able to form three H-bonds each to four
XX consecutive cytosines; do not contain two sequences of three consecutive
XX nucleotides each able to form three H-bonds to three consecutive
XX cytosines, and the ratio between residues able to form two H-bonds each
XX (2R) or three such bonds (3R) is given by 2R/3R = 0.33-0.72. The
XX oligonucleotides are used to modulate expression of genes, particularly
XX the genes for p53, ErbB-2, jund, jund, TGF-beta 1 or beta 2 to control
XX proliferation of primary cell cultures (e.g. bone marrow stem, liver or
XX kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The
XX oligonucleotides can also be used to analyse function of proteins (by
XX altering their expression or activity) and therapeutically, e.g. in cases

CC of cancer or (targeting TGF) for stimulating the immune system
XX
SQ Sequence 15 BP; 1 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Gy 936 CAAGCGCAAGCTGG 949
Db 14 CAAGCGCAAGCTGG 1
RESULT 573
AAAX31113/C
ID AAAX31113 standard; DNA; 15 BP.
XX
AC AAAX31113;
XX
XX 21-MAY-1999 (first entry)
DT
XX
DE Tag sequence of a transcript increased in colorectal cancer.
XX
XX Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;
XX diagnosis; prognosis; treatment; ss.
XX
OS Homo sapiens.
XX
XX WO9853319-A2.
XX
PD 26-NOV-1998.
XX
XX 20-MAY-1998; 98WO-USO10277.
XX
XX 21-MAY-1997; 97US-0047352P.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Vogelstein B, Kinzler KW;
XX
XX WPI; 1999-070161/06.
XX
XX Use of isolated gene transcripts - useful for developing products for the
XX diagnosis, prognosis and treatment of cancers, particularly colon and
XX pancreatic cancer.
XX
PS Claim 2; Page 31; 120pp; English.
XX
XX AAX30947-31815 represent tag sequences of transcripts that are
XX differentially expressed in colorectal cancer, in pancreatic cancer, or
XX in both. The tag sequences can be used to identify genes by matching the
XX tag to a gen data base member, or by using the tag sequences as probes to
XX isolate unidentified genes from cDNA libraries. The tag sequences can
XX also be used in a method for diagnosing colon or pancreatic cancer in a
XX sample suspected of being neoplastic. The method comprises comparing the
XX level of at least one transcript in a first sample of a tissue to a
XX second sample, where the first sample is a colonic tissue suspected of
XX being neoplastic and the second sample is a normal human colonic tissue.
XX The transcript is identified by a tag selected from AAX30947-31815. The
XX methods of the invention can be used in the diagnosis, prognosis and
XX treatment of cancer
XX
SQ Sequence 15 BP; 4 A; 6 C; 2 G; 3 T; 0 U; 0 Other;
Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Gy 367 GTGATGTCATCAT 380
Db 15 GCGATGTCATCAT 2

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RESULT 574
AAA07158/c
ID AAA07158 standard; DNA, 15 BP.
XX
AC AAA07158;
XX
DT 16-JUN-2000 (first entry)
XX
DE Probe for XELFI-1 alpha mRNA.
XX
DE Probe; Xenopus laevis; elongation factor-1 alpha chain; XELFI-1 alpha;
XX
DE biological activity screening; real-time monitoring; RNA transcription;
XX
DE RNA synthesis; detection; ss.
XX
OS Xenopus laevis.
XX
PN JP2000041700-A.
XX
PD 15-FEB-2000.
XX
PF 31-JUL-1998; 98JP-00218025.
XX
PR 31-JUL-1998; 98JP-00218025.
XX
PA (BUNS-) BUNSHI BIOHOTOINICS KENKYUSHO KK.
XX
DR WPI; 2000-295786/26.
XX
PT Determination and screening of biological activity of a drug, uses real-
XX
PT time monitoring of RNA transcription without electrophoresis.
XX
PS Example 1; Page 13; 25pp; Japanese.
XX
CC This sequence represents a probe for the mRNA encoding the Xenopus laevis
CC elongation factor-1 (XELFI-1 alpha) alpha chain. The invention relates to a
CC method for the determination and screening of the biological activity of
CC a drug, with real-time monitoring of RNA transcription and synthesis
CC without using electrophoresis. The method for the determination and
CC screening of the biological activity of a drug in an RNA transcription
CC and synthesis system, comprises: addition of the test drug to the system
CC to alter the transcription and synthesis of the RNA; and determining the
CC fluorescence of 2 probe sequences capable of hybridizing with the base
CC sequence of the transcribed and synthesized RNA, where one probe is a
CC donor probe labelled with an energy donor fluorescent molecule and the
CC other probe is an acceptor probe labelled with an energy acceptor
CC fluorescent molecule. The method is used for the determination and
CC screening of the biological activity of a drug. The method allows for the
CC automatic determination of the biological activity of a drug
XX
SQ Sequence 15 BP; 5 A; 2 C; 5 G; 3 T; 0 U; 0 Other;
XX
DB
OY 1155 CTTCAAGCAGCCCT 1168
DB 14 CTTCAAGTATGCCCT 1
XX
RESULT 575
AAA66946
ID AAA66946 standard; DNA, 15 BP.
XX
AC AAA66946;
XX
DT 19-OCT-2000 (first entry)
XX
DE Human leukocyte antigen A allele DNA probe A239A SEQ ID NO:4.
XX
DE Human leukocyte antigen; HLA; class I allele type; probe; PCR primer;
XX
DE amplification; hybridisation; organ transplant; gene typing; diagnosis;
XX
DE ss.

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XX
OS Homo sapiens.
XX
PN WO200031295-A1.
XX
PD 02-JUN-2000.
XX
PF 07-OCT-1999; 99WO-IP005527.
XX
PR 26-NOV-1998; 98JP-00335151.
XX
PA (SHIO ) SHIONOGI & CO LTD.
XX
PT Moribe T, Kaneshige T;
XX
DR WPI; 2000-400097/34.
XX
PT Simple, rapid and accurate method for distinguishing HLA class I allele
XX
PT type with possibility of mechanization and automation, applicable in
XX
PT judging donor-recipient compatibility during organ transplant and disease
XX
PT diagnosis.
XX
PS Claim 8; Page 50; 83pp; Japanese.
XX
CC The present invention describes a method for distinguishing a human
XX
CC leukocyte antigen (HLA) class I antigen or allele by a combination of
XX
CC polymerase chain reaction (PCR) using a primer pair whereby all HLA-A, -B
XX
CC or -C alleles can be amplified or using reverse hybridisation analysis
XX
CC comprising a DNA probe covalently bonded to microtitre plate wells which
XX
CC are hybridisable specifically with the base sequence of at least one
XX
CC specific HLA-A, -B or -C allele. The method is applicable in gene typing,
XX
CC judging donor-recipient compatibility during organ transplant and
XX
CC correlation analysis for diagnosis of various diseases. The method is
XX
CC simple, rapid and accurate, with possibility of mechanisation and
XX
CC automation, without the problems encountered by using the prior-art
XX
CC techniques. AAA66943 to AAA67072 represent oligonucleotide probes and PCR
XX
CC primers for use in the method of the present invention
XX
SQ Sequence 15 BP; 4 A; 3 C; 8 G; 0 T; 0 U; 0 Other;
XX
DB
OY 1307 AGGAGGAGCCGAG 1320
DB 2 AGGAGGAGCCGAG 15
XX
RESULT 576
AAF45174/c
ID AAF45174 standard; DNA, 15 BP.
XX
AC AAF45174;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGFBP2 oligonucleotide #13.
XX
DE Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX
DE cytostatic; dermatological; cardiac; virucide; ophthalmological; keloid;
XX
DE skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pituitary;
XX
DE IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilarsis;
XX
DE growth factor mediated cell proliferation; ichthyosis; seborrhoea; rubea;
XX
DE keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX
DE hyperneovascular condition; hyperplasia; kidney disease;
XX
DE neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.

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XX PF 21-JUN-2000; 2000WO-AU000693.
XX XX
XX PR 21-JUN-1999; 99US-0140345P.
XX XX
XX PA (MURDOCH CHILDRENS RES INST.
XX XX
XX PI Wraight CJ, Werther GA, Edmondson SR;
XX XX
XX DR WPI; 2001-041421/05.
XX XX
XX PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
XX PT inhibits or reduces growth factor mediated cell proliferation and/or
XX PT inflammation.
XX XX
XX PS Example 6; Page 34; 201pp; English.
XX XX
XX CC The present invention relates to a method for ameliorating the effects of
XX CC skin disorders. The method comprises contacting the skin with an
XX CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
XX CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX CC inhibiting or reducing growth factor mediated cell proliferation,
XX CC inflammation and/or other disorders. The present sequence is an
XX CC oligonucleotide which can be used to design the antisense
XX CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX CC F45161). The method is useful for ameliorating the effects of psoriasis,
XX CC ichthyosis, pityriasis, ruba, pilaris, seborrhoea, keloids, keratosis,
XX CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX CC hyperneovascular condition such as a neovascular condition of the retina,
XX CC brain or skin, growth factor-mediated malignancies, other sclerotic
XX CC disease, kidney disease, hyperproliferation of the inside of blood
XX CC vessels or any other hyperplasia
XX XX
XX SQ Sequence 15 BP; 6 A; 1 C; 8 G; 0 T; 0 U; 0 Other;
XX XX
XX Query Match 0.7%; Score 12.4; DB 1; Length 15;
XX Best Local Similarity 92.9%; Pred. No. 3.3e+02;
XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1008 CTTCTCTCTCTCTGC 1021
DB 14 CTTCTCTCTCTCTCC 1
XX
XX RESULT 577
XX AAF49868/c
XX ID AAF49868 standard; DNA; 15 BP.
XX XX
XX AC AAF49868;
XX XX
XX DT 30-MAR-2001 (first entry)
XX DE IGF-I oligonucleotide #828.
XX XX
XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX KW cytoostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX KW growth factor mediated cell proliferation; ichthyosis; seborrhoea; ruba;
XX KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX KW hyperneovascular condition; hyperplasia; kidney disease;
XX KW neovascular condition of the retina; ss.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200078341-A1.
XX XX
XX PD 28-DEC-2000.
XX XX
XX PF 21-JUN-2000; 2000WO-AU000693.
XX XX
XX PR 21-JUN-1999; 99US-0140345P.
XX XX
XX PI Wraight CJ, Werther GA, Edmondson SR;

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XX PA (MURDOCH CHILDRENS RES INST.
XX XX
XX PI Wraight CJ, Werther GA, Edmondson SR;
XX XX
XX DR WPI; 2001-041421/05.
XX XX
XX PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
XX PT inhibits or reduces growth factor mediated cell proliferation and/or
XX PT inflammation.
XX XX
XX PS Example 8; Page 66; 201pp; English.
XX XX
XX CC The present invention relates to a method for ameliorating the effects of
XX CC skin disorders. The method comprises contacting the skin with an
XX CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
XX CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX CC inhibiting or reducing growth factor mediated cell proliferation,
XX CC inflammation and/or other disorders. The present sequence is an
XX CC oligonucleotide which can be used to design the antisense
XX CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX CC F45161). The method is useful for ameliorating the effects of psoriasis,
XX CC ichthyosis, pityriasis, ruba, pilaris, seborrhoea, keloids, keratosis,
XX CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX CC hyperneovascular condition such as a neovascular condition of the retina,
XX CC brain or skin, growth factor-mediated malignancies, other sclerotic
XX CC disease, kidney disease, hyperproliferation of the inside of blood
XX CC vessels or any other hyperplasia
XX XX
XX SQ Sequence 15 BP; 0 A; 9 C; 4 G; 2 T; 0 U; 0 Other;
XX XX
XX Query Match 0.7%; Score 12.4; DB 1; Length 15;
XX Best Local Similarity 92.9%; Pred. No. 3.3e+02;
XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 15 GCGGCGAGCGCGGC 28
DB 14 GCGGCGAGCGAGGC 1
XX
XX RESULT 578
XX AAF52635/c
XX ID AAF52635 standard; DNA; 15 BP.
XX XX
XX AC AAF52635;
XX XX
XX DT 30-MAR-2001 (first entry)
XX DE IGF-I oligonucleotide #3595.
XX XX
XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX KW cytoostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX KW growth factor mediated cell proliferation; ichthyosis; seborrhoea; ruba;
XX KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX KW hyperneovascular condition; hyperplasia; kidney disease;
XX KW neovascular condition of the retina; ss.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200078341-A1.
XX XX
XX PD 28-DEC-2000.
XX XX
XX PF 21-JUN-2000; 2000WO-AU000693.
XX XX
XX PR 21-JUN-1999; 99US-0140345P.
XX XX
XX PA (MURDOCH CHILDRENS RES INST.
XX XX
XX PI Wraight CJ, Werther GA, Edmondson SR;

```

XX WPI; 2001-041421/05.
 DR Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 PS Example 8; Page 84; 201pp; English.
 XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, seborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 SQ Sequence 15 BP; 4 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 0.7%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 3.3e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1576 ATTCCATCCTTGAG 1589
 ID | |||||
 DB 14 ACTCCATCCTTGAG 1
 RESULT 579
 AAF54012/C
 ID AAF54012 standard; DNA; 15 BP.
 XX AAF54012;
 AC 30-MAR-2001 (first entry)
 DT IGF-I oligonucleotide #4972.
 XX
 DE Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cyostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; seborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 KM
 XX Homo sapiens.
 OS
 XX WO200078341-A1.
 FN
 XX 28-DEC-2000.
 PD
 XX 21-JUN-2000; 2000WO-AU000693.
 PF
 XX 21-JUN-1999; 99US-0140345P.
 PR
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 PA
 XX Wraight CJ, Werther GA, Edmondson SR;
 PI WPI; 2001-041421/05.
 DR
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering

PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 PS Example 8; Page 93; 201pp; English.
 XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, seborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 SQ Sequence 15 BP; 5 A; 3 C; 6 G; 1 T; 0 U; 0 Other;
 Query Match 0.7%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 3.3e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1403 GCTTCAGCTTCTCC 1416
 ID | |||||
 DB 15 GCTTCAGCTTCTCC 2
 RESULT 580
 AAF49641/C
 ID AAF49641 standard; DNA; 15 BP.
 XX AAF49641;
 AC 30-MAR-2001 (first entry)
 DT IGF-I oligonucleotide #601.
 XX
 DE Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cyostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; seborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 KM
 XX Homo sapiens.
 OS
 XX WO200078341-A1.
 FN
 XX 28-DEC-2000.
 PD
 XX 21-JUN-2000; 2000WO-AU000693.
 PF
 XX 21-JUN-1999; 99US-0140345P.
 PR
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 PA
 XX Wraight CJ, Werther GA, Edmondson SR;
 PI WPI; 2001-041421/05.
 DR
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.

PS Example 8; Page 64; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of

CC skin disorders. The method comprises contacting the skin with an

CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1

CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of

CC inhibiting or reducing growth factor mediated cell proliferation,

CC inflammation and/or other disorders. The present sequence is an

CC oligonucleotide which can be used to design the antisense

CC oligonucleotides of the present invention (see AAF45151 and AAF45153-

CC F45161). The method is useful for ameliorating the effects of psoriasis,

CC ichthyosis, pityriasis, ruba, pilaris, seborrheoa, keloids, keratosis,

CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a

CC hyperneovascular condition such as a neovascular condition of the retina,

CC brain or skin, growth factor-mediated malignancies, other sclerotic

CC disease, kidney disease, hyperproliferation of the inside of blood

CC vessels or any other hyperplasia

CC

SQ Sequence 15 BP; 5 A; 2 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 15;

Best Local Similarity 92.9%; Pred. No. 3.3e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1407 CAGCTTCCTCCCA 1420

Db 15 CGGCTTCTCTCCA 2

RESULT 581

AAF49643/c

ID AAF49643 standard; DNA; 15 BP.

XX AAF49643;

AC

XX 30-MAR-2001 (first entry)

DE IGF-I oligonucleotide #603.

XX

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;

KW cyostatic; dermatological; cardiant; virucide; ophthalmological; keloid;

KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;

KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;

KW growth factor mediated cell proliferation; ichthyosis; seborrheoa; ruba;

KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;

KW hyperneovascular condition; hyperplasia; kidney disease;

KW neovascular condition of the retina; ss.

XX

OS Homo sapiens.

XX

XX WO200078341-A1.

PN

XX 28-DEC-2000.

PD

XX 21-JUN-2000; 2000WO-AU000693.

PF

XX 21-JUN-1999; 99US-0140345P.

PR

XX (MURDOCH CHILDRENS RES INST.

PA

XX Wraight CJ, Werther GA, Edmondson SR;

PI

XX WPI; 2001-041421/05.

DR

XX

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering

PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that

PT inhibits or reduces growth factor mediated cell proliferation and/or

PT inflammation.

XX

XX Example 8; Page 64; 201pp; English.

PS

XX The present invention relates to a method for ameliorating the effects of

CC skin disorders. The method comprises contacting the skin with an

CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1

CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of

CC inhibiting or reducing growth factor mediated cell proliferation,

CC inflammation and/or other disorders. The present sequence is an

CC oligonucleotide which can be used to design the antisense

CC oligonucleotides of the present invention (see AAF45151 and AAF45153-

CC F45161). The method is useful for ameliorating the effects of psoriasis,

CC ichthyosis, pityriasis, ruba, pilaris, seborrheoa, keloids, keratosis,

CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a

CC hyperneovascular condition such as a neovascular condition of the retina,

CC brain or skin, growth factor-mediated malignancies, other sclerotic

CC disease, kidney disease, hyperproliferation of the inside of blood

CC vessels or any other hyperplasia

CC

SQ Sequence 15 BP; 5 A; 2 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 15;

Best Local Similarity 92.9%; Pred. No. 3.3e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1406 TCAGCTTCTCTCC 1419

Db 14 TCGGCTTCTCTCC 1

RESULT 582

AAF54013/c

ID AAF54013 standard; DNA; 15 BP.

XX AAF54013;

AC

XX 30-MAR-2001 (first entry)

DE IGF-I oligonucleotide #4973.

XX

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;

KW cyostatic; dermatological; cardiant; virucide; ophthalmological; keloid;

KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;

KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;

KW growth factor mediated cell proliferation; ichthyosis; seborrheoa; ruba;

KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;

KW hyperneovascular condition; hyperplasia; kidney disease;

KW neovascular condition of the retina; ss.

XX

OS Homo sapiens.

XX

XX WO200078341-A1.

PN

XX 28-DEC-2000.

PD

XX 21-JUN-2000; 2000WO-AU000693.

PF

XX 21-JUN-1999; 99US-0140345P.

PR

XX (MURDOCH CHILDRENS RES INST.

PA

XX Wraight CJ, Werther GA, Edmondson SR;

PI

XX WPI; 2001-041421/05.

DR

XX

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering

PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that

PT inhibits or reduces growth factor mediated cell proliferation and/or

PT inflammation.

XX

XX Example 8; Page 93; 201pp; English.

PS

XX The present invention relates to a method for ameliorating the effects of

CC skin disorders. The method comprises contacting the skin with an

CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1

CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of

CC inhibiting or reducing growth factor mediated cell proliferation,

CC inflammation and/or other disorders. The present sequence is an

CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1

CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of

CC inhibiting or reducing growth factor mediated cell proliferation,

CC inflammation and/or other disorders. The present sequence is an

CC oligonucleotide which can be used to design the antisense

CC oligonucleotides of the present invention (see AAF45151 and AAF45153-

CC F45161). The method is useful for ameliorating the effects of psoriasis,

CC ichthyosis, pityriasis, ruba, pilaris, seborrheoa, keloids, keratosis,

CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a

CC hyperneovascular condition such as a neovascular condition of the retina,

CC brain or skin, growth factor-mediated malignancies, other sclerotic

CC disease, kidney disease, hyperproliferation of the inside of blood

CC vessels or any other hyperplasia

CC

SQ Sequence 15 BP; 5 A; 2 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 15;

Best Local Similarity 92.9%; Pred. No. 3.3e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1406 TCAGCTTCTCTCC 1419

Db 14 TCGGCTTCTCTCC 1

RESULT 582

AAF54013/c

ID AAF54013 standard; DNA; 15 BP.

XX AAF54013;

AC

XX 30-MAR-2001 (first entry)

DE IGF-I oligonucleotide #4973.

XX

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;

KW cyostatic; dermatological; cardiant; virucide; ophthalmological; keloid;

KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;

KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;

KW growth factor mediated cell proliferation; ichthyosis; seborrheoa; ruba;

KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;

KW hyperneovascular condition; hyperplasia; kidney disease;

KW neovascular condition of the retina; ss.

XX

OS Homo sapiens.

XX

XX WO200078341-A1.

PN

XX 28-DEC-2000.

PD

XX 21-JUN-2000; 2000WO-AU000693.

PF

XX 21-JUN-1999; 99US-0140345P.

PR

XX (MURDOCH CHILDRENS RES INST.

PA

XX Wraight CJ, Werther GA, Edmondson SR;

PI

XX WPI; 2001-041421/05.

DR

XX

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering

PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that

PT inhibits or reduces growth factor mediated cell proliferation and/or

PT inflammation.

XX

XX Example 8; Page 93; 201pp; English.

PS

XX The present invention relates to a method for ameliorating the effects of

CC skin disorders. The method comprises contacting the skin with an

CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1

CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of

CC inhibiting or reducing growth factor mediated cell proliferation,

CC inflammation and/or other disorders. The present sequence is an

CC oligonucleotide which can be used to design the antisense
CC oligonucleotide of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
CC
XX Sequence 15 BP; 5 A; 3 C; 6 G; 1 T; 0 U; 0 Other;
SQ
Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1403 GCTTCAGCTCTCC 1416
DB 14 GGTTCAGCTCTCC 1
RESULT 583
AAF45225/c
ID AAF45225 standard; DNA; 15 BP.
AC AAF45225;
XX
XX 30-MAR-2001 (first entry)
DT
XX
DE IGFBP2 oligonucleotide #64.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cyostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200078341-A1.
XX
XX 28-DEC-2000.
XX
XX 21-JUN-2000; 2000WO-AU000693.
XX
XX 21-JUN-1999; 99US-0140345P.
XX
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX
XX Wraight CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
XX inhibits or reduces growth factor mediated cell proliferation and/or
XX inflammation.
XX
XX Example 6; Page 34; 201pp; English.
XX
XX The present invention relates to a method for ameliorating the effects of
XX skin disorders. The method comprises contacting the skin with an
XX antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX inhibiting or reducing growth factor mediated cell proliferation,
XX inflammation and/or other disorders. The present sequence is an
XX oligonucleotide which can be used to design the antisense
XX oligonucleotide of the present invention (see AAF45151 and AAF45153-
XX F45161). The method is useful for ameliorating the effects of psoriasis,
XX ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
XX neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX hyperneovascular condition such as a neovascular condition of the retina,
XX brain or skin, growth factor-mediated malignancies, other sclerotic
XX disease, kidney disease, hyperproliferation of the inside of blood
XX vessels or any other hyperplasia
XX
XX Sequence 15 BP; 5 A; 3 C; 6 G; 1 T; 0 U; 0 Other;
SQ
Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 15 GCGGCGA6CGGCGC 28
DB 14 GCGGCGGCGGCGC 1

CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
CC
XX Sequence 15 BP; 0 A; 10 C; 4 G; 1 T; 0 U; 0 Other;
SQ
Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 15 GCGGCGA6CGGCGC 28
DB 14 GCGGCGGCGGCGC 1
RESULT 584
AAF52480
ID AAF52480 standard; DNA; 15 BP.
AC AAF52480;
XX
XX 30-MAR-2001 (first entry)
DT
XX
DE IGF-1 oligonucleotide #3440.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cyostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200078341-A1.
XX
XX 28-DEC-2000.
XX
XX 21-JUN-2000; 2000WO-AU000693.
XX
XX 21-JUN-1999; 99US-0140345P.
XX
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX
XX Wraight CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
XX inhibits or reduces growth factor mediated cell proliferation and/or
XX inflammation.
XX
XX Example 8; Page 83; 201pp; English.
XX
XX The present invention relates to a method for ameliorating the effects of
XX skin disorders. The method comprises contacting the skin with an
XX antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX inhibiting or reducing growth factor mediated cell proliferation,
XX inflammation and/or other disorders. The present sequence is an
XX oligonucleotide which can be used to design the antisense
XX oligonucleotide of the present invention (see AAF45151 and AAF45153-
XX F45161). The method is useful for ameliorating the effects of psoriasis,
XX ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
XX neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX hyperneovascular condition such as a neovascular condition of the retina,
XX brain or skin, growth factor-mediated malignancies, other sclerotic
XX disease, kidney disease, hyperproliferation of the inside of blood
XX vessels or any other hyperplasia
XX
XX Sequence 15 BP; 0 A; 10 C; 4 G; 1 T; 0 U; 0 Other;
SQ
Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 15 GCGGCGA6CGGCGC 28
DB 14 GCGGCGGCGGCGC 1

CC vessels or any other hyperplasia
XX Sequence 15 BP; 4 A; 5 C; 3 G; 3 T; 0 U; 0 Other;
SQ

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 719 CCACAGAGACCATG 732
Db 2 CCACAGAGACCTTG 15
|||||

RESULT 585
AAF52681/c
ID AAF52681 standard; DNA; 15 BP.
XX
AC AAF52681;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGF-1 oligonucleotide #3641.
XX

KM Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KM cytosstatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KM skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KM IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KM growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KM keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KM hyperneovascular condition; hyperplasia; kidney disease;
KM neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wraight CJ, Werther GA, Edmondson SR;
XX
DR WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
PS Example 8; Page 84; 201pp; English.
XX

CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC neoplasia, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
CC
XX Sequence 15 BP; 0 A; 4 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1315 CCAGAGACGGCCC 1328
Db 14 CCAGAGACGACGCC 1
|||||

RESULT 586
AAF54011/c
ID AAF54011 standard; DNA; 15 BP.
XX
AC AAF54011;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGF-1 oligonucleotide #4971.
XX

KM Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KM cytosstatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KM skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KM IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KM growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KM keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KM hyperneovascular condition; hyperplasia; kidney disease;
KM neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wraight CJ, Werther GA, Edmondson SR;
XX
DR WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
PS Example 8; Page 93; 201pp; English.
XX

CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC neoplasia, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
CC
XX Sequence 15 BP; 5 A; 2 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1405 TTCAGCTTCTCCTC 1418
| | | | | | | | | |
Db 14 TTCAGCTTCTCCTC 1

RESULT 587
AAFA9866/C
ID AAF49866 standard; DNA; 15 BP.
AC AAF49866;
XX
XX 30-MAR-2001 (first entry)
DE IGF-1 oligonucleotide #826.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytoskeletal; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; seborrhoea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
XX Homo sapiens.
OS
XX WO200078341-A1.
PN
XX 28-DEC-2000.
PD
XX 21-JUN-2000; 2000WO-AU000693.
PF
XX 21-JUN-1999; 99US-0140345P.
PR
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX Wraight CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
DR
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
XX Example 8; Page 66; 201pp; English.
PS
XX The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC P45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, seborrhoea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
XX Sequence 15 BP; 0 A; 7 C; 5 G; 3 T; 0 U; 0 Other;
SQ

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 CGGCGAGCGGGCA 29
| | | | | | | | | |
Db 15 CGGCGAGCGAGCA 2

RESULT 588
AAF52634/C
ID AAF52634 standard; DNA; 15 BP.
AC AAF52634;
XX
XX 30-MAR-2001 (first entry)
DE IGF-1 oligonucleotide #3594.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytoskeletal; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; seborrhoea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
XX Homo sapiens.
OS
XX WO200078341-A1.
PN
XX 28-DEC-2000.
PD
XX 21-JUN-2000; 2000WO-AU000693.
PF
XX 21-JUN-1999; 99US-0140345P.
PR
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX Wraight CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
DR
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
XX Example 8; Page 84; 201pp; English.
PS
XX The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC P45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, seborrhoea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
XX Sequence 15 BP; 4 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
SQ

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1576 ATTCCATCCTTGAG 1589
| | | | | | | | | |
Db 15 ACTCCATCCTTGAG 2

RESULT 589
AAF54010/C
ID AAF54010 standard; DNA; 15 BP.

XX	AAFS4010;
XX	
DT	30-MAR-2001 (first entry)
DE	
XX	IGF-I oligonucleotide #4970.
XX	
OS	Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX	Cyclosteric; dermatological; cardiant; vitruclide; ophthalmological; keloid;
KW	skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW	IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW	growth factor mediated cell proliferation; ichthyosis; seborrhoea; rubra;
KW	keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW	hyperneovascular condition; hyperplasia; kidney disease;
XX	neovascular condition of the retina; ss.
XX	
XX	Homo sapiens.
XX	
XX	MO200078341-A1.
PD	
XX	28-DEC-2000.
XX	
PF	21-JUN-2000; 2000WO-AU000693.
XX	
XX	21-JUN-1999; 99US-0140345P.
XX	
PA	(MURDOCH CHILDRENS RES INST.
XX	
PI	Wraight CJ, Werther GA, Edmondson SR;
DR	WPI; 2001-041421/05.
XX	
PT	Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT	UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT	inhibits or reduces growth factor mediated cell proliferation and/or
PT	inflammation.
PS	
XX	Example 8; Page 93; 201pp; English.
XX	
CC	The present invention relates to a method for ameliorating the effects of
CC	skin disorders. The method comprises contacting the skin with an
CC	antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
CC	receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC	inhibiting or reducing growth factor mediated cell proliferation,
CC	inflammation and/or other disorders. The present sequence is an
CC	oligonucleotide of the present invention (see AAF45151 and AAF45153-
CC	45161). The method is useful for ameliorating the effects of psoriasis,
CC	ichthyosis, pityriasis, rubra, pilaris, seborrhoea, keloids, keratosis,
CC	neoplasias, scleroderma, wart, benign growths, cancers of the skin, a
CC	hyperneovascular condition such as a neovascular condition of the retina,
CC	brain or skin, growth factor-mediated malignancies, other sclerotic
CC	disease, kidney disease, hyperproliferation of the inside of blood
XX	vessels or any other hyperplasia
XX	
SO	Sequence 15 BP; 5 A; 1 C; 7 G; 2 T; 0 U; 0 Other;
QY	Query Match 0.7%; Score 12.4; DB 1; Length 15;
	Best Local Similarity 92.9%; Pred. No. 3.3e+02;
	Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB	1405 TTGAGCTTCCTCCTC 1418
	15 TTGAGCTTCCTCCC 2
RESULT 590	
ID	AAF45222/c
XX	AAF45222 standard; DNA; 15 BP.
AC	AAF45222;
XX	
DT	30-MAR-2001 (first entry)

XX	IGFBP2 oligonucleotide #61.
DE	
XX	Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KM	cytostatic; dermatological; cardiant; vitruide; ophthalmological; keloid;
KM	skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pilyriasis;
KM	IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KM	growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KM	keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KM	hyperneovascular condition; hyperplasia; kidney disease;
KM	neovascular condition of the retina; ss.
OS	
XX	Homo sapiens.
XX	
PM	WO200078341-A1.
XX	
PD	28-DEC-2000.
XX	
PF	21-JUN-2000; 2000WO-AU000693.
XX	
PR	21-JUN-1999; 99US-0140345P.
XX	
PA	(MURD-) MURDOCH CHILDRENS RES INST.
PI	Wraight CJ, Werther GA, Edmondson SR;
XX	
DR	WPI; 2001-041421/05.
XX	
PT	Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT	UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT	inhibits or reduces growth factor mediated cell proliferation and/or
PT	inflammation.
XX	
PS	Example 6; Page 34; 201pp; English.
XX	
CC	The present invention relates to a method for ameliorating the effects of
CC	skin disorders. The method comprises contacting the skin with an
CC	antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
CC	receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC	inhibiting or reducing growth factor mediated cell proliferation,
CC	inflammation and/or other disorders. The present sequence is an
CC	oligonucleotide which can be used to design the antisense
CC	oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC	F4161). The method is useful for ameliorating the effects of psoriasis,
CC	ichthyosis, pilyriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC	neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC	hyperneovascular condition such as a neovascular condition of the retina,
CC	brain or skin, growth factor-mediated malignancies, other sclerotic
CC	disease, kidney disease, hyperproliferation of the inside of blood
CC	vessels or any other hyperplasia
XX	
SQ	Sequence 15 BP; 0 A; 11 C; 3 G; 1 T; 0 U; 0 Other;
XX	
Query Match	0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity	92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
QY	17 GGCGAGGCGGGCAG 30
DB	15 GGCGGGCGGGCAG 2
XX	
RESULT 591	
AAFS2679/c	
ID	AAFS2679 standard; DNA, 15 BP.
XX	
AAFS2679;	
XX	
AC	
XX	
DT	30-MAR-2001 (first entry)
XX	
DE	IGF-I oligonucleotide #3639.
XX	
XX	Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;

KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wright CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
PS Example 8; Page 84; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, ptyriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
CC
SQ Sequence 15 BP; 0 A; 5 C; 6 G; 4 T; 0 U; 0 Other;
Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1316 CAGAGGACGGCCCC 1329
DB 15 CAGAGGACGACCCCC 2
RESULT 592
AAF45172/C
ID AAF45172 standard; DNA; 15 BP.
XX
AC AAF45172;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGFBP2 oligonucleotide #11.
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;

KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wright CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
PS Example 6; Page 34; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, ptyriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
CC
SQ Sequence 15 BP; 7 A; 0 C; 8 G; 0 T; 0 U; 0 Other;
Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1009 TTCTTCTCTCTGCC 1022
DB 15 TTCTTCTCTCTGCC 2
RESULT 593
AAF52482
ID AAF52482 standard; DNA; 15 BP.
XX
AC AAF52482;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGF-I oligonucleotide #3442.
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX

OS Homo sapiens.
 XX WO200078341-A1.
 PN 28-DEC-2000.
 PD 21-JUN-2000; 2000WO-AU000693.
 XX 21-JUN-1999; 99US-0140345P.
 PR (MURDOCH CHILDRENS RES INST.
 XX Wraight CJ, Werther GA, Edmondson SR;
 PI WPI; 2001-041421/05.
 DR
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX
 PS Example 8; Page 83; 201pp; English.
 XX
 CC The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design cell proliferation,
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC leishmaniasis, pityriasis, rubea, pilaris, seborrhoea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 CC
 SQ Sequence 15 BP; 4 A; 5 C; 3 G; 3 T; 0 U; 0 Other;
 XX
 QY
 Query Match 0.7%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 3.3e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 DB 720 CACAGAGACCATGC 733
 1 CACAGAGACCTGC 14
 XX
 RESULT 594
 AAF70390/C
 ID AAF70390 standard; DNA; 15 BP.
 XX
 AC AAF70390;
 XX
 DT 20-APR-2001 (first entry)
 XX
 DE Human DRD2 allele specific oligonucleotide primer SEQ ID NO:133.
 XX
 KW Human; dopamine receptor D2; DRD2; polymorphism; allele specific;
 KW drug target isogene; detection; single nucleotide polymorphism; SNP;
 KW genotype; schizophrenia; Parkinson's disease; myoclonus dystonia; MD;
 KW probe; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200105832-A1.
 XX
 PD 25-JAN-2001.
 XX
 PF 19-JUL-2000; 2000WO-US019644.
 XX

PR 19-JUL-1999; 99US-0144493P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Chew A, Denton RR, Duda A, Nandabalan K, Stephens JC;
 XX WPI; 2001-091967/10.
 DR
 XX
 PS Claim 15; Page 24; 135pp; English.
 XX
 CC The present invention describes polynucleotides comprising single
 CC nucleotide polymorphisms (SNPs) in the human dopamine receptor D2 (DRD2).
 CC The polynucleotides may be used in assays to detect and characterize
 CC polymorphisms in DRD2 that affect its expression and activity and are
 CC involved in disorders such as schizophrenia, Parkinson's and myoclonus
 CC dystonia (MD). This information would be useful for studying the
 CC biological function of DRD2 as well as in identifying drugs targeting
 CC this protein for the treatment of disorders related to its abnormal
 CC expression or function. Polymorphisms in the DRD2 gene affect the
 CC advantageous to detect polymorphisms in the DRD2 gene and how those
 CC polymorphisms are combined in different copies of the gene. AAF70261 to
 CC AAF70308 represent human DRD2 allele specific oligonucleotide probes, and
 CC AAF70309 to AAF70404 represent human DRD2 allele specific oligonucleotide
 CC primers which are used in the detection of DRD2 polymorphisms. AAF70405
 CC to AAF70452 represent oligonucleotide primers for the detection of human
 CC DRD2 polymorphisms which are given in the exemplification of the present
 CC invention. AAF70453 to AAF70538 represent PCR primers for the human DRD2
 CC gene which are used in examples from the present invention
 CC
 SQ Sequence 15 BP; 1 A; 8 C; 2 G; 4 T; 0 U; 0 Other;
 XX
 QY
 Query Match 0.7%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 3.3e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 DB 879 ATGGGCCAGTGAG 892
 14 AGGGGCCAGTGAGA 1
 XX
 RESULT 595
 AAF69430
 ID AAF69430 standard; DNA; 15 BP.
 XX
 AC AAF69430;
 XX
 DT 18-APR-2001 (first entry)
 XX
 DE Human IL4Ralpha gene probe #70.
 XX
 KW Polymorphism; human; interleukin 4 receptor-alpha; IL4R-alpha;
 KW allergic disease; probe; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200104270-A1.
 XX
 PD 18-JAN-2001.
 XX
 PF 13-JUL-2000; 2000WO-US019094.
 XX
 PR 13-JUL-1999; 99US-0143435P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Chew A, Denton RR, Duda A, Nandabalan K, Stephens JC;
 XX Windemuth AK;
 XX

DR WPI, 2001-103078/11.
XX New isolated polynucleotide useful for the identification of therapeutics
PT in allergic diseases is new.
XX
PS Claim 15; Page 43; 188pp; English.
XX
CC The present invention relates to polymorphisms of the human interleukin 4
CC receptor-alpha gene (IL4R-alpha; see AAF57718 for the reference
CC sequence). Polynucleotides comprising polymorphic gene variants are
CC useful for therapeutic purposes. For example, where a patient may benefit
CC from expression of a particular IL4Ralpha protein isoform, an expression
CC vector encoding the isoform may be administered to the patient. It may
CC desirable to decrease or block expression of a particular IL4Ralpha
CC isogene, which may be done by turning off by transforming a targeted
CC organ, tissue or cell population with an expression vector that expresses
CC high levels of untranslatable mRNA for the isogene. Specific therapeutics
CC identified by these methods may be useful for allergic diseases. The
CC present sequence is a probe for human IL4R-alpha
CC
XX
SQ Sequence 15 BP; 2 A; 5 C; 7 G; 1 T; 0 U; 0 Other;
XX
Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1299 GGGCCACGAGGAGG 1312
Db 1 GGCCACGTGGAGG 14
XX
RESULT 596
AAF69387/c
ID AAF69387 standard; DNA; 15 BP.
XX
AC AAF69387;
XX
DT 18-APR-2001 (first entry)
XX
DE Human IL4Ralpha gene probe #27.
XX
KW Polymorphism; human; interleukin 4 receptor-alpha; IL4R-alpha;
KW allergic disease; probe; ss.
XX
OS Homo sapiens.
XX
PN MO200104270-A1.
XX
PD 18-JAN-2001.
XX
PF 13-JUL-2000; 2000WO-US019094.
XX
PR 13-JUL-1999; 99US-0143435P.
XX
PA (GENA-) GENA1SSANCE PHARM INC.
XX
PI Chew A, Denton RR, Duda A, Nandabalan K, Stephens JC;
PI Windemuth AK;
XX
DR WPI; 2001-103078/11.
XX
PT New isolated polynucleotide useful for the identification of therapeutics
PT in allergic diseases is new.
XX
PS Claim 15; Page 42; 188pp; English.
XX
CC The present invention relates to polymorphisms of the human interleukin 4
CC receptor-alpha gene (IL4R-alpha; see AAF57718 for the reference
CC sequence). Polynucleotides comprising polymorphic gene variants are
CC useful for therapeutic purposes. For example, where a patient may benefit
CC from expression of a particular IL4Ralpha protein isoform, an expression
CC vector encoding the isoform may be administered to the patient. It may
CC desirable to decrease or block expression of a particular IL4Ralpha

CC isogene, which may be done by turning off by transforming a targeted
CC organ, tissue or cell population with an expression vector that expresses
CC high levels of untranslatable mRNA for the isogene. Specific therapeutics
CC identified by these methods may be useful for allergic diseases. The
CC present sequence is a probe for human IL4R-alpha
CC
XX
SQ Sequence 15 BP; 1 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
XX
Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1235 TCCAGACCCGAGGC 1248
Db 14 TCCAGCCCGAGGC 1
XX
RESULT 597
AAF69537
ID AAF69537 standard; DNA; 15 BP.
XX
AC AAF69537;
XX
DT 18-APR-2001 (first entry)
XX
DE Human IL4Ralpha gene probe #177.
XX
KW Polymorphism; human; interleukin 4 receptor-alpha; IL4R-alpha;
KW allergic disease; probe; ss.
XX
OS Homo sapiens.
XX
PN MO200104270-A1.
XX
PD 18-JAN-2001.
XX
PF 13-JUL-2000; 2000WO-US019094.
XX
PR 13-JUL-1999; 99US-0143435P.
XX
PA (GENA-) GENA1SSANCE PHARM INC.
XX
PI Chew A, Denton RR, Duda A, Nandabalan K, Stephens JC;
PI Windemuth AK;
XX
DR WPI; 2001-103078/11.
XX
PT New isolated polynucleotide useful for the identification of therapeutics
PT in allergic diseases is new.
XX
PS Claim 15; Page 45; 188pp; English.
XX
CC The present invention relates to polymorphisms of the human interleukin 4
CC receptor-alpha gene (IL4R-alpha; see AAF57718 for the reference
CC sequence). Polynucleotides comprising polymorphic gene variants are
CC useful for therapeutic purposes. For example, where a patient may benefit
CC from expression of a particular IL4Ralpha protein isoform, an expression
CC vector encoding the isoform may be administered to the patient. It may
CC desirable to decrease or block expression of a particular IL4Ralpha
CC isogene, which may be done by turning off by transforming a targeted
CC organ, tissue or cell population with an expression vector that expresses
CC high levels of untranslatable mRNA for the isogene. Specific therapeutics
CC identified by these methods may be useful for allergic diseases. The
CC present sequence is a probe for human IL4R-alpha
CC
XX
SQ Sequence 15 BP; 2 A; 8 C; 4 G; 1 T; 0 U; 0 Other;
XX
Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1451 CAGGTGACGCCCC 1464
III -|||||

DB 1 CAGCTGACGCCCC 14

RESULT 598
AAF73926
ID AAF73926 standard; DNA; 15 BP.
XX
AC AAF73926;
XX
DT 30-APR-2001 (first entry)
XX
DE Human SLC6A4 allele-specific oligonucleotide primer #46.
XX
KM Solute carrier family 6 neurotransmitter transporter, serotonin 4; SLC6A4;
XX genotyping; allele specific oligonucleotide; ss.
OS Homo sapiens.
XX
PN WO200109161-A1.
PD 08-FEB-2001.
PF 31-JUL-2000; 2000WO-US020638.
XX
PR 29-JUL-1999; 99US-0146290P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Denton RR, Duda A, Nandabalan K, Sanchis A, Stephens JC;
XX
DR WPI; 2001-123317/13.
XX
PT New isolated polynucleotide comprising a polymorphic variant for the
PT solute carrier family 6 neurotransmitter transporter, serotonin member 4
PT gene for identifying drugs for treating disorders related to expression
PT of the protein.
XX
PS Claim 12; Page 21; 152pp; English.
XX
CC The present invention relates to a polymorphic variant of a reference
CC sequence for the solute carrier family 6 neurotransmitter transporter,
CC serotonin member 4 (SLC6A4) gene or a fragment of it or a sequence
CC complementary to the first sequence. The invention is used in producing a
CC recombinant organism that can be used to express SLC6A4 for protein
CC structure analysis and binding studies. A composition comprising a
CC genotyping oligonucleotide is used to detect a polymorphism in the SLC6A4
CC gene
XX
SQ Sequence 15 BP; 1 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1471 TTGACCTGCCTCC 1484
DB 1 TTGAGCTGCCTCC 14

RESULT 599
AAF73930
ID AAF73930 standard; DNA; 15 BP.
XX
AC AAF73930;
XX
DT 30-APR-2001 (first entry)
XX
DE Human SLC6A4 allele-specific oligonucleotide primer #50.
XX
KM Solute carrier family 6 neurotransmitter transporter, serotonin 4; SLC6A4;
KM genotyping; allele specific oligonucleotide; ss.
XX
OS Homo sapiens.

XX
PN WO200109161-A1.
XX
PD 08-FEB-2001.
XX
PF 31-JUL-2000; 2000WO-US020638.
XX
PR 29-JUL-1999; 99US-0146290P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Denton RR, Duda A, Nandabalan K, Sanchis A, Stephens JC;
XX
DR WPI; 2001-123317/13.
XX
PT New isolated polynucleotide comprising a polymorphic variant for the
PT solute carrier family 6 neurotransmitter transporter, serotonin member 4
PT gene for identifying drugs for treating disorders related to expression
PT of the protein.
XX
PS Claim 12; Page 21; 152pp; English.
XX
CC The present invention relates to a polymorphic variant of a reference
CC sequence for the solute carrier family 6 neurotransmitter transporter,
CC serotonin member 4 (SLC6A4) gene or a fragment of it or a sequence
CC complementary to the first sequence. The invention is used in producing a
CC recombinant organism that can be used to express SLC6A4 for protein
CC structure analysis and binding studies. A composition comprising a
CC genotyping oligonucleotide is used to detect a polymorphism in the SLC6A4
CC gene
XX
SQ Sequence 15 BP; 2 A; 5 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1471 TTGACCTGCCTCC 1484
DB 2 TTGAGCTGCCTCC 15

RESULT 600
ADV36833/C
ID ADV36833 standard; RNA; 15 BP.
XX
AC ADV36833;
XX
DT 10-FEB-2005 (first entry)
XX
DE Human anti-HER2 NCH ribozyme substrate sequence #806.
XX
KM Enzymatic nucleic acid molecule; gene expression; down regulation;
KM protein-tyrosine-phosphatase-1b; PTP-1B; methionine aminopeptidase;
KM MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
KM beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
KM c-erbB2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
KM hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
KM amberyzyme; zinzyme; DNazyme; cancer; breast cancer; Alzheimer's disease;
KM diabetes; obesity; cardiac disease; heart disease; age-related disease;
KM hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
KM ss.
XX
OS Homo sapiens.
XX
PN WO200116312-A2.
XX
PD 08-MAR-2001.
XX
PF 30-AUG-2000; 2000WO-US023998.
XX
PR 31-AUG-1999; 99US-0151713P.
PR 27-SEP-1999; 99US-00406643.

```

PR 27-SEP-1999; 99US-0156236P.
PR 27-SEP-1999; 99US-0156467P.
PR 08-NOV-1999; 99US-00436430.
PR 06-DEC-1999; 99US-0169100P.
PR 29-DEC-1999; 99US-00474432.
PR 29-DEC-1999; 99US-0173612P.
PR 30-DEC-1999; 99US-00476387.
PR 04-FEB-2000; 2000US-00498824.
PR 20-FEB-2000; 2000US-00531025.
PR 14-APR-2000; 2000US-0197769P.
PR 23-MAY-2000; 2000US-00578223.
PR 09-AUG-2000; 2000US-00636385.
PA
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Mcawiggen J, Usman N, Blatt L, Beigelman L, Burgin A;
PI Kapelsky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;
XX
XX WPI; 2001-244406/25.
XX
XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules
XX are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
XX obesity and heart disease.
XX
XX Example 7, Page 488; 717pp; English.
XX
XX The present invention relates to the use of enzymatic nucleic acid
XX molecules (e.g. ribozymes) to modulate gene expression. The invention of
XX also methods for their use to down regulate or inhibit the expression of
XX genes encoding protein-tyrosine-phosphatase-1b (PTN-1B), methionine
XX aminopeptidase (MEAP-2), human telomerase (hTERT), protein kinase C
XX alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
XX receptor-2 (HER2/c-erbB2/neu), phospholamban (PLN), presenilin-1 (ps-1),
XX presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
XX nucleic acid molecules used to inhibit the expression of the said genes
XX include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,
XX zincyme, and/or DNAzyme motifs. The methods of the invention are useful
XX for treating cancer, in particular breast cancer, Alzheimer's disease,
XX diabetes, obesity, cardiac diseases e.g. heart disease, age-related
XX diseases, hepatitis B infections, and hepatitis and hepatocellular
XX carcinoma. The enzymatic nucleic acid molecules can also be used as
XX diagnostic tools to examine genetic drift and mutations within diseased
XX cells and to detect the presence of specific RNA in a cell. The present
XX sequence represents a substrate/target sequence for an anti-HER2 NCH
XX ribozyme used in the examples of the present invention. Note, Some SEQ ID
XX Nos are repeated more than once in the specification, but these have
XX different sequences associated with them.
XX
XX
XX Sequence 15 BP; 5 A; 3 C; 5 G; 0 T; 2 U; 0 Other;
XX
XX Query Match 0.7%; Score 12.4; DB 1; Length 15;
XX Best Local Similarity 92.9%; Pred. No. 3.3e+02;
XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0
XX
XX QY 1055 TTATCCAGCAGGTC 1068
XX |||||||||
XX 14 TTTTCCAGCAGGTC 1
XX
XX
XX RESULT 601
XX ABL46309
XX ID ABL46309 standard; DNA; 15 BP.
XX AC ABL46309;
XX
XX 26-APR-2002 (first entry)
XX
XX Mouse scavenger receptor class B type 1 oligonucleotide SEQ ID NO:276.
XX
XX Nucleic acid accessible hybridisation site; detection; hybridisation;
XX characterisation; identification; nucleic acid structure; diagnosis;
XX PCR primer; probe; ss.
XX

```

XX	Mus sp.
OS	Synthetic.
XX	
PN	WO200198537-A2.
XX	
PD	27-DEC-2001.
XX	
PJ	15-JUN-2001; 2001WO-US019401.
XX	
PR	17-JUN-2000; 2000US-0212308P.
XX	
PR	15-JUN-2001; 2001US-00212308.
XX	
PA	(THIR-) THIRD WAVE TECHNOLOGIES INC.
XX	
PI	Lymichev V, Allawi H, Dong F, Neri BP, Vener IT;
XX	
DR	WPI; 2002-049698/06.
XX	
PT	Identifying oligonucleotides hybridizing to nucleic acids containing
PT	secondary structure, useful in clinical diagnosis, comprises identifying
PT	primers that interact with the target to form an extension product under
XX	amplification conditions.
XX	
PS	Claim 48; Fig 79A; 40pp; English.
XX	
CC	The present invention describes a method for identifying oligonucleotides
CC	with desired hybridisation properties to nucleic acid targets containing
CC	secondary structure. The method comprises amplifying a target nucleic
CC	acid having at least one accessible and one inaccessible site. Primers
CC	that form an extension product are identified as the oligonucleotides
CC	which can interact with the folded target nucleic acid. Oligonucleotides
CC	from the present invention can be used in novel detection methods for
CC	clinical diagnostic purposes, including the detection and identification
CC	of pathogenic organisms (e.g. HIV). The method allows the ability to
CC	rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent
CC	sequences used in the exemplification of the present invention
XX	
SQ	Sequence 15 BP; 2 A; 4 C; 4 G; 5 T; 0 U; 0 Other;
XX	
Query Match	0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity	92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative	0; Mismatches 1; Indels 0; Gaps 0
DG	669 CATCTGGGCCTCG 682 2 CATCTTGGTCCTGG 15
RESULT 602	
AAD43755	
ID	AAD43755 standard; DNA; 15 BP.
XX	
AC	AAD43755;
XX	
DT	14-NOV-2002 (first entry)
XX	
DE	Human AGR2 gene polymorphism detecting ASO probe #3.
XX	
KM	Human; angiotensin receptor 2; forensic application; drug response;
KW	AGR2; congenital abnormality of kidney and urinary tract; CAKUT;
KM	cardiovascular disorder; premature ovarian failure; gene therapy; POF;
XX	polymorphism; ASO; allele-specific oligonucleotide; probe; ss.
OS	Homo sapiens.
XX	
PN	WO200263045-A1.
XX	
PD	15-AUG-2002.
XX	
PF	02-FEB-2001; 2001WO-US003620.
XX	
PR	02-FEB-2001; 2001WO-US003620.

XX (GENA-) GENAISANCE PHARM INC.
XX Chew A, Choi JY, Koshy B, Stephens JC,
XX WPI; 2002-636599/68.
XX Novel genetic variants of angiotensin receptor 2 isogenes, useful in
PT therapeutic purposes and in screening for drugs targeting the angiotensin
PT receptor protein.
XX
XX Claim 16; Page 20; 69pp; English.
XX
XX The invention relates to genetic variants of human angiotensin receptor 2
CC (AGTR2) isogenes and methods for detecting variants of AGTR2 gene.
CC Polynucleotides of the invention are useful in studying the expression
CC and biological function of AGTR2 and in developing drugs targeting AGTR2
CC protein. Methods of the invention are useful for studying population
CC diversity, anthropological lineage, the significance of diversity and
CC lineage at the phenotypic level, paternity testing, forensic applications
CC and for identifying associations between AGTR2 genetic variations and a
CC trait such as levels of drug response or susceptibility to disease. It is
CC useful in developing diagnostic tests and therapeutic treatments for
CC cardiovascular disorders, congenital abnormalities of kidney and urinary
CC tract (CAKUT) and premature ovarian failure (POF). The invention is
CC useful in gene therapy. The present sequence is an allele-specific
CC oligonucleotide (ASO) probe used to detect human AGTR2 gene polymorphisms
XX
XX Sequence 15 BP; 1 A; 6 C; 2 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 991 TGCGTGCCTTCCA 1004
Db 1 TGGCTTCCCTTCCA 14
XX
XX RESULT 603
ABK32066/c
XX ABK32066 standard; DNA; 15 BP.
XX
XX ABK32066;
XX
XX 23-APR-2002 (first entry)
XX
XX Human colon cancer SAGE tag #167.
XX
XX Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag;
XX serial analysis of gene expression; diagnostic; prognostic; probe;
XX cancer marker; ss.
XX
XX Homo sapiens.
XX
XX U66333152-B1.
XX
XX 25-DEC-2001.
XX
XX 20-MAY-1998; 98US-00081646.
XX
XX 20-MAY-1998; 98US-00081646.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Vogelstein B, Kinzler KW, Zhang L, Zhou W;
XX WPI; 2002-153821/20.
XX
XX New human nucleic acid containing specific SAGE tags, useful as
PT diagnostic markers for cancer, also derived probes.
XX
XX Disclosure; Col 24; 161pp; English.
XX

XX The invention relates to an isolated, purified human nucleic acid (I)
CC that has the same sequence as a mRNA found in humans and is a SAGE
CC (serial analysis of gene expression) tag comprising a single stranded
CC probe containing at least 10 consecutive nucleotides. SAGE tags, are
CC diagnostic and prognostic markers of cancer, especially of the colon and
CC pancreas. ABK31900-ABK322770 represent human colon and pancreatic cancer
CC SAGE tags of the invention
XX
XX Sequence 15 BP; 4 A; 6 C; 2 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 367 GTGATGTGATCAT 360
Db 15 GCGATGTGATCAT 2
XX
XX RESULT 604
ACA09887
XX ID ACA09887 standard; RNA; 15 BP.
XX
XX ACA09887;
XX
XX 03-JUN-2003 (first entry)
XX
XX
XX Necrosis factor kappa B sub-unit modulating enzyme target #80.
XX
XX Enzymatic nucleic acid; nuclear factor kappa B; NFkB; lipozyme; zinkzyme;
XX G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;
XX lung cancer; prostate cancer; colorectal cancer; brain cancer;
XX osteopagel cancer; stomach cancer; bladder cancer; pancreatic cancer;
XX cervical cancer; head and neck cancer; ovarian cancer; melanoma;
XX lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
XX chemotherap; paclitaxel; docetaxel; cisplatin; methotrexate;
XX cyclophosphamide; doxorubin; fluorouracil carboxiplatin; edatrexate;
XX gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
XX rheumatoid arthritis; restenosis; Crohn's disease; obesity; lechaemia;
XX gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
XX transplant/graft rejection; reperfusion injury; glomerulonephritis;
XX allergic airway inflammation; inflammatory bowel disease; infection; ss.
XX
XX Homo sapiens.
XX
XX US202177568-A1.
XX
XX 28-NOV-2002.
XX
XX 23-MAY-2001; 2001US-00864785.
XX
XX 07-DEC-1992; 92US-00987132.
XX 18-MAY-1994; 94US-00245466.
XX 15-AUG-1994; 94US-00291932.
XX 23-DEC-1996; 96US-00777916.
XX
XX (STIN/) STINGHCOMB D T.
XX (MCSW/) MCSWIGEN J.
XX (DRAP/) DRAPER K G.
XX
XX Stinchcomb DT, Mcswiggen J, Draper KG;
XX WPI; 2003-340953/32.
XX
XX Novel enzymatic nucleic acid molecules which down regulates expression of
PT a sequence encoding a subunit of nuclear factor kappa B useful for
PT treating cancer, inflammatory disorders and autoimmune diseases.
XX
XX Claim 3; Page 61; 72pp; English.
XX
XX The invention describes an enzymatic nucleic acid molecule (I) which down
CC regulates expression of a sequence encoding a subunit of nuclear factor
CC

CC kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat
 CC cancer and is useful for down-regulating RBL-A activity in a cell, for
 CC treating a patient having a condition associated with the level of RBL-A.
 CC (I) is useful for cleaving RNA comprising a sequence of RBL-A gene, in
 CC the presence of a divalent cation, especially Mg²⁺. The enzymatic and
 CC antisense nucleic acid molecules are useful for treating breast, lung,
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
 CC multidrug resistant cancer. The method involves use of other drug
 CC therapies such as monoclonal antibodies, RBL-A-specific inhibitors or
 CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,
 CC cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate,
 CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic
 CC acid molecules are also useful for treating inflammatory disease such as
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
 CC rejection, gene therapy applications, ischemia/reperfusion injury
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or
 CC infection. This sequence represents the substrate of a novel enzymatic
 CC nucleic acid molecule

XX SQ Sequence 15 BP; 2 A; 6 C; 1 G; 0 T; 6 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 15;

Best Local Similarity 57.1%; Pred. No. 3.3e+02;

Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1410 CTCTCTCCCAATG 1423

Db 2 CUUCUCCUCCAUUG 15

RESULT 605

ACA09888 standard; RNA; 15 BP.

AC ACA09888;

DT 03-JUN-2003 (first entry)

DE Necrosis factor kappa B sub-unit modulating enzyme target #81.

XX Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;
 KW G-cleaver; amberzyme; cancer; RBL-A activity; breast cancer; human;
 KW lung cancer; prostate cancer; colorectal cancer; brain cancer;
 KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;
 KW lymphoma; glioma; multidrug resistant cancer; RBL-A-specific inhibitor;
 KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
 KW cyclophosphamide; doxorubicin; fluorouracil carboplatin; edatrexate;
 KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
 KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
 KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
 KW transplant/graft rejection; reperfusion injury; glomerulonephritis;
 KW allergic airway inflammation; inflammatory bowel disease; infection; ss.

XX Homo sapiens.

XX US2002177568-A1.

PD 28-NOV-2002.

PF 23-MAY-2001; 2001US-00864785.

XX 07-DEC-1992; 92US-00987132.

PR 18-MAY-1994; 94US-00245466.

PR 15-AUG-1994; 94US-00291932.

PR 23-DEC-1996; 96US-00777916.

XX (STIN/) STINGCOMB D T.

PA (MCSM/) MCSMIGEN J.

PA (DRAP/) DRAPER K G.

XX Stinchcomb DT, Mcswigen J, Draper KG;

XX WPI; 2003-340953/32.

PT Novel enzymatic nucleic acid molecules which down regulates expression of
 PT a sequence encoding a subunit of nuclear factor kappa B useful for
 PT treating cancer, inflammatory disorders and autoimmune diseases.

PS Claim 3; Page 61; 72pp; English.

XX The invention describes an enzymatic nucleic acid molecule (I) which down
 CC regulates expression of a sequence encoding a subunit of nuclear factor
 CC kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat
 CC cancer and is useful for down-regulating RBL-A activity in a cell, for
 CC treating a patient having a condition associated with the level of RBL-A.
 CC (I) is useful for cleaving RNA comprising a sequence of RBL-A gene, in
 CC the presence of a divalent cation, especially Mg²⁺. The enzymatic and
 CC antisense nucleic acid molecules are useful for treating breast, lung,
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
 CC multidrug resistant cancer. The method involves use of other drug
 CC therapies such as monoclonal antibodies, RBL-A-specific inhibitors or
 CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,
 CC cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate,
 CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic
 CC acid molecules are also useful for treating inflammatory disease such as
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
 CC rejection, gene therapy applications, ischemia/reperfusion injury
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or
 CC infection. This sequence represents the substrate of a novel enzymatic
 CC nucleic acid molecule

XX SQ Sequence 15 BP; 1 A; 7 C; 1 G; 0 T; 6 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 15;

Best Local Similarity 57.1%; Pred. No. 3.3e+02;

Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1410 CTCTCTCCCAATG 1423

Db 1 CUUCUCCUCCAUUG 14

RESULT 606

ABX94796/C standard; DNA; 15 BP.

AC ABX94796;

DT 08-JUL-2003 (first entry)

DE Beta-actin PCR primer #2.

XX Androgen receptor; human; acne; acneform skin disorder; acne rosacea;
 KW antisense; steroid hormone receptor; steroid hormone metabolising enzyme;
 KW 5alpha-reductase; dermatological; antisborrheic; sebaceous gland;
 KW phosphorocholate; RT-PCR; primer; beta-actin; ss.

XX Unidentified.

PN WO2003017917-A2.

PD 06-MAR-2003.

PF 23-AUG-2002; 2002WO-EP009452.

PR 23-AUG-2001; 2001DE-01041443.

PA (RINA-) RINA TECHNOLOGIEN GMBH.
PA (ZOUB/) ZOUBOULIS C C.
XX Zouboulis CC;
XX WPI; 2003-278606/27.
DR
XX
PT Use of non-viral agents for treating acne or acneform skin conditions,
PT particularly antisense oligonucleotides directed against androgen
PT receptor or 5alpha reductase.
XX
XX Example 1; Page 18; 36pp; German.
XX
CC This invention describes a novel method for treatment of acne and
CC acneform skin disorders, including rosacea, using a non-viral active
CC agent, prepared by molecular biological methods. The method comprises an
CC antisense oligonucleotide; (stabilised) ribozyme; (mirror) aptamer;
CC chimeric RNA/DNA oligonucleotide; naked plasmid DNA or DNA encapsulated
CC in a liposome, especially an antisense oligonucleotide specific for a
CC gene that encodes a steroid hormone receptor or steroid hormone
CC metabolising enzyme, particularly the androgen receptor and/or 5alpha-
CC reductase. The products of the invention have dermatological and
CC antiandrogenic activity and can inhibit the androgen-induced stimulation
CC of sebaceous gland activity. The method of the invention provides
CC effective treatment with reduced side effects and without the
CC difficulties associated with systemic administration. This sequence
CC represents a RT-PCR primer used to amplify the beta-actin gene, which is
CC used as a control during the amplification of the human androgen receptor
CC described in the disclosure of the invention
XX
SQ Sequence 15 BP; 0 A; 4 C; 8 G; 3 T; 0 U; 0 Other;
Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 134 GCCCCAGGCGCCAG 147
DB 14 GCCCCAGGCGCCAG 1
RESULT 607
ADL50873
ID ADL50873 standard; RNA; 15 BP.
XX
AC ADL50873;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human PKR substrate sequence #1987.
XX
KM antisense oligonucleotide; neurite growth inhibitor; NOGO;
KM proteoglycan D2 receptor; PTGDR; IkappaB kinase; IKK;
KM central nervous system injury; CNS injury; spinal cord injury; cancer;
KM melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
KM restenosis; asthma; Crohn's disease; diabetes; obesity;
KM autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KM graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KM allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KM substrate; db.
XX
OS Undifferentiated.
XX
PN WO200281628-A2.
XX
PD 17-OCT-2002.
XX
PF 03-APR-2002; 2002WO-US010512.
XX
XX 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.
XX

XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Chowrira B, Haeblerli P, Mcawiggen J, Fosnaugh K;
XX
XX WPI; 2003-058513/05.
DR
XX
PT Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or
PT protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
XX Claim 59; SEQ ID NO 4406; 317pp; English.
XX
CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection,
CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human PKR
CC substrate sequence.
XX
SQ Sequence 15 BP; 0 A; 7 C; 2 G; 0 T; 6 U; 0 Other;
Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 57.1%; Pred. No. 3.3e+02;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 105 CCCTCCCTGCTGCT 118
DB 1 CCCCTCCCTGCTGCT 14
RESULT 608
ADP64570
ID ADP64570 standard; DNA; 15 BP.
XX
AC ADP64570;
XX
DT 26-AUG-2004 (first entry)
XX
DE VIC probe for typing SNP260 in a disease sensitivity gene.
XX
XX disease-sensitive gene; single nucleotide polymorphism; SNP;
KM linkage disequilibrium analysis; type II diabetes sensitive gene; probe;
KM ss.
XX
OS Homo sapiens.
XX
PN WO2004049234-A1.
XX
PD 10-JUN-2004.
XX
PF 21-NOV-2003; 2003WO-JP014888.
XX
XX 22-NOV-2002; 2002JP-00339901.
XX
PA (BIOS-) APPLIED BIOSYSTEMS JAPAN LTD.
PA (FUJI) FUJITSU LTD.
PA (ITAK/) ITAKURA M.
XX
PI Itakura M, Kato H, Katashima R, Shinohara S, Nomura K;
XX
DR WPI; 2004-460856/43.
XX

PT Identifying disease-sensitive gene, involves selecting single nucleotide
PT polymorphism (SNP) marker which are not unevenly distributed over
PT candidate regions of gene, and subjecting to linkage disequilibrium
PT analysis.
XX
XX Disclosure; SEQ ID NO 11; 53bp; Japanese.
XX
CC The invention relates to a method of identifying (M1) a disease-sensitive
CC gene using single nucleotide polymorphisms (SNPs) marker, by subjecting a
CC disease sensitive SNPs marker to linkage disequilibrium analysis and
CC specifying the region where linkage disequilibrium is observed and the
CC SNPs marker is contained in the candidate region, where SNP markers are
CC not unevenly distributed over the entire candidate regions of disease
CC sensitive gene. (M1) is useful for identifying a disease-sensitive
CC gene, e.g. for identifying type II diabetes sensitive gene. This sequence
CC represents a VIC-labelled probe to identify SNP260 in a disease
CC sensitivity gene used in the method of the invention.
XX
SQ Sequence 15 BP; 6 A; 3 C; 2 G; 4 T; 0 U; 0 Other;
XX
Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 65 TCAGCTTCAAAA 78
Db 1 TCAGCTTCAAAA 14
XX
RESULT 609
ADQ31062
ID ADQ31062 standard; DNA; 15 BP.
XX
AC ADQ31062;
XX
DT 23-SEP-2004 (first entry)
DE C-fos mRNA detection capture oligonucleotide.
XX
KW analyte detection; detection; probe; detection probe; reporter;
KW capture oligonucleotide; human; c-fos; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 15
FT /*tag= a
FT /mod_base= OTHER
FT /note= "3, labelled with red oxazine dye (RO)"
FT
XX
XX WO2004057023-A1.
XX
XX 08-JUL-2004.
XX
XX 19-DEC-2003; 2003WO-BP014661.
XX
XX 20-DEC-2002; 2002EP-00028582.
XX
XX 13-JAN-2003; 2003US-0439439P.
XX
XX (EVOT-) EVOTEC OAI AG.
XX
XX Himnah S, Lambue D, Droege S, Jaeger S, Gall K;
XX
XX WPI; 2004-543305/52.
XX
XX
XX Detecting an analyte such as protein or nucleic acid, useful for
XX screening drugs, comprises probe detection of captured analyte where
XX surplus probe signal is quenched and/or differential emission wavelength
XX of labeled support is measured.
XX
XX Example 1; Page 20; 61pp; English.
XX

CC The present invention describes a method for detecting an analyte in a
CC sample. The method comprises: (a) providing detection probes being
CC labelled with a first reporter, where the detection probes are capable of
CC binding to the analyte; (b) providing a solid support; (c) providing
CC capture probes being bound or capable of binding to the solid support,
CC where the capture probes are capable of binding to the analyte, and so
CC concentrating the analyte on the solid support; (d) contacting the sample
CC with the detection probes, the solid support; (e) detecting the detection
CC probes is conducted in the presence of quenching probes binding to
CC surplus detection probes not being bound to the analyte and thereby
CC quenching at least partially an emission of the first reporter of said
CC surplus detection probes, and/or (ii) the solid support is labelled with
CC a second reporter different from the first reporter, imaging the sample
CC at an emission wavelength of the second reporter, generating a mask
CC obtained from imaging the sample at the emission wavelength of the second
CC reporter and applying this mask to an image of the sample used for
CC detecting the detection probes. The present sequence represents a capture
CC oligonucleotide used in the detection of c-fos mRNA, which is used in an
CC example from the present invention.
XX
SQ Sequence 15 BP; 1 A; 5 C; 7 G; 2 T; 0 U; 0 Other;
XX
Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1449 GGCAGGTGCAGCCC 1462
Db 1 GGCAGGTGCAGCCC 14
XX
RESULT 610
ADQ11821/c
ID ADQ11821 standard; DNA; 15 BP.
XX
AC ADQ11821;
XX
DT 07-OCT-2004 (first entry)
DE Poly gly linker coding sequence, SEQ ID 302.
XX
XX
XX Muscular; Muscular; Gene Therapy; Antidiabetic; Anorectic; Myostatin;
XX myostatin-binding peptide; growth/differentiation factor 8; GDF-8;
XX skeletal muscle mass; muscle-wasting disease; muscular dystrophy;
XX amyotrophic lateral sclerosis; congestive obstructive pulmonary disease;
XX chronic heart failure; cancer; AIDS; renal failure; uremia;
XX rheumatoid arthritis; age-related sarcopenia; muscle-wasting;
XX spinal chord injury; stroke; bone fracture; aging; diabetes; obesity;
XX hyperglycaemia; bone loss; osteoporosis; de.
XX
XX Synthetic.
XX
XX WO2004058988-A2.
XX
XX 15-JUL-2004.
XX
XX 19-DEC-2003; 2003WO-US040781.
XX
XX 20-DEC-2002; 2002US-0435923P.
XX
XX (AMGE-) AMGEN INC.
XX
XX Han H, Min H, Boone TC;
XX
XX WPI; 2004-525896/50.
XX
XX
XX New binding agent which inhibits myostatin, useful for treating muscular
XX dystrophy, amyotrophic lateral sclerosis, congestive obstructive
XX pulmonary disease, stroke, aging, diabetes, obesity, osteoporosis.
XX
XX Example 2; SEQ ID NO 302; 287pp; English.
XX

CC The present invention relates to novel binding agents comprising at least
CC one peptide capable of binding myostatin and inhibiting its activity. In
CC one embodiment, the binding agent comprises at least one myostatin-
CC binding peptide attached directly or indirectly to at least one vehicle
CC such as a polymer or an Fc domain. Myostatin (also known as
CC growth/differentiation factor 8, GDF-8) is a transforming growth factor-
CC beta (TGF-beta) family member known to be involved in regulation of
CC skeletal muscle mass. The binding agents increase lean muscle mass when
CC administered to animals and decrease fat to muscle ratios. The binding
CC agents are useful for treating muscle-wasting disease, e.g. muscular
CC dystrophy, amyotrophic lateral sclerosis, congestive obstructive
CC pulmonary disease, chronic heart failure, cancer, AIDS, renal failure,
CC uremia, rheumatoid arthritis, age-related sarcopenia, muscle-wasting due
CC to prolonged bedrest, spinal cord injury, stroke, bone fracture, or
CC aging, and myosin-related metabolic disorder, e.g. diabetes, obesity,
CC hyperglycaemia, bone loss, or osteoporosis. The present sequence is a
CC linker peptide coding sequence used to illustrate the invention.

XX
SQ Sequence 15 BP; 1 A; 0 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1276 ACCACGACTCTCCAC 1289
DB 15 ACCACGACTCTCCAC 2

RESULT 611
ADS12596/c
ID ADS12596 standard; DNA; 15 BP.
XX
AC ADS12596;
XX
DT 16-DEC-2004 (first entry)
XX
DE Reverse RT-PCR primer used to amplify human beta-actin DNA SegID.
XX
KW PCR; primer; 89; microarray; inflammatory bowel disease; Crohn's disease;
XX ulcerative colitis; screening method; antiinflammatory; antiulcer;
XX RT-PCR; real-time PCR; beta-actin.
XX
OS Homo sapiens.
XX
PN EPI462527-A1.
XX
PD 29-SEP-2004.
XX
PF 26-MAR-2003; 2003EP-00006943.
XX
PR 26-MAR-2003; 2003EP-00006943.
XX
PA (CONA-) CONARIS RES INST AG.
XX
PI Costello C, Ma N, Schreiber SD, Seegert D;
XX WPI; 2004-663617/65.
XX
DR WPI; 2004-663617/65.
XX
PT New diagnostic composition comprising specific nucleic acid molecules,
XX useful for diagnosing or developing a compound for treating inflammatory
XX bowel diseases or related disease e.g., Crohn's disease and ulcerative
XX colitis.
XX
PS Example 1; SEQ ID NO 6; 63pp; English.
XX
CC This invention relates to a novel diagnostic composition that comprises
CC nucleic acid molecules bound to a solid support (or microarray), wherein
CC each nucleic acid can hybridise to an mRNA of a gene that shows abnormal
CC expression in an gastrointestinal condition. Specifically, it refers to
CC DNA oligos useful for preparing a microarray chip for the diagnosis of
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis or a
CC disposition thereof. The present invention describes nucleic acid

CC molecules useful for screening methods to identify compounds that can be
CC used for therapy or to prevent progression of the aforementioned
CC conditions. As such, the pharmaceutical compositions developed
CC according to exhibit antiinflammatory and antiulcer activities. This
CC oligonucleotide sequence is an RT-PCR primer used to amplify human beta-
CC actin, an endogenous control gene used in an exemplification of the
CC invention.

XX
SQ Sequence 15 BP; 0 A; 4 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 134 GCCCCAGGCGCCAG 147
DB 14 GCCCCAGGCGCCAG 1

RESULT 612
ADV95329/c
ID ADV95329 standard; DNA; 15 BP.
XX
AC ADV95329;
XX
DT 24-FEB-2005 (first entry)
XX
DE Sequence #1 from human BMP-4 DNA.
XX
KW Methanol Yeast; gene expression; cloning; bone morphogenetic protein-4;
XX BMP-4; de.
XX
OS Homo sapiens.
XX
PN CN1513979-A.
XX
PD 21-JUL-2004.
XX
PF 20-MAY-2003; 2003CN-00136581.
XX
PR 20-MAY-2003; 2003CN-00136581.
XX
PA (UVFU-) UNIV FUJIAN.
XX
PI Zhang Y, Chen Y, Huang Y;
XX WPI; 2004-710695/70.
XX
DR WPI; 2004-710695/70.
XX
PT High efficiency expression of recombinant human bone forming protein 4
XX and 7 using methanol yeast.
XX
PS Disclosure; Fig 1; 14pp; Chinese.
XX
CC The invention relates to a technique for using methanol yeast to
CC efficiently express human bone morphogenetic proteins (BMPs). The method
CC includes using the plasmids pBluescript KS-BMP4 and pBluescript KS-BMP7
CC containing human BMP-4 and BMP-7 cDNA sequences as template. PCR
CC amplification, fixed-point mutation to the arginine codon in the
CC sequence, and cloning it to methanol yeast expression plasmid pPIC9K. The
CC method further comprises transforming this plasmid into methanol yeast
CC GS115. The method is useful for using methanol yeast to efficiently
CC express human bone morphogenetic protein. This sequence represents a
CC sequence from BMP-4 DNA.
XX
SQ Sequence 15 BP; 5 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1402 AGCTTCAGCTTCTC 1415
DB 15 AGCTTCAGCTTCTC 2

```

ID      ADVY26280 standard; DNA; 15 BP.
AC      ADVY26280/c
XX      ADVY26280;
DT      10-MAR-2005 (first entry)
XX      Human beta-actin control reverse primer.
DE      ss; primer; inflammatory bowel disease; Crohn's disease;
KW      ulcerative colitis; gastrointestinal-gen.; inflammation;
KM      antiinflammatory; diagnosis; DNA polymorphism; PCR.
XX      Homo sapiens.
OS      WO2004109288-A1.
PN      16-DEC-2004.
PD      03-JUN-2004; 2004WO-SE000861.
PF      06-JUN-2003; 2003GB-00013081.
PR      26-NOV-2003; 2003GB-00027427.
PP      (ASTR ) ASTRAZENECA AB.
PA      Corneliussen B, Schreiber S, Stoll M;
PI      WPI; 2005-057661/06.
PX      Identifying a compound capable of modulating the action of the DLG5
PT      protein comprises subjecting one or more test compounds to a screen
PR      comprising DLG5 polypeptide, its homologue or fragment.
XX      Example 3; SEQ ID NO 172; 79pp; English.
PS      The invention relates to identifying a compound capable of modulating the
XX      action of the DLG5 protein comprising subjecting one or more test
CC      compounds to a screen comprising a DLG5 polypeptide appearing as
CC      ADY66112, its homologue or fragment. Also included are identifying a
CC      potential anti-inflammatory bowel disease (anti-IBD) therapeutic
CC      compounds, screening for a compound potentially useful for treating IBD,
CC      a cell comprising a reporter gene under the control of the DLG5 promoter,
CC      testing potential therapeutic agents for the ability to suppress IBD
CC      phenotype, identifying inhibitors of transcription of DLG5, preparing a
CC      pharmaceutical composition and diagnosing IBD or determining
CC      susceptibility to develop IBD. The methods are useful for identifying a
CC      compound capable of modulating the action of the DLG5 protein or
CC      diagnosing IBD. The compound that is able to modulate that activity or
CC      amount of DLG5 and methods are useful for preparing a medicament for
CC      treating IBD, ulcerative colitis and Crohn's disease. The human gene
CC      encoding DLG5 is located on chromosome 10-q22.3. The present sequence is
CC      a control PCR primer used in expression analysis of the dlgs gene.
XX      SQ      Sequence 15 BP; 0 A; 4 C; 8 G; 3 T; 0 U; 0 Other;

Query Match          0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.3e+02;
Matches   13; Conservative    0; Mismatches     1; Indels     0; Gaps     0

QY      134 GCCCAGGCCGCAG 147
        |||||
DB      14 GCCCGAGCACCGAG 1

RESULT 614
ADY25936
ID      ADY25936 standard; DNA; 15 BP.
AC      ADY25936;

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[illegible]


```
XX 68; aptamer.
XX Synthetic.
XX WO2005019430-A2.
XX 03-MAR-2005.
XX 23-AUG-2004; 2004WO-US027284.
XX 22-AUG-2003; 2003US-0497104P.
XX (RERE-) RES DEV FOUND.
XX Ellington A, Manjula R;
XX WPI; 2005-202637/21.
XX Selecting aptamer beacons in vitro comprises generating a pool of single-
XX stranded nucleic acid species comprising a fluorophore F1, and a random
XX insert of N nucleotides.
XX Example 1; SEQ ID NO 7; 124pp; English.
XX The invention relates to a method of selecting aptamer beacons in vitro
XX which comprises generating a pool of single-stranded nucleic acid species
XX having a fluorophore F1, and a random insert of N nucleotides. The method
XX is useful for selecting aptamer beacons in vitro. The present sequence
XX represents a randomized DNA pool capture oligonucleotide.
XX Sequence 15 BP; 6 A; 2 C; 4 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 0.7%; Score 12.4; DB 1; Length 15;
XX Best Local Similarity 92.9%; Pred. No. 3.3e+02;
XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 397 ATGAGCAGCAGTGAC 410
XX 2 ATGAGCAGCAGTGAC 15
XX
XX RESULT 616
XX ID ADY52800 standard; DNA; 15 BP.
XX AC ADY52800;
XX 19-MAY-2005 (first entry)
XX Human CHRNA2 gene P52 detecting reverse ASO primer, SEQ ID NO: 13.
XX Selectable marker; pharmaceutical; gene therapy; diagnosis;
XX SNP detection; cognitive disorder; nootropic; neurological disease;
XX dementia; Alzheimers disease; neuroprotective; degeneration;
XX Parkinsons disease; antiparkinsonian;
XX cholinergic receptor; nicotinic, alpha polypeptide 2; CHRNA2; primer; ss.
XX Homo sapiens.
XX OS
XX US2005048543-A1.
XX 03-MAR-2005.
XX 09-JUL-2004; 2004US-00887650.
XX 11-JUL-2003; 2003US-0486331P.
XX (AERS/) AERSENG J.
XX (ATHA/) ATHANASIOU M.
XX (BRAI/) BRAIN C.
XX (COHE/) COHEN N.
XX (DAIN/) DAIN B.
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```
PA (DENT/) DENTON R R.
PA (JUDS/) JUDSON R S.
PA (OZDE/) OZDEMIR V.
PA (REED/) REED C R.
XX Aerssens J, Athanasio M, Brain C, Cohen N, Dain B, Denton RR;
XX Judson RS, Ozdemir V, Reed CR;
XX WPI; 2005-202086/21.
XX Determining whether an individual has a response marker I or II comprises
XX PT determining whether the individual has zero copies or at least one copy
XX of any of the CHRNA2 haplotypes.
XX Claim 42; SEQ ID NO 13; 52pp; English.
XX The present invention relates to a method for determining whether an
XX individual has a response marker I or II. The method involves determining
XX whether the individual has zero copies or at least one copy of any of the
XX cholinergic receptor, nicotinic, alpha polypeptide 2 (CHRNA2) haplotypes.
XX The composition and methods are useful for diagnosing and treating a
XX cognitive disorder, e.g. mild or moderate dementia of the Alzheimer's
XX type, or dementia associated with Parkinson's disease. The method of the
XX invention is also useful for predicting the expected therapeutic response
XX of an individual to treatment with galantamine and for gene therapy. The
XX present sequence is the human CHRNA2 gene polymorphic site 2 (P52)
XX detecting allele-specific oligonucleotide (ASO) primer.
XX Sequence 15 BP; 0 A; 3 C; 5 G; 6 T; 0 U; 1 Other;
XX
XX Query Match 0.7%; Score 12.4; DB 1; Length 15;
XX Best Local Similarity 92.9%; Pred. No. 3.3e+02;
XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 671 TCTGGGTCTGTGCT 684
XX 2 TCTGGGTCTGTGCT 15
XX
XX RESULT 617
XX ID ADZ45541/c
XX ADZ45541 standard; DNA; 15 BP.
XX AC ADZ45541;
XX 30-JUN-2005 (first entry)
XX Murine factor IX directed antibody CDR1 DNA SEQ ID NO 245.
XX bispecific antibody; blood coagulation factor VIII; bleeding;
XX fibrinolysis; blood coagulation factor X; blood-coagulation factor IX;
XX factor VIII deficiency; von Willebrands disease; hemostatic;
XX immunostimulator; antibody engineering; ds; gene.
XX Mus musculus.
XX OS
XX WO2005035756-A1.
XX 21-APR-2005.
XX 08-OCT-2004; 2004WO-JP014911.
XX 10-OCT-2003; 2003WO-JP013062.
XX 14-OCT-2003; 2003WO-JP013123.
XX (CHUS ) CHUGAI SEIYAKU KK.
XX Hattori K, Kojima T, Miyazaki T, Soeda T;
XX WPI; 2005-315563/32.
XX P-PSDB; ADZ45542.
XX Novel bispecific antibody substituting for function of cofactor that
```

PT enhances enzyme reaction, and recognizing both enzyme and substrates of
PT enzyme, useful for treating hemophilia A.
XX
XX Disclosure; SEQ ID NO 245; 69bp; Japanese.
XX
CC This invention describes a novel bispecific antibody which can act as a
CC cofactor to enhance an enzyme reaction and can recognize the enzyme and
CC the enzyme substrate. The antibody specifically binds to blood
CC coagulation factor VIII. The invention also describes a composition
CC comprising the antibody and a carrier, a kit useful in preventing and/or
CC treating bleeding associated with a disorder or from a disease caused by
CC bleeding. The composition includes blood coagulation factor VIII. The
CC antibody of the invention can be a blood-coagulation fibrinolytic related
CC factor including blood-coagulation factor VIII, blood coagulation factor
CC X, or blood-coagulation factor IX. The antibody comprises a complementary
CC determining region (CDR) of anti-blood-coagulation factor IX/Xa factor
CC antibody. The novel antibody or composition is useful for preventing
CC and/or treating a disease accompanying bleeding, or the disease resulting
CC from bleeding, where the disease accompanying bleeding or the disease
CC resulting from bleeding develops and/or progresses by an active reduction
CC or deletion of the blood coagulation factor VIII. The disease the
CC develops and/or progresses by an active reduction or deletion of the
CC blood coagulation factor VIII and/or activation blood coagulation factor
CC VIII, is hemophilia A or von Willebrand disease, where the hemophilia is
CC an acquired hemophilia A. This sequence encodes a fragment of the
CC antibody described in the method of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 15 BP; 3 A; 5 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 30 GTGCATCCAGAGC 43
DB 15 GTGCATCCAGAGC 2

RESULT 618
AEA40005/c
ID AEA40005 standard; DNA; 15 BP.
XX
AC AEA40005;
XX
DT 28-JUL-2005 (first entry)
XX
DE DNA encoding TNF resistant monoclonal antibody VH region, D2VH CDR1.
XX
KW tumor necrosis factor; TNF; monoclonal antibody; D2 mAb;
KW light chain variable region; heavy chain variable region; D2VH; ds.
XX
OS unidentified.
XX
FT Key Location/Qualifiers
FT CDS 1..15
FT /*tag= a
FT /product= "CDR1 of D2VH"
XX
XX CN1544467-A.
XX
XX 10-NOV-2004.
XX
XX 13-NOV-2003; 2003CN-01105920.
XX
XX 13-NOV-2003; 2003CN-01105920.
XX
XX (UFO-) UNIV FOURTH MILITARY MEDICAL.
XX
XX Jin B, Liu X, Yang K;
XX

DR WPI; 2005-153079/17.
DR P-PsDB; AEA40006.
XX
XX Variable region gene of high neutralization activity monoclonal antibody
PT of tumor necrosis factor and its preparation.
XX
PS Claim 1; Page 3; 20pp; Chinese.
XX
XX The invention relates to a method for preparing variable region genes of
CC high neutralization activity tumor necrosis factor (TNF) resistant
CC monoclonal antibody (D2 mAb). The method comprises using recombinant
CC human TNF immune BALB/c mouse to prepare a plurality of mouse anti-TNF
CC monoclonal antibody, carrying out an extracorporeal blocking-up
CC experiment to screen anti-TNF monoclonal antibody with high
CC neutralization activity. By cloning the monoclonal antibody light chain
CC and heavy chain variable region (VL and VH respectively) genes, the
CC monoclonal antibody light chain and heavy chain variable region gene
CC sequence and amino acid sequence can be obtained, and the utility of the
CC gene sequence and protein sequence can be confirmed. This sequence
CC represents DNA encoding the complementarity determining region, CDR1 of
CC D2VH.
XX
SQ Sequence 15 BP; 4 A; 4 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 30 GTGCATCCAGAGC 43
DB 15 GTGCATCCAGAGC 2

RESULT 619
AEB21700/c
ID AEB21700 standard; DNA; 15 BP.
XX
AC AEB21700;
XX
DT 08-SEP-2005 (first entry)
XX
DE Anti-Nogo-antibody A2A10/3 CDR 1 DNA SEQ ID NO 22.
XX
KW neuroprotective; nootropic; cerebroprotective; vasotropic;
KW antiparkinsonian; anticonvulsant; protein production; therapeutic;
KW pharmaceutical; amyloidosis; metabolic disorder;
KW cerebrovascular ischemia; cardiovascular disease; neurological disease;
KW brain injury; injury; spinal cord injury; vulnertary; dementia;
KW peripheral neuropathy; parkinsons disease; Huntingtons chorea;
KW genetic disorder; Creutzfeldt Jakob disease; infection;
KW motor neurone disease; cns-gen.; muscular-gen.; myositis;
KW antiinflammatory; inflammation; musculoskeletal disease;
KW Alzheimers disease; degeneration; antibody; heavy chain variable region;
KW ds.
XX
XX unidentified.
XX
XX WO2005061545-A2.
XX
XX 07-JUL-2005.
XX
XX 20-DEC-2004; 2004WO-GB005343.
XX
XX 22-DEC-2003; 2003GB-00029684.
XX
XX 22-DEC-2003; 2003GB-00029711.
XX
XX (GLAX) GLAXO GROUP LTD.
XX
XX Hussain I, PyinJha RK;
XX
XX WPI; 2005-522181/53.
XX
XX P-PsDB; AEB21682.
XX

PT Modulating production of amyloidogenic peptide in, e.g. Alzheimer's
PT disease, by contacting cell and Nogo polypeptide with Nogo antagonist.
XX
PS Disclosure; SEQ ID NO 22; 53pp; English.
XX
CC The invention describes a method of modulating production of an
CC amyloidogenic peptide comprising contacting a cell which is expressing
CC the precursor from which the amyloidogenic peptide is derived and a Nogo
CC polypeptide, with a Nogo antagonist. Also described are: use of a Nogo
CC antagonist in the manufacture of a medicament for the treatment or
CC prophylaxis of a disease involving amyloidosis; and a method of treatment
CC or prophylaxis of Alzheimer's disease comprising administering to the
CC human in need an anti-Nogo antibody. The invention is used for modulating
CC production of amyloidogenic peptide in, e.g. Alzheimer's disease, stroke,
CC traumatic brain injury and spinal cord injury, fronto-temporal dementias,
CC peripheral neuropathy, Parkinson's disease, Huntington's disease,
CC Creutzfeldt-Jakob disease, amyotrophic lateral sclerosis, multiple
CC sclerosis, or inclusion body myositis. The invention provides an
CC unexpected route for therapeutic intervention in particularly Alzheimer's
CC disease. This sequence encodes anti-Nogo-antibody 2A10/3 heavy chain
CC complementarily determining region (CDR) 1.
XX
SQ Sequence 15 BP; 4 A; 4 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 15 GTGCATCCAGAGC 2
RESULT 620
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ID AEB08734 standard; DNA; 15 BP.
XX
AC AEB08734;
XX
DT 08-SEP-2005 (first entry)
XX
DE antibody 2A10 heavy chain CDR DNA SEQ ID NO 22.
XX
KW cerebroprotective; vasotropic; neuroprotective; vulnerary; nootropic;
KW antiparkinsonian; anticonvulsant; neuroleptic; antibody engineering;
KW pharmaceutical; cerebrovascular ischemia; cardiovascular disease;
KW neurological disease; brain injury; injury; spinal cord injury;
KW Alzheimer's disease; degeneration; dementia; neuropathy;
KW parkinsons disease; Huntingtons chorea; genetic disorder;
KW multiple sclerosis; immune disorder; Creutzfeldt Jakob disease;
KW infection; schizophrenia; psychiatric disorder; motor neurone disease;
KW cns-gen.; muscular-gen.; ds.
XX
OS Unidentified.
XX
PN WO2005061544-A2.
XX
PD 07-JUL-2005.
XX
PF 20-DEC-2004; 2004WO-GB005325.
XX
PR 22-DEC-2003; 2003GB-00029684.
XX
PR 22-DEC-2003; 2003GB-00029711.
XX
PA (GLAXO) GLAXO GROUP LTD.
XX
PI Ellis JH, Bon-Duval A, Grundy RI, Hussain F, Mcadam R;
PI Plumptre C, Pirinjah RK, Wilson PA;
XX
DR WPI; 2005-479448/48.
XX
DR P-PSDB; AEB08717.
XX
PT New antibody or its functional fragment that binds with and neutralizes

PT human neurite outgrowth useful for treating or prophylaxis of stroke and
PT other neurological disease e.g. traumatic brain injury, spinal cord
PT injury, Alzheimer's disease.
XX
PS Disclosure; SEQ ID NO 22; 143pp; English.
XX
CC The invention describes an antibody (A1) or its functional fragment, that
CC binds with and neutralizes human neurite outgrowth (NOCO). Also described
CC are: providing a first vector encoding a heavy chain of the antibody;
CC providing a second vector encoding a light chain of the antibody; co-
CC transfected a mammalian host cell with the first and second vectors;
CC culturing the host cell in culture media (preferably serum free) under
CC conditions permissive to the secretion of the antibody from the host cell
CC into the culture media; recovering (and optionally purifying) the
CC secreted antibody; and promoting axonal sprouting involving contacting a
CC human axon with an anti-NOCO antibody. The antibody is useful in the
CC preparation of a medicament for treating or prophylaxis of stroke and
CC other neurological disease/disorders (e.g. traumatic brain injury, spinal
CC cord injury, Alzheimer's disease, frontotemporal dementias (taupathies),
CC peripheral neuropathy, Parkinson's disease, Huntington's disease and
CC multiple sclerosis); Creutzfeldt-Jakob disease (CJD), Schizophrenia,
CC amyotrophic lateral sclerosis (ALS), inclusion body myositis. The
CC antibody inhibits neurodegeneration and/or promotes functional recovery
CC in a human patient suffering, or at risk of developing, stroke or other
CC neurological diseases/disorder. This sequence encodes an antibody 2A10
CC heavy chain complementarily region (CDR) that can be used in the creation
CC of anti-NOCO-antibody of the invention.
XX
SQ Sequence 15 BP; 4 A; 4 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 30 GTGCATCCAGAGC 43
DB 15 GTGCATCCAGAGC 2
RESULT 621
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AC AEB99140;
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DT 23-FEB-2006 (first entry)
XX
DE Human c-fos FRET quencher oligonucleotide #4.
XX
KW analyte detection; drug screening; c-fos; ss.
XX
OS Homo sapiens.
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OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 15 /*tag= a
FT /note= "Red oxazine dye labeled"
XX
PN WO2005121359-A1.
XX
PD 22-DEC-2005.
XX
PF 11-JUN-2004; 2004WO-EP006344.
XX
PF 11-JUN-2004; 2004WO-EP006344.
XX
PR 11-JUN-2004; 2004WO-EP006344.
XX
PA (EVOTEC) EVOTEC AG.
XX
PI Hinnaah SC, Lambroe D, Droegge S, Jaeger S, Gall K, Stuermer W;
PI Schaefer M;
XX
DR WPI; 2006-056856/06.
XX

XX Detecting (nucleic acid) analytes in a sample, useful in high throughput
 PT screening and diagnostics, comprises contacting the sample with detection
 PT probes, solid support and capture probes, and detecting by confocal
 PT observation.

XX Example 1; Page 22; 54pp; English.

XX The invention relates to a method of detecting analytes in a sample
 CC comprising providing a solid support, providing capture probes bound or
 CC capable of being bound to the support, providing detection probes capable
 CC of binding to the analytes, contacting the sample with the probes and
 CC solid support, and detecting through confocal observation the analytes
 CC which are bound to the detection probes. The method is useful for
 CC detecting (and optionally quantifying) analytes in a sample. The analytes
 CC are preferably nucleic acids. The method may comprise adding a
 CC potentially pharmaceutically active substance or drug modulates the
 CC sample and analyzing whether the substance or drug modulates the
 CC generation of the analytes. The method is useful in screening for
 CC potentially pharmaceutically active substances, in diagnostics, or in
 CC determining any potential side effects of drugs. The method is suitable
 CC for detecting low concentrations of nucleic acid analytes without
 CC amplification steps, and with direct detection of the analytes in a
 CC homogeneous format without washing or other separation steps. The method
 CC is suitable for high throughput applications such as mass diagnostics and
 CC drug testing and development. The present sequence represents a human c-
 CC fos FRBT quencher oligonucleotide.

XX Sequence 15 BP; 1 A; 5 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 15;

Best Local Similarity 92.9%; Fred.No. 3.3e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 GGTGTGTGCAGCCC 14

Search completed: June 12, 2006, 06:15:46
 Job time : 15 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2006, 06:09:50 ; Search time 10 Seconds
(without alignments)
3.457 Million cell updates/sec

Title: US-09-930-503A-6

Perfect score: 1766
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Scoring table:
IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 508 seqs, 9787 residues

Total number of hits satisfying chosen parameters: 1016

Minimum DB seq length: 8
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 488 summaries

Database : us-09-930-503a-6.sl.rge4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	30	1.7	CO800306	ACCESSION:CO800306
3	28	1.6	CS174800	ACCESSION:CS174800
4	27	1.5	CO800305	ACCESSION:CO800305
5	27	1.5	CO800321	ACCESSION:CO800321
6	27	1.5	CS174801	ACCESSION:CS174801
7	25.8	1.5	CO800314	ACCESSION:CO800314
8	25.2	1.4	AR109708	ACCESSION:AR109708
9	24.8	1.4	134577	ACCESSION:134577
10	24.8	1.4	136528	ACCESSION:136528
11	24.8	1.4	176284	ACCESSION:176284
12	24.2	1.4	AR109715	ACCESSION:AR109715
13	24	1.4	AR109808	ACCESSION:AR109808
14	24	1.4	CS186499	ACCESSION:CS186499
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16	24	1.4	AR150645	ACCESSION:AR150645
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40	21.8	1.2	27	ACCESSION:E37242
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ORGANISM	synthetic construct other sequences; artificial sequences.
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TITLE Gerbil neurokinin 1 receptor
JOURNAL Patent: WO 2005090401-A 3 29-SEP-2005;
Astrazeneca AB (SE)

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		PAT 28-APR-2004

DEFINITION	Sequence 1 from facenc
ACCESSION	CQ800305
VERSION	CQ800305.1 GI:46849171
KEYWORDS	

SOURCE	ORGANISM	REFERENCE
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synthetic construct	synthetic construct	1
other sequences; artificial sequences.	other sequences; artificial sequences.	1

AUTHORS
Gibbins, J.M., Lowry, P.J., Graham, G.J. and Page, N.M.
TITLE
Treatment of vascular diseases
PARIENT: WO 2004030695-A 4 15-Apr-2004;
UNIVERSITY OF READING (GB)
LOCATION/CH3145690

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VERSION	CQ800321.1				
KEYWORDS	GI:46849187				
SOURCE	.				
ORGANISM	synthetic construct				
	synthetic construct				

REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES
1	Gibbins, J. M., Lowry, P. J., Graham, G. J. and Page, N. M.	Treatment of vascular diseases	Patent: WO 2004/030695-A 20 15-APR-2004;	1
		University of Reading (GB)		37
		Location/Qualifiers		

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Db 27 CTACTCAACCCAGAGACCATGCCAG 1

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ACCESSION	CS174801						
VERSION	CS174801.1						GI:77625636

SOURCE ORGANISM	synthetic construct synthetic construct other sequences; artificial sequences
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AUTHORS Dirmota, T.
TITLE Gerbil neurokinin 1 receptor
JOURNAL Patent: WO 2005090401-A 4 29-SEP-2005;
AstraZeneca AB (SE)

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LOCUS				
CQ800314				

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VERSION      CQ800314.1  GI:46849180
KEYWORDS
SOURCE       synthetic construct

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REFERENCE
AUTHORS
1
Gibbins, J.M., Lowry, P.J., Graham, G.J. and Page, N.M

TITLE Treatment of vascular diseases
JOURNAL Patent: WO 2004030695-A 13 15-APR-2004;
University of Reading (GB)
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LOCUS Sequence 132 from patent US 6114139.
DEFINITION ARI09708
ACCESSION ARI09708 GI:12825984
VERSION ARI09708.1 GI:12825984
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 30)
AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.
TITLE G-protein coupled receptor protein and a DNA encoding the receptor
JOURNAL Patent: US 6114139-A 132 05-SEP-2000;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.4%; Score 25.2; DB 1; Length 30;
Best Local Similarity 90.0%; Pred. No. 23;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 979 TTGGCCATCTGCTGCTGCCCTTCACATC 1008
Db 1 TTGGCCATCTGCTGCTGCCCTTCACATC 30

RESULT 9
I34577 30 bp DNA linear PAT 06-FEB-1997
LOCUS Sequence 6 from patent US 5596088.
DEFINITION I34577
ACCESSION I34577 GI:1825368
VERSION I34577.1 GI:1825368
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 30)
AUTHORS Boucher,R.C., Weisman,G.A., Turner,J.T., Harden,T.K., Parr,C.E.,
Sullivan,D.M., Erb,L.J. and Lustig,K.D.
TITLE DNA Encoding the human P.sub.2U receptor and null cells expressing
P.sub.2U receptors
JOURNAL Patent: US 5596088-A 6 21-JAN-1997;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.4%; Score 24.8; DB 1; Length 30;
Best Local Similarity 76.7%; Pred. No. 26;
Matches 23; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 979 TTGGCCATCTGCTGCTGCCCTTCACATC 1008
Db 1 TTGGCCATCTGCTGCTGCCCTTCACATC 1008

Db 30 TTGGCCCTCWCCTKCTGCTTSCACGTC 1

RESULT 10
I36528/c 30 bp DNA linear PAT 13-MAY-1997
LOCUS Sequence 6 from patent US 5607836.
DEFINITION I36528
ACCESSION I36528 GI:2086353
VERSION I36528.1 GI:2086353
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 30)
AUTHORS Boucher,R.C., Weisman,G.A., Turner,J.T., Harden,T.K., Parr,C.E.,
Sullivan,D.M., Erb,L.J. and Lustig,K.D.
TITLE Methods of detecting compounds which bind to the P.sub.2U receptor
JOURNAL Patent: US 5607836-A 6 04-MAR-1997;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.4%; Score 24.8; DB 1; Length 30;
Best Local Similarity 76.7%; Pred. No. 26;
Matches 23; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 979 TTGGCCATCTGCTGCTGCCCTTCACATC 1008
Db 30 TTGGCCCTCWCCTKCTGCTTSCACGTC 1

RESULT 11
I76284/c 30 bp DNA linear PAT 03-APR-1998
LOCUS Sequence 6 from patent US 5691156.
DEFINITION I76284
ACCESSION I76284 GI:3012438
VERSION I76284.1 GI:3012438
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 30)
AUTHORS Boucher,R.C., Weisman,G.A., Turner,J.T., Harden,T.K., Parr,C.E.,
Sullivan,D.M., Erb,L.J. and Lustig,K.D.
TITLE Method of inhibiting cell growth with the P.sub.2U receptor
JOURNAL Patent: US 5691156-A 6 25-NOV-1997;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.4%; Score 24.8; DB 1; Length 30;
Best Local Similarity 76.7%; Pred. No. 26;
Matches 23; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 979 TTGGCCATCTGCTGCTGCCCTTCACATC 1008
Db 30 TTGGCCCTCWCCTKCTGCTTSCACGTC 1

RESULT 12
ARI09715 30 bp DNA linear PAT 14-FEB-2001
LOCUS Sequence 139 from patent US 6114139.
DEFINITION ARI09715
ACCESSION ARI09715 GI:12825991
VERSION ARI09715.1 GI:12825991
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 30)

AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.
TITLE G-protein coupled receptor protein and a DNA encoding the receptor
JOURNAL Patent: US 6114139-A 139 05-SEP-2000;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.4%; Score 24.2; DB 1; Length 30;
Best Local Similarity 89.7%; Pred. No. 32;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 979 TTGCCATCTGCTGGCTGCCCTTCCACAT 1007
Db 1 TTGGCATCTGCTGGCTGCCCTTCCACGT 29

RESULT 13
LOCUS ARI09808 24 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 232 from patent US 6114139.
ACCESSION ARI09808
VERSION ARI09808.1 GI:12826084
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.
TITLE G-protein coupled receptor protein and a DNA encoding the receptor
JOURNAL Patent: US 6114139-A 232 05-SEP-2000;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.4%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 979 TTGCCATCTGCTGGCTGCCCTTC 1002
Db 1 TTGGCATCTGCTGGCTGCCCTTC 24

RESULT 14
LOCUS CS186499 24 bp DNA linear PAT 04-NOV-2005
DEFINITION Sequence 5 from Patent WO2005100986.
ACCESSION CS186499
VERSION CS186499.1 GI:80748371
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 other sequences; artificial sequences.

AUTHORS Golz,S.
TITLE Diagnostic and therapeutics for diseases associated with
JOURNAL lachykinin receptor 1(tacr1)
PATENT: WO 2005100986-A 5 27-OCT-2005;
Bayer Healthcare AG (DE)
FEATURES Location/Qualifiers
source 1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="probe"

Query Match 1.4%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 296 CCTGCAAAATGTCCTTTGGGAG 319

Db 1 CCTGCAAAATGTCCTTTGGGAG 24

RESULT 15
LOCUS ARI09637/c 29 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 61 from patent US 6114139.
ACCESSION ARI09637
VERSION ARI09637.1 GI:12825913
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 29)
AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.
TITLE G-protein coupled receptor protein and a DNA encoding the receptor
JOURNAL Patent: US 6114139-A 61 05-SEP-2000;
FEATURES Location/Qualifiers
source 1..29
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.4%; Score 24; DB 1; Length 29;
Best Local Similarity 72.4%; Pred. No. 32;
Matches 21; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 979 TTGCCATCTGCTGGCTGCCCTTCCACAT 1007
Db 29 TTCRYNTCTGCTGGCTGCCCTTCTCMT 1

RESULT 16
LOCUS ARI50645/c 29 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 32 from patent US 6228984.
ACCESSION ARI50645
VERSION ARI50645.1 GI:15115236
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 29)
AUTHORS Hinuma,S., Habata,Y., Kawamata,Y., Hosoya,M., Fujii,R., Fukusumi,S. and Kitada,C.
TITLE Polypeptides their production and use
JOURNAL Patent: US 6228984-A 32 08-MAY-2001;
FEATURES Location/Qualifiers
source 1..29
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.4%; Score 24; DB 1; Length 29;
Best Local Similarity 72.4%; Pred. No. 32;
Matches 21; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 979 TTGCCATCTGCTGGCTGCCCTTCCACAT 1007
Db 29 TTCRYNTCTGCTGGCTGCCCTTCTCMT 1

RESULT 17
LOCUS E11515/c 29 bp DNA linear PAT 29-SEP-1997
DEFINITION primer for screening novel G protein(guanine nucleotide-binding
protein) coupling type receptor protein from rabbit stomach pylorus
smooth muscle.
E11515
ACCESSION E11515.1 GI:22025151
VERSION E11515.1
KEYWORDS JP 196154682-A/3.
SOURCE unidentified
ORGANISM unidentified sequences.

REFERENCE 1 (bases 1 to 29)
 AUTHORS Hinuma,K., Fujii,A. and Kawamata,Y.
 TITLE NEW G PROTEIN COUPLED TYPE RECEPTOR PROTEIN, ITS PRODUCTION AND
 JOURNAL Patent: JP 1996154682-A 3 18-JUN-1996;
 TAKEDA CHEM IND LTD

COMMENT
 OS None
 OC Artificial sequences.
 PN JP 1996154682-A/3
 PD 18-JUN-1996
 PP 02-DEC-1994 JP 1994299792
 P1 HINUMA KUNIJU, FUJII AKIRA, KAWAMATA YUJI
 PC C12N15/09,A61K48/00,C07K14/705,C12P21/02,G01N33/566; CC
 strandedness: Single;
 CC topology: linear;
 CC hypothetical: No;
 CC anti-sense: Yes;
 FH Key
 FT Location/Qualifiers

FEATURES
 source Location/Qualifiers
 FT 1..29 /organism='Artificial sequences'.
 1..29 /mol_type='genomic DNA'
 /db_xref='taxon:32644'

Query Match 1.4%; Score 24; DB 1; Length 29;
 Best Local Similarity 72.4%; Pred. No. 32;
 Matches 21; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 979 TTGGCCATCTGCTGCGCTGCCCTTCACAT 1007
 |||:::|||||:|||||:|:|:
 Db 29 TTCRYSNCTGCTGCTGCGCTGCCTCWT 1

RESULT 18
 E16194/c 29 bp DNA linear PAT 28-JUL-1999
 LOCUS E16194
 DEFINITION primer.
 ACCESSION E16194
 VERSION E16194.1 GI:5710877
 KEYWORDS JP 1998146192-A/18.
 SOURCE unidentified
 ORGANISM unclassified
 1 (bases 1 to 29)
 Hinuma,K., Habatake,Y., Kawamata,Y., Hosoya,M., Fujii,A.,
 Fukuzumi,M. and Kitada,C.
 NEW PHYSIOLOGICALLY ACTIVE SUBSTANCE, ITS PRODUCTION AND USE
 Patent: JP 1998146192-A 18 02-JUN-1998;
 TAKEDA CHEM IND LTD

COMMENT
 OS None
 OC Artificial sequences.
 PN JP 1998146192-A/18
 PD 02-JUN-1998
 PP 26-DEC-1995 JP 1996348328
 PR 28-DEC-1995 JP 95P 343371, 15-MAR-1996 JP 96P 59419, PR
 12-AUG-1996 JP 96P 211805, 18-SEP-1996 JP 96P 246573 PI
 HINUMA KUNIJU, HABATAKE YUUCO, KAWAMATA YUJI, HOSOTA MASAKI, PI
 FUJII AKIRA,
 PI FUKUZUMI MASASHI, KITADA CHIHIRO
 PC C12N15/09,A61K31/70,A61K31/70,A61K31/70,A61K31/70,
 PC A61K31/70,
 PC A61K35/76,A61K38/00,A61K48/00,C07H21/00,C07K14/47,C12N5/10, PC
 C12P21/02,
 PC C12Q1/02,G01N33/566, (C12N5/10,C12R1:91), (C12P21/02,C12R1:91);
 CC strandedness: Single;
 CC topology: linear;
 CC hypothetical: No;
 FH Key
 FT Location/Qualifiers
 FT source 1..29 /organism='Artificial sequences'.
 FT

FEATURES
 source Location/Qualifiers
 FT 1..29 /organism='unidentified'
 /mol_type='genomic DNA'
 /db_xref='taxon:32644'

Query Match 1.4%; Score 24; DB 1; Length 29;
 Best Local Similarity 72.4%; Pred. No. 32;
 Matches 21; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 979 TTGGCCATCTGCTGCGCTGCCCTTCACAT 1007
 |||:::|||||:|||||:|:|:
 Db 29 TTCRYSNCTGCTGCTGCGCTGCCTCWT 1

RESULT 19
 E27220/c 29 bp DNA linear PAT 18-JUN-2001
 LOCUS E27220
 DEFINITION Novel physiologically active substance, process for producing the
 same and utilization thereof.
 ACCESSION E27220
 VERSION E27220.1 GI:13025237
 KEYWORDS JP 199909286-A/11.
 SOURCE unidentified
 ORGANISM unclassified
 unclassified sequences.
 1 (bases 1 to 29)
 Shuji,H. and Shoji,F.
 Novel physiologically active substance, process for producing the
 same and utilization thereof
 Patent: JP 199909286-A 11 19-JAN-1999;
 TAKEDA CHEM IND LTD

COMMENT
 OS Unidentified
 PN JP 199909286-A/11
 PD 19-JAN-1999
 PP 27-APR-1998 JP 1998117189

QY 979 TTGGCCATCTGCTGCGCTGCCCTTCACAT 1007
 |||:::|||||:|||||:|:|:
 Db 29 TTCRYSNCTGCTGCTGCGCTGCCTCWT 1

RESULT 20
 E28278/c 29 bp DNA linear PAT 18-JUN-2001
 LOCUS E28278
 DEFINITION Utilization of peptide.
 ACCESSION E28278
 VERSION E28278.1 GI:13025312
 KEYWORDS JP 1999071300-A/18.

SOURCE unidentified
ORGANISM unidentified
REFERENCE unclassified sequences.
AUTHORS 1 (bases 1 to 29)
TITLE Shuji,H., Ryo,F., Yuji,K. and Hirokazu,M.
JOURNAL Utilization of peptide
Patent: JP 199071300-A 18 16-MAR-1999;
TAKEDA CHEM IND LTD
COMMENT OS Unidentified
PN JP 199071300-A/18
PD 16-MAR-1999
PF 22-JUN-1998 JP 1998175007
PI SHUJI HINUMA, RYO FUJII, YUJI KAWAMATA, HIROKAZU MATSUMOTO PC
A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00, PC
A61K38/00,
PC A61K38/00,A61K38/00,C07K7/08,C07K14/705//C12N15/09,C12P21/02,
PC (C12P21/02,C12R1:91),A61K37/02,A61K37/02,A61K37/02,A61K37/02,
PC A61K37/02,
PC A61K37/02,A61K37/02,A61K37/02,A61K37/02,C12N15/00 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..29
FEATURES
source Location/Qualifiers
1..29 /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 1.4%; Score 24; DB 1; Length 29;
Best Local Similarity 72.4%; Pred. No. 32;
Matches 21; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
Qy 979 TTGGCCATCTGCTGCTGCCCTTCACAT 1007
Db 29 TTCRYSNCTCTGCTGCTGCCCTTCCTCMT 1
RESULT 21
AR300947/c 29 bp DNA 1linear PAT 12-JUN-2003
LOCUS AR300947
DEFINITION Sequence 61 from patent US 6538107.
ACCESSION AR300947
VERSION AR300947.1 GI:31688620
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 29)
AUTHORS Hinuma,S., Ito,Y. and Fujii,R.
TITLE G protein coupled receptor protein production, and use thereof
JOURNAL Patent: US 6538107-A 61 25-MAR-2003;
Takeda Chemical Industries, Ltd.; Osaka;
JPX;
FEATURES
source Location/Qualifiers
1..29 /organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.4%; Score 24; DB 1; Length 29;
Best Local Similarity 72.4%; Pred. No. 32;
Matches 21; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
Qy 979 TTGGCCATCTGCTGCTGCCCTTCACAT 1007
Db 29 TTCRYSNCTCTGCTGCTGCCCTTCCTCMT 1
RESULT 22
AR583779/c 29 bp DNA 1linear PAT 15-DEC-2004
LOCUS AR583779

DEFINITION Sequence 32 from patent US 6794491.
ACCESSION AR583779
VERSION AR583779.1 GI:56621382
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 29)
AUTHORS Hinuma,S., Habata,Y., Kawamata,Y., Hosoya,M., Fujii,R., Fukusumi,S.
TITLE Polypeptides, their production and use
JOURNAL Patent: US 6794491-A 32 21-SEP-2004;
Takeda Chemical Industries, Ltd.; Osaka;
JPX;
FEATURES
source Location/Qualifiers
1..29 /organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.4%; Score 24; DB 1; Length 29;
Best Local Similarity 72.4%; Pred. No. 32;
Matches 21; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
Qy 979 TTGGCCATCTGCTGCTGCCCTTCACAT 1007
Db 29 TTCRYSNCTCTGCTGCTGCCCTTCCTCMT 1
RESULT 23
AR651208/c 29 bp DNA 1linear PAT 20-APR-2005
LOCUS AR651208
DEFINITION Sequence 32 from patent US 6881545.
ACCESSION AR651208
VERSION AR651208.1 GI:62795419
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 29)
AUTHORS Hinuma,S., Habata,Y., Kawamata,Y., Hosoya,M., Fujii,R., Fukusumi,S.
TITLE Polypeptides, their production and use
JOURNAL Patent: US 6881545-A 32 19-APR-2005;
Takeda Chemical Industries, Ltd.; Osaka;
JPX;
FEATURES
source Location/Qualifiers
1..29 /organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.4%; Score 24; DB 1; Length 29;
Best Local Similarity 72.4%; Pred. No. 32;
Matches 21; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
Qy 979 TTGGCCATCTGCTGCTGCCCTTCACAT 1007
Db 29 TTCRYSNCTCTGCTGCTGCCCTTCCTCMT 1
RESULT 24
AR109661 27 bp DNA 1linear PAT 14-FEB-2001
LOCUS AR109661
DEFINITION Sequence 85 from patent US 6114139.
ACCESSION AR109661
VERSION AR109661.1 GI:12825937
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 27)
AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.
TITLE G-protein coupled receptor protein and a DNA encoding the receptor
JOURNAL Patent: US 6114139-A 85 05-SEP-2000;

FEATURES
source
Location/Qualifiers
1..27
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.3%; Score 23.8; DB 1; Length 27;
Best Local Similarity 92.6%; Pred. No. 29;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 979 TTGGCATCTGCTGGCTGCCCTTCAC 1005
Db 1 TTGGCATCTGCTGGCTGCCCTTCAC 27

RESULT 25
117149/c 117149 24 bp DNA linear PAT 03-APR-1996
LOCUS Sequence 4 from patent US 5484886.
DEFINITION 117149
ACCESSION 117149 GI:1252057
VERSION 117149.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 24)
TITLE Fong, T.M. and Strader, C.D.
JOURNAL Human neurokinin-1 receptor
Patent: US 5484886-A 4 16-JAN-1996;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.3%; Score 23; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1105 ATGTACAACCCCATCATCTACTG 1127
Db 24 ATGTACAACCCCATCATCTACTG 2

RESULT 26
AX468718/c AX468718 24 bp DNA linear PAT 16-JUL-2002
LOCUS Sequence 34 from Patent WO0213799.
DEFINITION AX468718
ACCESSION AX468718
VERSION AX468718.1 GI:21901488
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS 1
TITLE synthetic construct
JOURNAL other sequences; artificial sequences.
1 Henry, J.L., Cahill, C.M. and Yaahpal, K.
Oligonucleotides and other modulators of the nk-1 receptor pathway
Patent: WO 0213799-A 34 21-FEB-2002;
FEATURES Location/Qualifiers
source 1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match
Best Local Similarity 1.3%; Score 23; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1105 ATGTACAACCCCATCATCTACTG 1127
Db 24 ATGTACAACCCCATCATCTACTG 2

RESULT 27
117150/c 117150 24 bp DNA linear PAT 03-APR-1996
LOCUS Sequence 5 from patent US 5484886.
DEFINITION 117150
ACCESSION 117150
VERSION 117150.1 GI:1252058
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 24)
TITLE Fong, T.M. and Strader, C.D.
JOURNAL Human neurokinin-1 receptor
Patent: US 5484886-A 5 16-JAN-1996;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.3%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 35;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1051 AAGTTATCCAGCAGGCTTACTG 1074
Db 24 AAGTTATCCAGCAGGCTTACTG 1

RESULT 28
AR109658 AR109658 27 bp DNA linear PAT 14-FEB-2001
LOCUS Sequence 82 from patent US 6114139.
DEFINITION AR109658
ACCESSION AR109658
VERSION AR109658.1 GI:12825934
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 27)
TITLE Hinuma, S., Hosoya, M., Fujii, R., Ohtaki, T., Fukusumi, S. and Ohgi, K.
JOURNAL G-protein coupled receptor protein and a DNA encoding the receptor
Patent: US 6114139-A 82 05-SEP-2000;
FEATURES Location/Qualifiers
source 1..27
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.3%; Score 22.2; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 49;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 979 TTGGCATCTGCTGGCTGCCCTTCAC 1005
Db 1 TTGGCATCTGCTGGCTGCCCTTCAC 27

RESULT 29
AR109660 AR109660 27 bp DNA linear PAT 14-FEB-2001
LOCUS Sequence 84 from patent US 6114139.
DEFINITION AR109660
ACCESSION AR109660
VERSION AR109660.1 GI:12825936
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 27)
TITLE Hinuma, S., Hosoya, M., Fujii, R., Ohtaki, T., Fukusumi, S. and Ohgi, K.
JOURNAL G-protein coupled receptor protein and a DNA encoding the receptor
Patent: US 6114139-A 84 05-SEP-2000;
FEATURES Location/Qualifiers
source 1..27

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/organism="unknown"
/mol_type="unassigned DNA"

Query Match
  1.3%; Score 22.2; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 49;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 979 TTGGCCATCTGCTGCTGCCCTTCAC 1005
Db 1 TTGGCCATCTGCTGCTGCCCTTCAC 27

RESULT 30
LOCUS ARI09595 27 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 2 from patent US 6114139.
ACCESSION ARI09595
VERSION ARI09595.1 GI:12825871
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 27)
AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.
TITLE G-protein coupled receptor protein and a DNA encoding the receptor
JOURNAL Patent: US 6114139-A 2 05-SEP-2000;
FEATURES
    Location/Qualifiers
        1..27
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match
  1.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 56;
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 979 TTGGCCATCTGCTGCTGCCCTTCAC 1005
Db 27 TTGGCCATCTGCTGCTGCCCTTCAC 1

RESULT 31
LOCUS ARI09652 27 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 76 from patent US 6114139.
ACCESSION ARI09652
VERSION ARI09652.1 GI:12825928
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 27)
AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.
TITLE G-protein coupled receptor protein and a DNA encoding the receptor
JOURNAL Patent: US 6114139-A 76 05-SEP-2000;
FEATURES
    Location/Qualifiers
        1..27
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match
  1.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 56;
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 979 TTGGCCATCTGCTGCTGCCCTTCAC 1005
Db 1 TTGGCCATCTGCTGCTGCCCTTCAC 27

RESULT 32
LOCUS ARI50643 27 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 30 from patent US 6228984.
ACCESSION ARI50643
```

```

VERSION ARI50643.1 GI:15115234
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS Hinuma,S., Habata,Y., Kawamata,Y., Hosoya,M., Fujii,R., Fukusumi,S.
and Kitada,C.
TITLE Polypeptides their production and use
JOURNAL Patent: US 6228984-A 30 08-MAY-2001;
FEATURES
    Location/Qualifiers
        1..27
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match
  1.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 56;
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 979 TTGGCCATCTGCTGCTGCCCTTCAC 1005
Db 27 TTGGCCATCTGCTGCTGCCCTTCAC 1

RESULT 33
LOCUS E11748 27 bp DNA linear PAT 29-SEP-1997
DEFINITION Primer for screening rabbit guanine nucleotide-binding protein
coupling type receptor protein.
ACCESSION E11748
VERSION E11748.1 GI:22025384
KEYWORDS JP 1996193099-A/3.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 27)
AUTHORS Hinuma,K., Fujii,A. and Kawamata,Y.
TITLE NEW G PROTEIN COUPGATED RECEPTOR PROTEIN, ITS PRODUCTION AND USE
JOURNAL Patent: JP 1996193099-A 3 30-JUL-1996;
COMMENT TAKEDA CHEM IND LTD
OS None
OC Artificial sequences.
PM JP 1996193099-A/3
PD 30-JUL-1996
PR 24-AUG-1995 JP 1995215798
PR 14-NOV-1994 JP 94P 279545
PI HINUMA KUNIJU, FUJII AKIRA, KAWAMATA YUJI
PC C07K14/705, C07H21/04, C12N1/21, C12N5/10, C12N15/09, PC
C12Q1/00//A61K48/00,
PC C12Q1/68;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: Yes;
FH Key
FT source
    Location/Qualifiers
        1..27
            /organism="Artificial sequences".
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"

Query Match
  1.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 56;
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 979 TTGGCCATCTGCTGCTGCCCTTCAC 1005
Db 27 TTGGCCATCTGCTGCTGCCCTTCAC 1
```

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RESULT 34
E12466/c
LOCUS      E12466      27 bp      DNA      linear      PAT 27-APR-1998
DEFINITION PCR primer for selective amplification and cloning of the family of
ACCESSION   E12466
VERSION     E12466.1 GI:3251299
KEYWORDS    JP 1997000268-A/2.
SOURCE      unidentified
ORGANISM    unidentified
REFERENCE   1 (bases 1 to 27)
AUTHORS     Hinuma,K., Hosoya,M., Fujii,A., Otaki,T., Fukuzumi,M. and
            Ooyoshi,K.
TITLE       NEW G PROTEIN COUPLATION TYPE RECEPTOR PROTEIN, ITS PRODUCTION AND
JOURNAL     TAKEDA CHEM IND LTD
COMMENT      OS None
            OC Artificial sequences.
            PN JP 1997000268-A/2
            PD 07-JAN-1997
            PR 10-AUG-1995 JP 1995224544
            PR 11-AUG-1994 JP 94P 189272, 11-AUG-1994 JP 94P 189273, PR
            11-AUG-1994 JP 94P 189274, 30-SEP-1994 JP 94P 236356, PR
            30-SEP-1994 JP 94P 236357, 02-NOV-1994 JP 94P 270017, PR
            28-DEC-1994 JP 94P 326611, 20-JAN-1995 JP 95P 7177, PR
            16-MAR-1995 JP 95P 57186, 19-APR-1995 JP 95P 93989, PI
            HINUMA KUNITI, HOSoya MASAki, FUJII AKIRA, OTAKI TETSUYA, PI
            FUKUZUMI MASASHI, OYOSHI KAZUHIRO
PC          C12N15/09, C07H21/04, C12N1/21, G01N33/53, G01N33/566//C07K14/705,
PC          C07K16/28,
PC          C12P21/02, C12P21/08, C12Q1/68, (C12N1/21, C12R1:19), (C12P21/02,
PC          C12R1:19);
CC          strandedness: Single;
CC          topology: linear;
FH          Location/Qualifiers
FT          source      1..27
FT          misc_feature 1..27 /organism='Artificial sequences' FT
FT          FT          /note='degenerate primer based on conserved
FT          amino acid
FT          sequences of the sixth transmembrane domain of
FT          known G
FT          protein-coupled receptors'.
FEATURES
source      1..27
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"

Query Match      1.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 56;
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      979 TTGGCCATCTGCTGCTGCCCTTCAC 1005
DB      27 TTGGCMTCTGCTGANTGCCYWCNAC 1

RESULT 35
E12660/c
LOCUS      E12660      27 bp      DNA      linear      PAT 27-APR-1998
DEFINITION Primer.
ACCESSION   E12660
VERSION     E12660.1 GI:3251492
KEYWORDS    JP 1997048800-A/4.
SOURCE      unidentified
ORGANISM    unidentified
REFERENCE   1 (bases 1 to 27)
AUTHORS     Hinuma,K., Fujii,A., Fukuzumi,M., Otaki,T., Hosoya,M., Oogi,K. and
            Onda,H.

```

```

TITLE       GALANIN RECEPTOR PROTEIN, ITS PRODUCTION AND USE
JOURNAL     TAKEDA CHEM IND LTD
COMMENT      OS None
            OC Artificial sequences.
            PN JP 1997048800-A/4
            PD 18-FEB-1997
            PR 12-OCT-1995 JP 1995289215
            PR 13-OCT-1994 JP 94P 247599, 28-DEC-1994 JP 94P 326610, PR
            31-MAY-1995 JP 95P 134412
            PI HINUMA KUNITI, FUJII AKIRA, FUKUZUMI MASASHI, OTAKI TETSUYA,
            PI HOSoya MASAki, OOGI KAZUHIRO, ONDA HARUO
PC          C07K14/72, C07H21/04, C12N5/10, C12N15/09, C12P21/02, PC
            G01N33/566//A61K38/00
PC          A61K38/00, A61K38/00, (C12P21/02, C12R1:91);
CC          strandedness: Single;
CC          topology: linear;
CC          hypothetical: No;
FH          Location/Qualifiers
FT          source      1..27
FT          FT          /organism='Artificial sequences'.
FT          Location/Qualifiers
FT          1..27
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"

Query Match      1.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 56;
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      979 TTGGCCATCTGCTGCTGCCCTTCAC 1005
DB      27 TTGGCMTCTGCTGANTGCCYWCNAC 1

RESULT 36
E14221/c
LOCUS      E14221      27 bp      DNA      linear      PAT 28-JUL-1999
DEFINITION Primer.
ACCESSION   E14221
VERSION     E14221.1 GI:5708904
KEYWORDS    JP 1997278798-A/5.
SOURCE      unidentified
ORGANISM    unidentified
REFERENCE   1 (bases 1 to 27)
AUTHORS     Hinuma,K., Sakamoto,J. and Hosoya,M.
TITLE       NEW G PROTEIN COUPLATED TYPE RECEPTOR PROTEIN, ITS PRODUCTION AND
JOURNAL     USE THEREOF
            Patent: JP 1997278798-A 5 28-OCT-1997;
            TAKEDA CHEM IND LTD
COMMENT      OS None
            OC Artificial sequences.
            PN JP 1997278798-A/5
            PD 28-OCT-1997
            PR 07-FEB-1997 JP 1997024190
            PR 07-FEB-1996 JP 96P 21562
            PI HINUMA KUNITI, SAKAMOTO JUNICHI, HOSoya MASAki PC
            C07K14/705, A61K38/00, C07H21/04, C07K16/28, C12N1/21, C12N15/09, PC
            C12P21/02,
PC          G01N33/566//A61K48/00, C12Q1/68, (C12N1/21, C12R1:19), (C12P21/02,
PC          C12R1:19);
CC          strandedness: Single;
CC          topology: linear;
FH          Location/Qualifiers
FT          source      1..27
FT          FT          /organism='Artificial sequences'.
FT          Location/Qualifiers
FT          1..27
            /organism="unidentified"

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/mol_type="genomic DNA"  
/db_xref="taxon:32644"
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Query Match	1.2%	Score 21.8;	DB 1;	Length 27;
Best Local Similarity	74.1%	Pred. No. 56;		
Matches 20; Conservative	4;	Mismatches 3;	Indels 0;	Gaps 0

Oy	979	TTCGCATCTGCTGGCTGCCCTTCCAC	1005
		::: :::	
Db	27	TTTGCCMTCTGCTGCGTGCCTYYWCNAC	1

RESULT 37
E16192/c

Query Match	1.2%	Score 21.8;	DB 1;	Length 27;
Best Local Similarity	74.1%;	Pred. No. 56;		
Matches 20;	Conservative 4;	Mismatches 3;	Indels 0;	Gaps 0;

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Qy      979 TTGCGCATCTGCTGSGCTGCGCCCTTCAC 1005
      ||||:||||| ||||: |||
Db      27  TTTCGCMTCTGCTGSGNTGCGCCYYWCNAC 1
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RESULT 38	27 bp	DNA	linear	PAT 18-JUN-2001
E27218/c				
LOCUS				
DEFINITION	Novel Physiologically active substance, process for producing the same and utilization thereof.			
ACCESSION	E27218			
VERSION	E27218.1	GI:13025235		
KEYWORDS	JP 1999009286-A/9.			

SOURCE ORGANISM	unidentified unidentified unclassified sequences
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JOURNAL Patent: JP 1999009286-A 9 19-JAN-1999
TAKEDA CHEM IND LTD
OS Unidentified

FEATURES	F1	/organism= undencelled
Location/Qualifiers		

Query Match	1.2%	Score 21.8;	DB 1;	Length 27;
Best Local Similarity	74.1%;	Pred. No. 56;		
Matches 20; Conservative	4;	Mismatches 3;	Indels 0;	Gaps 0;

QY	979	TTCGCATCTGCTGCTGCCCTTCAC	1009
		:	
Db	27	TTTGCCMTCTGCTGNTGCCYYWCNAC	1

RESULT 39				
E28276/c				
LOCUS	E28276	27 bp	DNA	linear
DEFINITION	Utilization of peptide.			
ACCESSION	E28276			
VERSION	E28276.1	GI:1302510		
KEYWORDS	JP 1999071300-A/16.			
SOURCE	unidentified			
ORGANISM	unidentified			
REFERENCE	unclassified sequences.			
AUTHORS	1 (bases 1 to 27)			
TITLE	Shuji,H., Ryo,F., Yui,K. and Hirokazu,M.			
JOURNAL	Utilization of peptide			
	Patent: JP 1999071300-A 16 16-MAR-1999;			
	TAKEDA CHEM IND LTD			
COMMENT	OS Unidentified			

P1 SHUJI HINUMA, RYO FUJII, YUJI KAMAMATA, HIROKAZU MATSUMOTO PC
 A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, PC
 A61K38/00,
 PC A61K38/00, A61K38/00, C07K7/08, C07K14/705//C12N15/09, C12P21/02,
 PC C12P21/02, C12P21:91), A61K37/02, A61K37/02, A61K37/02, A61K37/02,
 PC A61K37/02,
 PC A61K37/02, A61K37/02, A61K37/02, A61K37/02, C12N15/00 CC
 Strandedness: Single;
 CC Topology: Linear;
 FH Key Location/Qualifiers

FT source 1..27 /organism='Unidentified'.
FT Location/Qualifiers
source 1..27 /organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 1.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 56;
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 979 TTGGCATCTGCTGGCTGCCCTTCAC 1005
Db 27 TTGGCMTCTGCTGANTGCCYWCNAC 1

RESULT 40
E37242 27 bp DNA linear PAT 31-JUN-2002
LOCUS Novel physiologically active substance, process for producing the
DEFINITION same and use thereof.
ACCESSION E37242
VERSION E37242.1 GI:18624793
KEYWORDS JP 2000159798-A/4.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 27)
AUTHORS Hinuma,S., Tatemoto,K., Hosoya,M., Habata,Y., Fujii,R. and
Kitada,C.
TITLE Novel physiologically active substance, process for producing the
same and use thereof
PATENT: JP 2000159798-A 4 13-JUN-2000;
JOURNAL TAKEDA CHEM IND LTD
OS Unidentified
PN JP 2000159798-A/4
PD 13-JUN-2000
PF 22-DEC-1998 JP 1998364656
PR

PI SHUJI HINUMA, KAZUHIKO TATEMOTO, MASAKI HOSOYA, YUGO HABATA, PI
RYO FUJII,
PI CHIEKO KITADA
PC C07K14/705,A61K31/00,A61K31/00,A61K31/00,A61K31/00,
PC A61K38/00,
PC A61K39/395,A61K39/395,C07K16/28,C12N1/21,C12N5/10,C12N5/09,
PC C12P1/02
PC G01N33/15,G01N33/577//C12P21/08,(C12N1/21,C12R1:19),(C12N5/10,
PC C12R1:91),
PC A61K37/02,C12N5/00,C12N15/00,(C12N5/00,C12R1:91) CC
Strandedness: Single;
CC Topology: linear;
FH Key Location/Qualifiers
FT source 1..27 /organism='unidentified'.
FEATURES
source 1..27 Location/Qualifiers
1..27 /organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 1.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 56;
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 979 TTGGCATCTGCTGGCTGCCCTTCAC 1005
Db 27 TTGGCMTCTGCTGANTGCCYWCNAC 1

RESULT 41
AR211515/c 27 bp DNA linear PAT 20-JUN-2002
LOCUS AR211515

DEFINITION Sequence 8 from patent US 6399325.
ACCESSION AR211515
VERSION AR211515.1 GI:21514857
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS Hinuma,S., Fujii,R., Fukusumi,S., Ohtaki,T., Hosoya,M., Ohgi,K. and
Onda,H.
TITLE DNA encoding a galanin receptor
PATENT: US 6399325-A 8 04-JUN-2002;
JOURNAL Location/Qualifiers
FEATURES
source 1..27 /organism='unknown'
/mol_type='unassigned DNA'

Query Match 1.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 56;
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 979 TTGGCATCTGCTGGCTGCCCTTCAC 1005
Db 27 TTGGCMTCTGCTGANTGCCYWCNAC 1

RESULT 42
AR266284/c 27 bp DNA linear PAT 10-APR-2003
LOCUS AR266284
DEFINITION Sequence 6 from patent US 6492324.
ACCESSION AR266284
VERSION AR266284.1 GI:29695138
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS Hinuma,S., Tatemoto,K., Hosoya,M., Habata,Y., Fujii,R. and
Kitada,C.
TITLE Aryl ligand polypeptides
PATENT: US 6492324-A 6 10-DEC-2002;
JOURNAL Takeda Chemical Industries, Ltd., Osaka;
WOX;

FEATURES
source 1..27 Location/Qualifiers
1..27 /organism='unknown'
/mol_type='genomic DNA'

Query Match 1.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 56;
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 979 TTGGCATCTGCTGGCTGCCCTTCAC 1005
Db 27 TTGGCMTCTGCTGANTGCCYWCNAC 1

RESULT 43
AR300905/c 27 bp DNA linear PAT 12-JUN-2003
LOCUS AR300905
DEFINITION Sequence 2 from patent US 6538107.
ACCESSION AR300905
VERSION AR300905.1 GI:31688578
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS Hinuma,S., Ito,Y. and Fujii,R.
TITLE G protein coupled receptor protein production, and use thereof
PATENT: US 6538107-A 2 25-MAR-2003;
JOURNAL Takeda Chemical Industries, Ltd., Osaka;
JPX;

FEATURES
source
Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Gaps 0;

OY 290 AACGAGCTGGCAATTGTCC 310
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1 AACGAGCTGGCAATTGTCC 21

Db 1 AACGAGCTGGCAATTGTCC 21

RESULT 49
LOCUS CS207679 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 387 from Patent WO2005109000.
ACCESSION CS207679
VERSION CS207679.1 GI:83413956
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Spittaels,K.F.
JOURNAL Patent: WO 2005109000-A 387 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)

FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Gaps 0;

OY 303 AATTGCTCTTGGGAGCTGC 323
|||||
1 AATTGCTCTTGGGAGCTGC 21

Db 1 AATTGCTCTTGGGAGCTGC 21

RESULT 50
LOCUS CS207680 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 388 from Patent WO2005109000.
ACCESSION CS207680
VERSION CS207680.1 GI:83413957
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Spittaels,K.F.
JOURNAL Patent: WO 2005109000-A 388 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)

FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Gaps 0;

OY 358 AACGTGTAAGTATGTGATC 378
|||||

Db 1 AACGTGTAAGTATGTGATC 21

RESULT 51
LOCUS CS207681 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 389 from Patent WO2005109000.
ACCESSION CS207681
VERSION CS207681.1 GI:83413958
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Spittaels,K.F.
JOURNAL Patent: WO 2005109000-A 389 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)

FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Gaps 0;

OY 463 AATACAGTGGTGAAGCTCACC 483
|||||
1 AATACAGTGGTGAAGCTCACC 21

Db 1 AATACAGTGGTGAAGCTCACC 21

RESULT 52
LOCUS CS207682 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 390 from Patent WO2005109000.
ACCESSION CS207682
VERSION CS207682.1 GI:83413959
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Spittaels,K.F.
JOURNAL Patent: WO 2005109000-A 390 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)

FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Gaps 0;

OY 475 AACTCAGCTATGCTGTCCAC 495
|||||
1 AACTCAGCTATGCTGTCCAC 21

Db 1 AACTCAGCTATGCTGTCCAC 21

RESULT 53
LOCUS CS207683 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 391 from Patent WO2005109000.
ACCESSION CS207683
VERSION CS207683.1 GI:83413960
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Spittaels, K. F.
JOURNAL Patent: WO 2005109000-A 391 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 494 ACAACGAATGGTACTACGGCC 514
Db 1 ACAACGAATGGTACTACGGCC 21

RESULT 54
LOCUS CS207684 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 392 from Patent WO2005109000.
ACCESSION CS207684
VERSION CS207684.1 GI:83413961
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Spittaels, K. F.
JOURNAL Patent: WO 2005109000-A 392 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 526 AAGTCCACAACCTCTTCCC 546
Db 1 AAGTCCACAACCTCTTCCC 21

RESULT 55
LOCUS CS207685 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 393 from Patent WO2005109000.
ACCESSION CS207685
VERSION CS207685.1 GI:83413962
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Spittaels, K. F.
JOURNAL Patent: WO 2005109000-A 393 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 643 ACAGCCACCAAGTGTATC 663
Db 1 ACAGCCACCAAGTGTATC 21

RESULT 56
LOCUS CS207686 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 394 from Patent WO2005109000.
ACCESSION CS207686
VERSION CS207686.1 GI:83413963
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Spittaels, K. F.
JOURNAL Patent: WO 2005109000-A 394 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 649 ACCAAAGTGTATCTGTGTC 669
Db 1 ACCAAAGTGTATCTGTGTC 21

RESULT 57
LOCUS CS207687 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 395 from Patent WO2005109000.
ACCESSION CS207687
VERSION CS207687.1 GI:83413964
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Spittaels, K. F.
JOURNAL Patent: WO 2005109000-A 395 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 652 AAAGTGTATCTGTGTCATC 672
Db 1 AAAGTGTATCTGTGTCATC 21

RESULT 58
LOCUS CS207688 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 396 from Patent WO2005109000.
ACCESSION CS207688
VERSION CS207688.1 GI:83413965

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
JOURNAL
FEATURES
source

synthetic construct
synthetic construct
other sequences; artificial sequences.
1
Spittaels, K.F.
Patent: WO 2005109000-A 396 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 713 ACTCAACACAGAGACCATGC 713
Db 1 ACTCAACACAGAGACCATGC 21

RESULT 59
CS207689 21 bp DNA linear PAT 08-DEC-2005
LOCUS
DEFINITION Sequence 397 from Patent WO2005109000.
ACCESSION CS207689
VERSION CS207689.1 GI:83413966
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
JOURNAL
FEATURES
source

synthetic construct
synthetic construct
other sequences; artificial sequences.
1
Spittaels, K.F.
Patent: WO 2005109000-A 397 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 797 ACCACATCTGTGACTGTGC 817
Db 1 ACCACATCTGTGACTGTGC 21

RESULT 60
CS207690 21 bp DNA linear PAT 08-DEC-2005
LOCUS
DEFINITION Sequence 398 from Patent WO2005109000.
ACCESSION CS207690
VERSION CS207690.1 GI:83413967
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
JOURNAL
FEATURES
source

synthetic construct
synthetic construct
other sequences; artificial sequences.
1
Spittaels, K.F.
Patent: WO 2005109000-A 398 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"

/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 811 ACTGTGCTGATCTACTTCCTC 831
Db 1 ACTGTGCTGATCTACTTCCTC 21

RESULT 61
CS207691 21 bp DNA linear PAT 08-DEC-2005
LOCUS
DEFINITION Sequence 399 from Patent WO2005109000.
ACCESSION CS207691
VERSION CS207691.1 GI:83413968
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
JOURNAL
FEATURES
source

synthetic construct
synthetic construct
other sequences; artificial sequences.
1
Spittaels, K.F.
Patent: WO 2005109000-A 399 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 857 ACACCGTAGTGGGATCACAC 877
Db 1 ACACCGTAGTGGGATCACAC 21

RESULT 62
CS207692 21 bp DNA linear PAT 08-DEC-2005
LOCUS
DEFINITION Sequence 400 from Patent WO2005109000.
ACCESSION CS207692
VERSION CS207692.1 GI:83413969
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
JOURNAL
FEATURES
source

synthetic construct
synthetic construct
other sequences; artificial sequences.
1
Spittaels, K.F.
Patent: WO 2005109000-A 400 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 874 ACACTATGGGCGGAGATGC 894
Db 1 ACACTATGGGCGGAGATGC 21

RESULT 63
CS207693

LOCUS CS207693 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 401 from Patent WO2005109000.
ACCESSION CS207693
VERSION CS207693.1 GI:83413970
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 Spittaels,K.F.
AUTHORS Patent: WO 2005109000-A 401 17-NOV-2005;
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
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1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 876 ACTATGGGCGCATGCC 896
Db 1 ACTATGGGCGCATGCC 21

RESULT 64
LOCUS CS207694 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 402 from Patent WO2005109000.
ACCESSION CS207694
VERSION CS207694.1 GI:83413971
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 Spittaels,K.F.
AUTHORS Patent: WO 2005109000-A 402 17-NOV-2005;
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 920 ACGAGCAAGTCTGCCAAGC 940
Db 1 ACGAGCAAGTCTGCCAAGC 21

RESULT 65
LOCUS CS207695 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 403 from Patent WO2005109000.
ACCESSION CS207695
VERSION CS207695.1 GI:83413972
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 Spittaels,K.F.
AUTHORS Patent: WO 2005109000-A 403 17-NOV-2005;
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
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1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

source 1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1025 ACATCAACCGATCTCTACC 1045
Db 1 ACATCAACCGATCTCTACC 21

RESULT 66
LOCUS CS207696 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 404 from Patent WO2005109000.
ACCESSION CS207696
VERSION CS207696.1 GI:83413973
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 Spittaels,K.F.
AUTHORS Patent: WO 2005109000-A 404 17-NOV-2005;
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1043 ACCTGAAGATTATCCAGC 1063
Db 1 ACCTGAAGATTATCCAGC 21

RESULT 67
LOCUS CS207697 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 405 from Patent WO2005109000.
ACCESSION CS207697
VERSION CS207697.1 GI:83413974
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 Spittaels,K.F.
AUTHORS Patent: WO 2005109000-A 405 17-NOV-2005;
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
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1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1048 AAGAGTTATCCAGCAGTC 1068
Db 1 AAGAGTTATCCAGCAGTC 21

RESULT 68
CS207698
LOCUS CS207698 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 406 from Patent WO2005109000.
ACCESSION CS207698
VERSION CS207698.1 GI:83413975
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Spittaels, K.F.
JOURNAL Patent: WO 2005109000-A 406 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1051 AAGTTATCCAGCAGGTCTAC 1071
Db 1 AAGTTATCCAGCAGGTCTAC 21
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RESULT 69
CS207699
LOCUS CS207699 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 407 from Patent WO2005109000.
ACCESSION CS207699
VERSION CS207699.1 GI:83413976
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Spittaels, K.F.
JOURNAL Patent: WO 2005109000-A 407 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1135 AATGACAGTTCGCTGCGGC 1155
Db 1 AATGACAGTTCGCTGCGGC 21
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RESULT 70
CS207700
LOCUS CS207700 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 408 from Patent WO2005109000.
ACCESSION CS207700
VERSION CS207700.1 GI:83413977
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Spittaels, K.F.
JOURNAL Patent: WO 2005109000-A 408 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

AUTHORS Spittaels, K.F.
JOURNAL Patent: WO 2005109000-A 408 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1214 AATGAATCCACCCGGTATC 1234
Db 1 AATGAATCCACCCGGTATC 21
|||||
|||||

RESULT 71
CS207701
LOCUS CS207701 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 409 from Patent WO2005109000.
ACCESSION CS207701
VERSION CS207701.1 GI:83413978
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Spittaels, K.F.
JOURNAL Patent: WO 2005109000-A 409 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1363 AACTGCTCTTCACGAAGTGAC 1383
Db 1 AACTGCTCTTCACGAAGTGAC 21
|||||
|||||

RESULT 72
CS207702
LOCUS CS207702 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 410 from Patent WO2005109000.
ACCESSION CS207702
VERSION CS207702.1 GI:83413979
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Spittaels, K.F.
JOURNAL Patent: WO 2005109000-A 410 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1377 AAGTACTCCAAGACCATGAC 1397
DB 1 AAGTGACTCCAAGACCATGAC 21

RESULT 73
LOCUS CS207703 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 411 from Patent WO2005109000.
ACCESSION CS207703
VERSION CS207703.1 GI:83413980
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Spittaels, K.F.
JOURNAL Patent: WO 2005109000-A 411 17-NOV-2005;
FEATURES Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
SOURCE 1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1387 AAGCCATGACAGAGAGCTTC 1407
DB 1 AAGACCATGACAGAGAGCTTC 21

RESULT 74
LOCUS CS207704 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 412 from Patent WO2005109000.
ACCESSION CS207704
VERSION CS207704.1 GI:83413981
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Spittaels, K.F.
JOURNAL Patent: WO 2005109000-A 412 17-NOV-2005;
FEATURES Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
SOURCE 1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1390 ACCATGACAGAGAGCTTCAGC 1410
DB 1 ACCATGACAGAGAGCTTCAGC 21

RESULT 75
LOCUS CS207705 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 413 from Patent WO2005109000.
ACCESSION CS207705
VERSION CS207705.1 GI:83413982
KEYWORDS

SOURCE
ORGANISM
REFERENCE 1
AUTHORS Spittaels, K.F.
JOURNAL Patent: WO 2005109000-A 413 17-NOV-2005;
FEATURES Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
SOURCE 1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1396 ACAGAGAGCTTCAGCTTCTCC 1416
DB 1 ACAGAGAGCTTCAGCTTCTCC 21

RESULT 76
LOCUS CS207706 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 414 from Patent WO2005109000.
ACCESSION CS207706
VERSION CS207706.1 GI:83413983
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Spittaels, K.F.
JOURNAL Patent: WO 2005109000-A 414 17-NOV-2005;
FEATURES Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
SOURCE 1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1497 AAATTCCTTCATCTGGAACC 1517
DB 1 AAATTCCTTCATCTGGAACC 21

RESULT 77
LOCUS CS207707 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 415 from Patent WO2005109000.
ACCESSION CS207707
VERSION CS207707.1 GI:83413984
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Spittaels, K.F.
JOURNAL Patent: WO 2005109000-A 415 17-NOV-2005;
FEATURES Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
SOURCE 1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1514 AACCATGAGAAACACCTTCAC 1534
1 AACCATGAGAAACACCTTCAC 21

RESULT 78
LOCUS CS207708 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 416 from Patent WO2005109000.
ACCESSION CS207708
VERSION CS207708.1 GI:83413985
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
1
AUTHORS Spitlaels, K.F.
JOURNAL Patent: WO 2005109000-A 416 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spitlaels, Koenraad Frederick F. (BE)
FEATURES
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1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1648 AATCACTGAACCTTGTCTGAGC 1668
1 AATCACTGAACCTTGTCTGAGC 21

RESULT 79
LOCUS CS207709 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 417 from Patent WO2005109000.
ACCESSION CS207709
VERSION CS207709.1 GI:83413986
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
1
AUTHORS Spitlaels, K.F.
JOURNAL Patent: WO 2005109000-A 417 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spitlaels, Koenraad Frederick F. (BE)
FEATURES
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1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1733 ACTTGGCTGCATGCGAGTGC 1753
1 ACTTGGCTGCATGCGAGTGC 21

RESULT 80
LOCUS CS207710 21 bp DNA linear PAT 08-DEC-2005

DEFINITION Sequence 418 from Patent WO2005109000.
CS207710
VERSION CS207710.1 GI:83413987
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
1
AUTHORS Spitlaels, K.F.
JOURNAL Patent: WO 2005109000-A 418 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spitlaels, Koenraad Frederick F. (BE)
FEATURES
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1. .21
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 290 AACGAGCTGGCAATTGTCC 310
1 AACGAGCTGGCAATTGTCC 21

RESULT 81
LOCUS CS207711 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 419 from Patent WO2005109000.
ACCESSION CS207711
VERSION CS207711.1 GI:83413988
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
1
AUTHORS Spitlaels, K.F.
JOURNAL Patent: WO 2005109000-A 419 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spitlaels, Koenraad Frederick F. (BE)
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1. .21
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 303 AATTGTCTTGGCGAGCTGC 323
1 AATTGTCTTGGCGAGCTGC 21

RESULT 82
LOCUS CS207712 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 420 from Patent WO2005109000.
ACCESSION CS207712
VERSION CS207712.1 GI:83413989
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
1
AUTHORS Spitlaels, K.F.
JOURNAL Patent: WO 2005109000-A 420 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spitlaels, Koenraad Frederick F. (BE)
FEATURES
source
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match      1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      358 AACGTGATGATGATGATC 378
Db      1 AACGTGATGATGATGATC 21

RESULT 83
LOCUS      CS207713      21 bp      DNA      linear      PAT 08-DEC-2005
DEFINITION Sequence 421 from Patent WO2005109000.
ACCESSION  CS207713
VERSION     CS207713.1 GI:83413990
KEYWORDS
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 Spittaels,K.F.
AUTHORS     Patent: WO 2005109000-A 421 17-NOV-2005;
JOURNAL     Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
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SOURCE      1..21
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              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="synthetic oligonucleotide"

Query Match      1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      463 AATACAGTGTGATGATGATC 483
Db      1 AATACAGTGTGATGATGATC 21

RESULT 84
LOCUS      CS207714      21 bp      DNA      linear      PAT 08-DEC-2005
DEFINITION Sequence 422 from Patent WO2005109000.
ACCESSION  CS207714
VERSION     CS207714.1 GI:83413991
KEYWORDS
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 Spittaels,K.F.
AUTHORS     Patent: WO 2005109000-A 422 17-NOV-2005;
JOURNAL     Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
SOURCE      1..21
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="synthetic oligonucleotide"

Query Match      1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      475 AACTTCACTATGCTGTCCAC 495
Db      1 AACTTCACTATGCTGTCCAC 21
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RESULT 85
LOCUS      CS207715      21 bp      DNA      linear      PAT 08-DEC-2005
DEFINITION Sequence 423 from Patent WO2005109000.
ACCESSION  CS207715
VERSION     CS207715.1 GI:83413992
KEYWORDS
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 Spittaels,K.F.
AUTHORS     Patent: WO 2005109000-A 423 17-NOV-2005;
JOURNAL     Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
SOURCE      1..21
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="synthetic oligonucleotide"

Query Match      1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      494 ACAACGAATGTTACTACGCGC 514
Db      1 ACAACGAATGTTACTACGCGC 21

RESULT 86
LOCUS      CS207716      21 bp      DNA      linear      PAT 08-DEC-2005
DEFINITION Sequence 424 from Patent WO2005109000.
ACCESSION  CS207716
VERSION     CS207716.1 GI:83413993
KEYWORDS
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 Spittaels,K.F.
AUTHORS     Patent: WO 2005109000-A 424 17-NOV-2005;
JOURNAL     Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
SOURCE      1..21
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="synthetic oligonucleotide"

Query Match      1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      643 ACAGCCACCAAGTGTGATC 663
Db      1 ACAGCCACCAAGTGTGATC 21

RESULT 87
LOCUS      CS207717      21 bp      DNA      linear      PAT 08-DEC-2005
DEFINITION Sequence 425 from Patent WO2005109000.
ACCESSION  CS207717
VERSION     CS207717.1 GI:83413994
KEYWORDS
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 Spittaels,K.F.
AUTHORS
```

JOURNAL Patent: WO 2005109000-A 425 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spilttaels, Koenraad Frederick F. (BE)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 649 ACCAAGTGTGATCTGTGTC 669
Db 1 ACCAAGTGTGATCTGTGTC 21

RESULT 88
LOCUS CS207718 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 426 from Patent WO2005109000.
ACCESSION CS207718
VERSION CS207718.1 GI:83413995
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.
REFERENCE
AUTHORS
JOURNAL
Patent: WO 2005109000-A 426 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spilttaels, Koenraad Frederick F. (BE)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 652 AAAGTGTGATCTGTGTCATC 672
Db 1 AAAGTGTGATCTGTGTCATC 21

RESULT 89
LOCUS CS207719 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 427 from Patent WO2005109000.
ACCESSION CS207719
VERSION CS207719.1 GI:83413996
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.
REFERENCE
AUTHORS
JOURNAL
Patent: WO 2005109000-A 427 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spilttaels, Koenraad Frederick F. (BE)
FEATURES
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1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 713 ACTGACCAAGAGACATGC 733
Db 1 ACTGACCAAGAGACATGC 21

RESULT 90
LOCUS CS207720 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 428 from Patent WO2005109000.
ACCESSION CS207720
VERSION CS207720.1 GI:83413997
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.
REFERENCE
AUTHORS
JOURNAL
Patent: WO 2005109000-A 428 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spilttaels, Koenraad Frederick F. (BE)
FEATURES
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1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 797 ACCACATCTGTGTGACTGTGC 817
Db 1 ACCACATCTGTGTGACTGTGC 21

RESULT 91
LOCUS CS207721 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 429 from Patent WO2005109000.
ACCESSION CS207721
VERSION CS207721.1 GI:83413998
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.
REFERENCE
AUTHORS
JOURNAL
Patent: WO 2005109000-A 429 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spilttaels, Koenraad Frederick F. (BE)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 811 ACTGTGCTGATCTACTTCCTC 831
Db 1 ACTGTGCTGATCTACTTCCTC 21

RESULT 92
LOCUS CS207723 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 431 from Patent WO2005109000.
ACCESSION CS207723
VERSION CS207723.1 GI:83414000
KEYWORDS
SOURCE
synthetic construct

ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Spittaels, K.F.
JOURNAL Patent: WO 2005109000-A 431 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 874 ACACATGGCCAGTGAGATC 894
Db 1 ACACATGGCCAGTGAGATC 21

RESULT 93
LOCUS CS207724 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 432 from Patent WO2005109000.
ACCESSION CS207724
VERSION CS207724.1 GI:83414001
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Spittaels, K.F.
JOURNAL Patent: WO 2005109000-A 432 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 876 ACTATGGGCCAGTGATCCC 896
Db 1 ACTATGGGCCAGTGATCCC 21

RESULT 94
LOCUS CS207725 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 433 from Patent WO2005109000.
ACCESSION CS207725
VERSION CS207725.1 GI:83414002
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Spittaels, K.F.
JOURNAL Patent: WO 2005109000-A 433 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 920 ACGAGCAAGTCTGCGCAGC 940
Db 1 ACGAGCAAGTCTGCGCAGC 21

RESULT 95
LOCUS CS207726 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 434 from Patent WO2005109000.
ACCESSION CS207726
VERSION CS207726.1 GI:83414003
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Spittaels, K.F.
JOURNAL Patent: WO 2005109000-A 434 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1025 ACATCAACCCAGATCTCACC 1045
Db 1 ACATCAACCCAGATCTCACC 21

RESULT 96
LOCUS CS207727 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 435 from Patent WO2005109000.
ACCESSION CS207727
VERSION CS207727.1 GI:83414004
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Spittaels, K.F.
JOURNAL Patent: WO 2005109000-A 435 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1043 ACCTGAAGAGTTATCCAGC 1063
Db 1 ACCTGAAGAGTTATCCAGC 21

RESULT 97
LOCUS CS207728 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 436 from Patent WO2005109000.

ACCESSION CS207728
VERSION CS207728.1 GI:83414005
KEYWORDS
SOURCE
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Spittaels,K.F.
JOURNAL Patent: WO 2005109000-A 436 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
Source location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1048 AAGAATTATCCAGCAGCTC 1068
DB 1 AAGAATTATCCAGCAGCTC 21

RESULT 98
LOCUS CS207729 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 437 from Patent WO2005109000.
ACCESSION CS207729
VERSION CS207729.1 GI:83414006
KEYWORDS
SOURCE
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Spittaels,K.F.
JOURNAL Patent: WO 2005109000-A 437 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
Source location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1051 AAGTTATCCAGCAGCTTAC 1071
DB 1 AAGTTATCCAGCAGCTTAC 21

RESULT 99
LOCUS CS207732 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 440 from Patent WO2005109000.
ACCESSION CS207732
VERSION CS207732.1 GI:83414009
KEYWORDS
SOURCE
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Spittaels,K.F.
JOURNAL Patent: WO 2005109000-A 440 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
Source location/Qualifiers
1..21
/organism="synthetic construct"

/mol_type="unassigned DNA"
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/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 290 AACGAGCTGGCAAAATTGTC 310
DB 1 AACGAGCTGGCAAAATTGTC 21

RESULT 100
LOCUS CS207733 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 441 from Patent WO2005109000.
ACCESSION CS207733
VERSION CS207733.1 GI:83414010
KEYWORDS
SOURCE
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Spittaels,K.F.
JOURNAL Patent: WO 2005109000-A 441 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
Source location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 AATTGCTCTTTGGGACGCTGC 323
DB 1 AATTGCTCTTTGGGACGCTGC 21

RESULT 101
LOCUS CS207734 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 442 from Patent WO2005109000.
ACCESSION CS207734
VERSION CS207734.1 GI:83414011
KEYWORDS
SOURCE
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Spittaels,K.F.
JOURNAL Patent: WO 2005109000-A 442 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
Source location/Qualifiers
1..21
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 AACGTGATGATGATGATGATC 378
DB 1 AACGTGATGATGATGATGATC 21

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	JOURNAL	FEATURES	source
CS207735	Sequence 443 from Patent WO2005109000.	CS207735	CS207735.1	GI:83414012	synthetic construct	synthetic construct	other sequences; artificial sequences.	1	Spittaels,K.F.	Patent: WO 2005109000-A 443 17-NOV-2005; Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)	Location/Qualifiers
1	21 bp	DNA	linear	PAT 08-DEC-2005							
1.2%; Score 21; DB 1; Length 21;											
Best Local Similarity 100.0%; Pred. No. 40;											
Matches 21; Conservative 0; Mismatches 0; Gaps 0;											
1	21 bp	DNA	linear	PAT 08-DEC-2005							
1.2%; Score 21; DB 1; Length 21;											
Best Local Similarity 100.0%; Pred. No. 40;											
Matches 21; Conservative 0; Mismatches 0; Gaps 0;											
1	21 bp	DNA	linear	PAT 08-DEC-2005							
1.2%; Score 21; DB 1; Length 21;											
Best Local Similarity 100.0%; Pred. No. 40;											
Matches 21; Conservative 0; Mismatches 0; Gaps 0;											
1	21 bp	DNA	linear	PAT 08-DEC-2005							
1.2%; Score 21; DB 1; Length 21;											
Best Local Similarity 100.0%; Pred. No. 40;											
Matches 21; Conservative 0; Mismatches 0; Gaps 0;											
1	21 bp	DNA	linear	PAT 08-DEC-2005							
1.2%; Score 21; DB 1; Length 21;											
Best Local Similarity 100.0%; Pred. No. 40;											
Matches 21; Conservative 0; Mismatches 0; Gaps 0;											
1	21 bp	DNA	linear	PAT 08-DEC-2005							
1.2%; Score 21; DB 1; Length 21;											
Best Local Similarity 100.0%; Pred. No. 40;											
Matches 21; Conservative 0; Mismatches 0; Gaps 0;											
1	21 bp	DNA	linear	PAT 08-DEC-2005							
1.2%; Score 21; DB 1; Length 21;											
Best Local Similarity 100.0%; Pred. No. 40;											
Matches 21; Conservative 0; Mismatches 0; Gaps 0;											
1	21 bp	DNA	linear	PAT 08-DEC-2005							
1.2%; Score 21; DB 1; Length 21;											
Best Local Similarity 100.0%; Pred. No. 40;											
Matches 21; Conservative 0; Mismatches 0; Gaps 0;											
1	21 bp	DNA	linear	PAT 08-DEC-2005							
1.2%; Score 21; DB 1; Length 21;											
Best Local Similarity 100.0%; Pred. No. 40;											
Matches 21; Conservative 0; Mismatches 0; Gaps 0;											
1	21 bp	DNA	linear	PAT 08-DEC-2005							
1.2%; Score 21; DB 1; Length 21;											
Best Local Similarity 100.0%; Pred. No. 40;											
Matches 21; Conservative 0; Mismatches 0; Gaps 0;											
1	21 bp	DNA	linear	PAT 08-DEC-2005							
1.2%; Score 21; DB 1; Length 21;											
Best Local Similarity 100.0%; Pred. No. 40;											
Matches 21; Conservative 0; Mismatches 0; Gaps 0;											

FEATURES	Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)									
source	Location/Qualifiers									
	1..21									
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	/db_xref="taxon:32630"									
	/note="synthetic oligonucleotide"									
Query Match	1.2%; Score 21; DB 1; Length 21;									
Best Local Similarity	100.0%; Pred. No. 40;									
Matches	21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Oy	494 ACACGAATGTTACTACGCC 514									
Db	1 ACACGAATGTTACTACGCC 21									
RESULT 105										
LOCUS	CS207738 21 bp DNA linear PAT 08-DEC-2005									
DEFINITION	Sequence 446 from Patent WO2005109000.									
ACCESSION	CS207738									
VERSION	CS207738.1 GI:83414015									
KEYWORDS										
SOURCE	synthetic construct									
ORGANISM	synthetic construct									
REFERENCE	1									
AUTHORS	Spittaels, K.F.									
JOURNAL	Patent: WO 2005109000-A 446 17-NOV-2005; Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)									
FEATURES	Location/Qualifiers									
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	/mol_type="unassigned DNA"									
	/db_xref="taxon:32630"									
	/note="synthetic oligonucleotide"									
Query Match	1.2%; Score 21; DB 1; Length 21;									
Best Local Similarity	100.0%; Pred. No. 40;									
Matches	21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Oy	526 AAGTTCACCACTCTTCCC 546									
Db	1 AAGTTCACCACTCTTCCC 21									
RESULT 106										
LOCUS	CS207739 21 bp DNA linear PAT 08-DEC-2005									
DEFINITION	Sequence 447 from Patent WO2005109000.									
ACCESSION	CS207739									
VERSION	CS207739.1 GI:83414016									
KEYWORDS										
SOURCE	synthetic construct									
ORGANISM	synthetic construct									
REFERENCE	1									
AUTHORS	Spittaels, K.F.									
JOURNAL	Patent: WO 2005109000-A 447 17-NOV-2005; Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)									
FEATURES	Location/Qualifiers									
source	1..21									
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	/mol_type="unassigned DNA"									
	/db_xref="taxon:32630"									
	/note="synthetic oligonucleotide"									
Query Match	1.2%; Score 21; DB 1; Length 21;									
Best Local Similarity	100.0%; Pred. No. 40;									
Matches	21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Oy	643 ACAGCCACCAAGTGTCTATC 663									

Db 1 ACAGCCACCAAGTGTATC 21
|||||
RESULT 107
CS207740 21 bp DNA linear PAT 08-DEC-2005
LOCUS CS207740
DEFINITION Sequence 448 from Patent WO2005109000.
ACCESSION CS207740
VERSION CS207740.1 GI:83414017
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 Spittaels, K.F.
AUTHORS Patent: WO 2005109000-A 448 17-NOV-2005;
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 649 ACCAAGTGTATCTGTCTC 669
Db 1 ACCAAGTGTATCTGTCTC 21
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RESULT 108
CS207741 21 bp DNA linear PAT 08-DEC-2005
LOCUS CS207741
DEFINITION Sequence 449 from Patent WO2005109000.
ACCESSION CS207741
VERSION CS207741.1 GI:83414018
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 Spittaels, K.F.
AUTHORS Patent: WO 2005109000-A 449 17-NOV-2005;
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 652 AAAGTGTATCTGTCTATC 672
Db 1 AAAGTGTATCTGTCTATC 21
|||||
RESULT 109
CS207742 21 bp DNA linear PAT 08-DEC-2005
LOCUS CS207742
DEFINITION Sequence 450 from Patent WO2005109000.
ACCESSION CS207742
VERSION CS207742.1 GI:83414019
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 Spittaels, K.F.
AUTHORS Patent: WO 2005109000-A 450 17-NOV-2005;
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

other sequences; artificial sequences.
REFERENCE
1 Spittaels, K.F.
AUTHORS Patent: WO 2005109000-A 450 17-NOV-2005;
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 713 ACTCACCACAGACCATGC 733
Db 1 ACTCACCACAGACCATGC 21
|||||
RESULT 110
CS207743 21 bp DNA linear PAT 08-DEC-2005
LOCUS CS207743
DEFINITION Sequence 451 from Patent WO2005109000.
ACCESSION CS207743
VERSION CS207743.1 GI:83406147
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 Spittaels, K.F.
AUTHORS Patent: WO 2005109000-A 451 17-NOV-2005;
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 797 ACCACATCTGTGACTGTGC 817
Db 1 ACCACATCTGTGACTGTGC 21
|||||
RESULT 111
CS207744 21 bp DNA linear PAT 08-DEC-2005
LOCUS CS207744
DEFINITION Sequence 452 from Patent WO2005109000.
ACCESSION CS207744
VERSION CS207744.1 GI:83406347
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 Spittaels, K.F.
AUTHORS Patent: WO 2005109000-A 452 17-NOV-2005;
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 811 ACTGTGCTGATCTACTTCCTC 831
|||||
1 ACTGTGCTGATCTACTTCCTC 21

Db

RESULT 112
LOCUS CS207745 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 453 from Patent WO2005109000.
ACCESSION CS207745
VERSION CS207745.1 GI:83406348
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Spitlaels, K.F.
JOURNAL Patent: WO 2005109000-A 453 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spitlaels, Koenraad Frederick F. (BE)
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 857 ACACCGTAGTGGAGATCACAC 877
|||||
1 ACACCGTAGTGGAGATCACAC 21

Db

RESULT 113
LOCUS CS207746 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 454 from Patent WO2005109000.
ACCESSION CS207746
VERSION CS207746.1 GI:83406349
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Spitlaels, K.F.
JOURNAL Patent: WO 2005109000-A 454 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spitlaels, Koenraad Frederick F. (BE)
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 874 AACTATGGCCAGTGAGATC 894
|||||
1 AACTATGGCCAGTGAGATC 21

Db

RESULT 114
LOCUS CS207747 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 455 from Patent WO2005109000.
ACCESSION CS207747

VERSION CS207747.1 GI:83406350
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Spitlaels, K.F.
JOURNAL Patent: WO 2005109000-A 455 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spitlaels, Koenraad Frederick F. (BE)
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 876 ACTATGGCCAGTGAGATCCC 896
|||||
1 ACTATGGCCAGTGAGATCCC 21

Db

RESULT 115
LOCUS CS207748 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 456 from Patent WO2005109000.
ACCESSION CS207748
VERSION CS207748.1 GI:83406351
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Spitlaels, K.F.
JOURNAL Patent: WO 2005109000-A 456 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spitlaels, Koenraad Frederick F. (BE)
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 920 ACGAGCAAGTCTGTGCCAAGC 940
|||||
1 ACGAGCAAGTCTGTGCCAAGC 21

Db

RESULT 116
LOCUS CS207749 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 457 from Patent WO2005109000.
ACCESSION CS207749
VERSION CS207749.1 GI:83406352
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Spitlaels, K.F.
JOURNAL Patent: WO 2005109000-A 457 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spitlaels, Koenraad Frederick F. (BE)
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"

/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1025 ACATCAACCCAGATCTTACC 1045
Db 1 ACATCAACCCAGATCTTACC 21
|||||

RESULT 117
LOCUS CS207750 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 458 from Patent WO2005109000.
ACCESSION CS207750
VERSION CS207750.1 GI:83406353
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
AUTHORS Spittaels,K.F.
JOURNAL Patent: WO 2005109000-A 458 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1048 AAGAAGTTATCCAGCAGGTC 1068
Db 1 AAGAAGTTATCCAGCAGGTC 21
|||||

RESULT 119

CS207752 21 bp DNA linear PAT 08-DEC-2005
LOCUS CS207752
DEFINITION Sequence 460 from Patent WO2005109000.
ACCESSION CS207752
VERSION CS207752.1 GI:83406355
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
AUTHORS Spittaels,K.F.
JOURNAL Patent: WO 2005109000-A 460 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1051 AAGTTATCCAGCAGGTCCTAC 1071
Db 1 AAGTTATCCAGCAGGTCCTAC 21
|||||

RESULT 120
LOCUS CS207753 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 461 from Patent WO2005109000.
ACCESSION CS207753
VERSION CS207753.1 GI:83406356
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
AUTHORS Spittaels,K.F.
JOURNAL Patent: WO 2005109000-A 461 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1135 AATGACAGTTCCTGCGGC 1155
Db 1 AATGACAGTTCCTGCGGC 21
|||||

RESULT 121
LOCUS CS207754 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 462 from Patent WO2005109000.
ACCESSION CS207754
VERSION CS207754.1 GI:83406357
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
AUTHORS Spittaels,K.F.
JOURNAL Patent: WO 2005109000-A 462 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)

FEATURES
source
1..21
location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1214 AATGAATCCACCCGGTATC 1234
1 AATGAATCCACCCGGTATC 21

RESULT 122
CS207755 21 bp DNA linear PAT 08-DEC-2005
LOCUS
DEFINITION Sequence 463 from Patent WO2005109000.
ACCESSION CS207755
VERSION CS207755.1 GI:83406358
KEYWORDS
SOURCE
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS Spittaels,K.F.
JOURNAL Patent: WO 2005109000-A 463 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)

FEATURES
source
1..21
location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1363 AACTGCTCTTCACGAGTGAC 1383
1 AACTGCTCTTCACGAGTGAC 21

RESULT 123
CS207756 21 bp DNA linear PAT 08-DEC-2005
LOCUS
DEFINITION Sequence 464 from Patent WO2005109000.
ACCESSION CS207756
VERSION CS207756.1 GI:83406359
KEYWORDS
SOURCE
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS Spittaels,K.F.
JOURNAL Patent: WO 2005109000-A 464 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)

FEATURES
source
1..21
location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1377 AAGTACTCCAGACCATGAC 1397
1 AAGTACTCCAGACCATGAC 21

Db 1 AAGTACTCCAGACCATGAC 21

RESULT 124
CS207757 21 bp DNA linear PAT 08-DEC-2005
LOCUS
DEFINITION Sequence 465 from Patent WO2005109000.
ACCESSION CS207757
VERSION CS207757.1 GI:83406360
KEYWORDS
SOURCE
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS Spittaels,K.F.
JOURNAL Patent: WO 2005109000-A 465 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)

FEATURES
source
1..21
location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1387 AAGACATGACAGAGCTTC 1407
1 AAGACATGACAGAGCTTC 21

RESULT 125
CS207758 21 bp DNA linear PAT 08-DEC-2005
LOCUS
DEFINITION Sequence 466 from Patent WO2005109000.
ACCESSION CS207758
VERSION CS207758.1 GI:83406361
KEYWORDS
SOURCE
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS Spittaels,K.F.
JOURNAL Patent: WO 2005109000-A 466 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)

FEATURES
source
1..21
location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1390 ACCATGACAGAGCTTCAGC 1410
1 ACCATGACAGAGCTTCAGC 21

RESULT 126
CS207759 21 bp DNA linear PAT 08-DEC-2005
LOCUS
DEFINITION Sequence 467 from Patent WO2005109000.
ACCESSION CS207759
VERSION CS207759.1 GI:83406362
KEYWORDS
SOURCE
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Spittaels, K.F.
JOURNAL Patent: WO 2005109000-A 467 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1396 ACAGAGAGCTTCAGCTTCTCC 1416
DB 1 ACAGAGAGCTTCAGCTTCTCC 21
|||||
|||||

RESULT 127
LOCUS CS207760 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 468 from Patent WO2005109000.
ACCESSION CS207760
VERSION CS207760.1 GI:83406363
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Spittaels, K.F.
JOURNAL Patent: WO 2005109000-A 468 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1497 AAATCCCTTCATCTGGAAC 1517
DB 1 AAATCCCTTCATCTGGAAC 21
|||||
|||||

RESULT 128
LOCUS CS207761 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 469 from Patent WO2005109000.
ACCESSION CS207761
VERSION CS207761.1 GI:83406364
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Spittaels, K.F.
JOURNAL Patent: WO 2005109000-A 469 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1514 AACCATCAGAAACACCTTCAC 1534
DB 1 AACCATCAGAAACACCTTCAC 21
|||||
|||||

RESULT 129
LOCUS CS207762 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 470 from Patent WO2005109000.
ACCESSION CS207762
VERSION CS207762.1 GI:83406365
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Spittaels, K.F.
JOURNAL Patent: WO 2005109000-A 470 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1648 AATCATGCAACTTGTGCTGAGC 1668
DB 1 AATCATGCAACTTGTGCTGAGC 21
|||||
|||||

RESULT 130
LOCUS CS207763 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 471 from Patent WO2005109000.
ACCESSION CS207763
VERSION CS207763.1 GI:83406366
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Spittaels, K.F.
JOURNAL Patent: WO 2005109000-A 471 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1733 ACTTGGCTGCATGCGAGTGC 1753
DB 1 ACTTGGCTGCATGCGAGTGC 21
|||||
|||||

RESULT 131
LOCUS CS207764 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 472 from Patent WO2005109000.
ACCESSION CS207764
VERSION CS207764.1 GI:83406367

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Spittaels, K.F.
JOURNAL Patent: WO 2005109000-A 472 17-NOV-2005;
Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
source 1. . 21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 290 AACCAAGCTGGCAATTGTCC 310
Db 1 AACCAAGCTGGCAATTGTCC 21

RESULT 132
LOCUS CS207765 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 473 from Patent WO2005109000.
ACCESSION CS207765
VERSION CS207765.1 GI:83406368
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Spittaels, K.F.
JOURNAL Patent: WO 2005109000-A 473 17-NOV-2005;
Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
source 1. . 21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 AATTGCTCTTGGGACAGCTGC 323
Db 1 AATTGCTCTTGGGACAGCTGC 21

RESULT 133
LOCUS CS207766 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 474 from Patent WO2005109000.
ACCESSION CS207766
VERSION CS207766.1 GI:83406369
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Spittaels, K.F.
JOURNAL Patent: WO 2005109000-A 474 17-NOV-2005;
Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
source 1. . 21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 AACGTGTAGTGTGATGATC 378
Db 1 AACGTGTAGTGTGATGATC 21

RESULT 134
LOCUS CS207767 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 475 from Patent WO2005109000.
ACCESSION CS207767
VERSION CS207767.1 GI:83406370
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Spittaels, K.F.
JOURNAL Patent: WO 2005109000-A 475 17-NOV-2005;
Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
source 1. . 21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 AATACAGTGTGTAACCTCACC 483
Db 1 AATACAGTGTGTAACCTCACC 21

RESULT 135
LOCUS CS207768 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 476 from Patent WO2005109000.
ACCESSION CS207768
VERSION CS207768.1 GI:83406371
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Spittaels, K.F.
JOURNAL Patent: WO 2005109000-A 476 17-NOV-2005;
Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
source 1. . 21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 475 AACTCACCCTATGCTGTCCAC 495
Db 1 AACTCACCCTATGCTGTCCAC 21

RESULT 136
LOCUS CS207769

LOCUS CS207769 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 477 from Patent WO2005109000.
ACCESSION CS207769
VERSION CS207769.1 GI:83406372
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Spittaels, K.F.
JOURNAL Patent: WO 2005109000-A 477 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 494 ACAACGAATGGTACTACGCGC 514
Db 1 ACAACGAATGGTACTACGCGC 21
RESULT 137
LOCUS CS207770 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 478 from Patent WO2005109000.
ACCESSION CS207770
VERSION CS207770.1 GI:83406373
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Spittaels, K.F.
JOURNAL Patent: WO 2005109000-A 478 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 643 ACAGCCACCAAGTGTGTCATC 663
Db 1 ACAGCCACCAAGTGTGTCATC 21
RESULT 138
LOCUS CS207771 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 479 from Patent WO2005109000.
ACCESSION CS207771
VERSION CS207771.1 GI:83406374
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Spittaels, K.F.
JOURNAL Patent: WO 2005109000-A 479 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 649 ACCAAGTGTGTCATCTGTGTC 669
Db 1 ACCAAGTGTGTCATCTGTGTC 21
RESULT 139
LOCUS CS207772 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 480 from Patent WO2005109000.
ACCESSION CS207772
VERSION CS207772.1 GI:83406375
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Spittaels, K.F.
JOURNAL Patent: WO 2005109000-A 480 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 652 AAAGTGTGTCATCTGTGTCATC 672
Db 1 AAAGTGTGTCATCTGTGTCATC 21
RESULT 140
LOCUS CS207773 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 481 from Patent WO2005109000.
ACCESSION CS207773
VERSION CS207773.1 GI:83406376
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Spittaels, K.F.
JOURNAL Patent: WO 2005109000-A 481 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 713 ACTCAACGACAGACCATGC 733
Db 1 ACTCAACGACAGACCATGC 21

RESULT 141
CS207774 21 bp DNA linear PAT 08-DEC-2005
LOCUS Sequence 482 from Patent WO2005109000.
DEFINITION CS207774
ACCESSION CS207774.1 GI:83406377
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 Spittaels, K.F.
AUTHORS Patent: WO 2005109000-A 482 17-NOV-2005;
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 797 ACCACATCTGTGACTGTGC 817
Db 1 ACCACATCTGTGACTGTGC 21

RESULT 142
CS207775 21 bp DNA linear PAT 08-DEC-2005
LOCUS Sequence 483 from Patent WO2005109000.
DEFINITION CS207775
ACCESSION CS207775.1 GI:83406378
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 Spittaels, K.F.
AUTHORS Patent: WO 2005109000-A 483 17-NOV-2005;
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 811 ACTGTGCTGATCTACTCTTC 831
Db 1 ACTGTGCTGATCTACTCTTC 21

RESULT 143
CS207776 21 bp DNA linear PAT 08-DEC-2005
LOCUS Sequence 484 from Patent WO2005109000.
DEFINITION CS207776
ACCESSION CS207776.1 GI:83406379
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 Spittaels, K.F.
AUTHORS Patent: WO 2005109000-A 484 17-NOV-2005;
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

AUTHORS Spittaels, K.F.
JOURNAL Patent: WO 2005109000-A 484 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 857 ACACCGTAGTGGGAAATCAGAC 877
Db 1 ACACCGTAGTGGGAAATCAGAC 21

RESULT 144
CS207777 21 bp DNA linear PAT 08-DEC-2005
LOCUS Sequence 485 from Patent WO2005109000.
DEFINITION CS207777
ACCESSION CS207777.1 GI:83406380
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 Spittaels, K.F.
AUTHORS Patent: WO 2005109000-A 485 17-NOV-2005;
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 874 AACTATGGGCGAGTGAGATC 894
Db 1 AACTATGGGCGAGTGAGATC 21

RESULT 145
CS207778 21 bp DNA linear PAT 08-DEC-2005
LOCUS Sequence 486 from Patent WO2005109000.
DEFINITION CS207778
ACCESSION CS207778.1 GI:83406381
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 Spittaels, K.F.
AUTHORS Patent: WO 2005109000-A 486 17-NOV-2005;
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 876 ACTATGGGCCAGTGATCCC 896
Db 1 ACTATGGGCCAGTGATCCC 21

RESULT 146
LOCUS CS207779 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 487 from Patent WO2005109000.
ACCESSION CS207779
VERSION CS207779.1 GI:83406382
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1 Spittaels, K.F.
AUTHORS Patent: WO 2005109000-A 487 17-NOV-2005;
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES Location/Qualifiers
1..21
source /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 920 ACGAGCAAGTCTCTGCCAAGC 940
Db 1 ACGAGCAAGTCTCTGCCAAGC 21

RESULT 147
LOCUS CS207780 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 488 from Patent WO2005109000.
ACCESSION CS207780
VERSION CS207780.1 GI:83406383
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1 Spittaels, K.F.
AUTHORS Patent: WO 2005109000-A 488 17-NOV-2005;
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES Location/Qualifiers
1..21
source /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1025 ACATCAACCCAGATCTTACC 1045
Db 1 ACATCAACCCAGATCTTACC 21

RESULT 148
LOCUS CS207781 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 489 from Patent WO2005109000.
ACCESSION CS207781
VERSION CS207781.1 GI:83406384
KEYWORDS

SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1 Spittaels, K.F.
AUTHORS Patent: WO 2005109000-A 489 17-NOV-2005;
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES Location/Qualifiers
1..21
source /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1043 ACCGAGAGAGTTATCCAGC 1063
Db 1 ACCGAGAGAGTTATCCAGC 21

RESULT 149
LOCUS CS207782 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 490 from Patent WO2005109000.
ACCESSION CS207782
VERSION CS207782.1 GI:83406385
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1 Spittaels, K.F.
AUTHORS Patent: WO 2005109000-A 490 17-NOV-2005;
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES Location/Qualifiers
1..21
source /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1048 AAGAAGTTATCCAGCAGTC 1068
Db 1 AAGAAGTTATCCAGCAGTC 21

RESULT 150
LOCUS CS207783 21 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 491 from Patent WO2005109000.
ACCESSION CS207783
VERSION CS207783.1 GI:83406386
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1 Spittaels, K.F.
AUTHORS Patent: WO 2005109000-A 491 17-NOV-2005;
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES Location/Qualifiers
1..21
source /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1051 AAGTTATCCAGCAGCTCTAC 1071
|||||
Db 1 AAGTTATCCAGCAGCTCTAC 21

RESULT 151
117155/c 117155 21 bp DNA linear PAT 03-APR-1996
LOCUS Sequence 10 from patent US 5484886.
ACCESSION 117155.1 GI:1252063
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 21)
AUTHORS Fong,T.M. and Strader,C.D.
TITLE Human neurokinin-1 receptor
JOURNAL Patent: US 5484886-A 10 16-JAN-1996;
FEATURES Location/Qualifiers
1..21
source /organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 559 TTGCGCAGTATCTACTCCATG 579
|||||
Db 21 TTGCGCAGTATCTACTCCATG 1

RESULT 152
117158/c 117158 21 bp DNA linear PAT 03-APR-1996
LOCUS Sequence 13 from patent US 5484886.
ACCESSION 117158
VERSION 117158.1 GI:1252066
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 21)
AUTHORS Fong,T.M. and Strader,C.D.
TITLE Human neurokinin-1 receptor
JOURNAL Patent: US 5484886-A 13 16-JAN-1996;
FEATURES Location/Qualifiers
1..21
source /organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 836 TGCCTGATGCTGCTATGCAT 856
|||||
Db 21 TGCCTGATGCTGCTATGCAT 1

RESULT 153
117160/c 117160 21 bp DNA linear PAT 03-APR-1996
LOCUS Sequence 15 from patent US 5484886.
ACCESSION 117160
VERSION 117160.1 GI:1252068
KEYWORDS

SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 21)
AUTHORS Fong,T.M. and Strader,C.D.
TITLE Human neurokinin-1 receptor
JOURNAL Patent: US 5484886-A 15 16-JAN-1996;
FEATURES Location/Qualifiers
1..21
source /organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 956 TGATGATTGCTGCTGTGCA 976
|||||
Db 21 TGATGATTGCTGCTGTGCA 1

RESULT 154
117162 117162 21 bp DNA linear PAT 03-APR-1996
LOCUS Sequence 17 from patent US 5484886.
ACCESSION 117162
VERSION 117162.1 GI:1252070
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 21)
AUTHORS Fong,T.M. and Strader,C.D.
TITLE Human neurokinin-1 receptor
JOURNAL Patent: US 5484886-A 17 16-JAN-1996;
FEATURES Location/Qualifiers
1..21
source /organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 924 GCAAGTCTTGCCAGCGCAA 944
|||||
Db 1 GCAAGTCTTGCCAGCGCAA 21

RESULT 155
117163 117163 21 bp DNA linear PAT 03-APR-1996
LOCUS Sequence 18 from patent US 5484886.
ACCESSION 117163
VERSION 117163.1 GI:1252071
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 21)
AUTHORS Fong,T.M. and Strader,C.D.
TITLE Human neurokinin-1 receptor
JOURNAL Patent: US 5484886-A 18 16-JAN-1996;
FEATURES Location/Qualifiers
1..21
source /organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 956 TGATGATTGCTGCTGTGCA 976

Db 1 TGATGATGTCGTGTGCA 21

RESULT	156			
LOCUS	117167/c			
DEFINITION	Sequence 22 from patent US 5464886.	21 bp	DNA	1 linear
ACCESSION	117167			
VERSION	117167.1			GI:1252075
KEYWORDS				
SOURCE	Unknown.			

Query Match	1.2%	Score 21;	DB 1;	Length 21;
Best local Similarity	100.0%	Pred. No. 40;		
Matches 21; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

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Oy      1567 AGGGAACATTCATCCTTG 1587
          |||||
Db      21  AGGAAACATTCATCCTTG 1

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RESULT 157			
AX468707			
LOCUS	AX468707	21 bp	DNA
DEFINITION	Sequence 23 from Patent WO0213799.		linear
ACCESSION	AX468707		
VERSION	AX468707.1	GI:21901477	

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Query Match Similarity      1.2%; Score 21; DB 1; Length 21;
Best Local Similarity      100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY		956	TGATGATTGTCTGGTGTGCA	976
Dd		1	TGATGATTGTCTGGTGTGCA	21

RESULT	158		
LOCUS	AX468708	21 bp	DNA
DEFINITION	Sequence 24 from Patent WO0213799.		linear
ACCESSION	AX468708		
VERSION	AX468708.1	GI:21901478	
KEYWORDS	.		
SOURCE	synthetic construct		
ORGANISM	synthetic construct		

REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES
1	Henry, J. L., Cahill, C. M. and Vashpal, K.	Oligonucleotides and other modulators of the nk-1 receptor pathway and therapeutic uses thereof	Patent: WO 0213799-A 24 21-FEB-2002;	Location/Qualifiers
	McGILL UNIVERSITY (CA)			1..*21-nc-"another" construct"

Query Match	1.2%	Score 21	DB 1	Length 21
Best Local Similarity	100.0%	Pred. No. 40		
Matches 21	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	924	GCAGTCTCTGCCAAGCGCAA	944
Db	1	GCAAGTCTCTGCCAAGCGCAA	21

RESULT 159	21 bp	DNA	linear	PAT 16-JUL-2002
AX468710/c				
LOCUS				
DEFINITION	Sequence 26 from Patent WO0213799.			

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Query Match Similarity      1.2%; Score 21; DB 1; Length 21;
Best Local Similarity      100.0%; Pred. No. 40;
Matches      21; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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Oy		956	TGATGATTGTCTGGTGTGCA	978
Dd		21	TGATGATTGTCTGGTGTGCA	1

[illegible]

REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	SOURCE
1	Henry, J. L., Cahill, C. M. and Yashpal, K.	Oligonucleotides and other modulators of the nk-1 receptor pathway	Patent: WO 0213799-A 28 21-FEB-2002;		
		and therapeutic uses thereof	McGILL UNIVERSITY (CA)		
		Location/Qualifiers			
					1. .21

JOURNAL Patent: WO 0213755-A 28 21-1
MC GILL UNIVERSITY (CA)
FEATURES Location/Qualifiers
source 1. .21

REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	SOURCE
1	Henry, J. L., Cahill, C. M. and Yashpal, K.	Oligonucleotides and other modulators of the nk-1 receptor pathway	Patent: WO 0213799-A 28 21-FEB-2002;		
		and therapeutic uses thereof	McGILL UNIVERSITY (CA)		
		Location/Qualifiers			
					1. .21

/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 836 TCGTGTGATTCGCTATGCTATG 856
DB 21 TCGTGTGATTCGCTATGCTATG 1

RESULT 161
AX468715/c
LOCUS AX468715 21 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 31 from Patent WO0213799.
ACCESSION AX468715
VERSION AX468715.1 GI:21901485
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Henry, J.L., Cahill, C.M. and Yashpal, K.
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway
JOURNAL and therapeutic uses thereof
Patent: WO 0213799-A 31 21-FEB-2002;
McGILL UNIVERSITY (CA)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 559 TTGCGCAGTATCTACTCCATG 579
DB 21 TTGCGCAGTATCTACTCCATG 1

RESULT 162
AX468717/c
LOCUS AX468717 21 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 33 from Patent WO0213799.
ACCESSION AX468717
VERSION AX468717.1 GI:21901487
KEYWORDS
SOURCE
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Henry, J.L., Cahill, C.M. and Yashpal, K.
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway
JOURNAL and therapeutic uses thereof
Patent: WO 0213799-A 33 21-FEB-2002;
McGILL UNIVERSITY (CA)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1051 AAGTTATCCAGCAGCTCTAC 1071
DB 21 AAGTTATCCAGCAGCTCTAC 1

RESULT 163
AX468722/c
LOCUS AX468722 21 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 38 from Patent WO0213799.
ACCESSION AX468722
VERSION AX468722.1 GI:21901492
KEYWORDS
SOURCE
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Henry, J.L., Cahill, C.M. and Yashpal, K.
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway
JOURNAL and therapeutic uses thereof
Patent: WO 0213799-A 38 21-FEB-2002;
McGILL UNIVERSITY (CA)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1567 AGGGAACATTCATCTCTG 1587
DB 21 AGGGAACATTCATCTCTG 1

RESULT 164
AX468724
LOCUS AX468724 21 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 40 from Patent WO0213799.
ACCESSION AX468724
VERSION AX468724.1 GI:21901494
KEYWORDS
SOURCE
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Henry, J.L., Cahill, C.M. and Yashpal, K.
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway
JOURNAL and therapeutic uses thereof
Patent: WO 0213799-A 40 21-FEB-2002;
McGILL UNIVERSITY (CA)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 205 TTGGAATGATTAAGTCTCTC 225
DB 1 TTGGAATGATTAAGTCTCTC 21

RESULT 165
AX468726/c
LOCUS AX468726 21 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 42 from Patent WO0213799.

ACCESSION AX468726
VERSION AX468726.1 GI:21901496
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Henry, J.L., Cahill, C.M. and Yashpal, K.
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway
JOURNAL Patent: WO 0213799-A 42 21-FEB-2002;
McGILL UNIVERSITY (CA)
FEATURES
source 1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 956 TGATGATTGTCGTGTGCA 976
Db 21 TGATGATTGTCGTGTGCA 1
|||||

RESULT 166
AX468727/c 21 bp DNA linear PAT 16-JUL-2002
LOCUS
DEFINITION Sequence 43 from Patent WO0213799.
ACCESSION AX468727
VERSION AX468727.1 GI:21901497
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Henry, J.L., Cahill, C.M. and Yashpal, K.
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway
JOURNAL Patent: WO 0213799-A 43 21-FEB-2002;
McGILL UNIVERSITY (CA)
FEATURES
source 1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 924 GCAAGTCTGCGCAAGCGCA 944
Db 21 GCAAGTCTGCGCAAGCGCA 1
|||||

RESULT 167
AX468729 21 bp DNA linear PAT 16-JUL-2002
LOCUS
DEFINITION Sequence 45 from Patent WO0213799.
ACCESSION AX468729
VERSION AX468729.1 GI:21901499
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Henry, J.L., Cahill, C.M. and Yashpal, K.
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway

JOURNAL and therapeutic uses thereof
Patent: WO 0213799-A 45 21-FEB-2002;
McGILL UNIVERSITY (CA)
FEATURES
source 1. .21
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 956 TGATGATTGTCGTGTGCA 976
Db 1 TGATGATTGTCGTGTGCA 21
|||||

RESULT 168
AX468731 21 bp DNA linear PAT 16-JUL-2002
LOCUS
DEFINITION Sequence 47 from Patent WO0213799.
ACCESSION AX468731
VERSION AX468731.1 GI:21901501
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Henry, J.L., Cahill, C.M. and Yashpal, K.
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway
JOURNAL Patent: WO 0213799-A 47 21-FEB-2002;
McGILL UNIVERSITY (CA)
FEATURES
source 1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 836 TGCTGTGATTGCTATGCA 856
Db 1 TGCTGTGATTGCTATGCA 21
|||||

RESULT 169
AX468734 21 bp DNA linear PAT 16-JUL-2002
LOCUS
DEFINITION Sequence 50 from Patent WO0213799.
ACCESSION AX468734
VERSION AX468734.1 GI:21901504
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Henry, J.L., Cahill, C.M. and Yashpal, K.
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway
JOURNAL Patent: WO 0213799-A 50 21-FEB-2002;
McGILL UNIVERSITY (CA)
FEATURES
source 1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 559 TTGCGCAGTATCTACTCCATG 579
1 TTGCGCAGTATCTACTCCATG 21

RESULT 170
LOCUS AX468736 21 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 52 from Patent WO0213799.
ACCESSION AX468736
VERSION AX468736.1 GI:21901506
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Henry,J.L., Cahill,C.M. and Yashpal,K.
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway
JOURNAL Patent: WO 0213799-A 52 21-FEB-2002;
MCGILL UNIVERSITY (CA)
FEATURES
source 1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1051 AAGTTTATCCAGCAGGTCTAC 1071
1 AAGTTTATCCAGCAGGTCTAC 21

RESULT 171
LOCUS AX468737 21 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 53 from Patent WO0213799.
ACCESSION AX468737
VERSION AX468737.1 GI:21901507
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Henry,J.L., Cahill,C.M. and Yashpal,K.
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway
JOURNAL Patent: WO 0213799-A 53 21-FEB-2002;
MCGILL UNIVERSITY (CA)
FEATURES
source 1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1105 ATGTACAACCCCATCATCTAC 1125
1 ATGTACAACCCCATCATCTAC 21

RESULT 172
LOCUS AX468741 21 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 57 from Patent WO0213799.
ACCESSION AX468741
VERSION AX468741.1 GI:21901511
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Henry,J.L., Cahill,C.M. and Yashpal,K.
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway
JOURNAL Patent: WO 0213799-A 57 21-FEB-2002;
MCGILL UNIVERSITY (CA)
FEATURES
source 1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1567 AGGAAATGATTAAGTCTTC 1587
1 AGGAAATGATTAAGTCTTC 21

RESULT 173
LOCUS AX468743 21 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 59 from Patent WO0213799.
ACCESSION AX468743
VERSION AX468743.1 GI:21901513
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Henry,J.L., Cahill,C.M. and Yashpal,K.
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway
JOURNAL Patent: WO 0213799-A 59 21-FEB-2002;
MCGILL UNIVERSITY (CA)
FEATURES
source 1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 TTGAAATGATTAAGTCTTC 225
21 TTGAAATGATTAAGTCTTC 1

RESULT 174
LOCUS AR109807 24 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 231 from patent US 6114139.
ACCESSION AR109807
VERSION AR109807.1 GI:12826083
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.
TITLE G-protein coupled receptor protein and a DNA encoding the receptor
JOURNAL Patent: US 6114139-A 231 05-SEP-2000;
FEATURES Location/Qualifiers
SOURCE 1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 59;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 979 TTGGCCATCTGCTGCGCTGCCCTTC 1002
Db 1 TTGGCCATCTGCTGCGCTGCCCTAC 24

RESULT 175
ARI09809 24 bp DNA linear PAT 14-FEB-2001
LOCUS Sequence 233 from patent US 6114139.
DEFINITION ARI09809
ACCESSION ARI09809.1 GI:12826085
VERSION
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 24)
AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.
TITLE G-protein coupled receptor protein and a DNA encoding the receptor
JOURNAL Patent: US 6114139-A 233 05-SEP-2000;
FEATURES Location/Qualifiers
SOURCE 1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 59;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 979 TTGGCCATCTGCTGCGCTGCCCTTC 1002
Db 1 TTGGCCATCTGCTGCGCTGCCCTAC 24

RESULT 176
ARI09813 24 bp DNA linear PAT 14-FEB-2001
LOCUS Sequence 237 from patent US 6114139.
DEFINITION ARI09813
ACCESSION ARI09813
VERSION ARI09813.1 GI:12826089
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 24)
AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.
TITLE G-protein coupled receptor protein and a DNA encoding the receptor
JOURNAL Patent: US 6114139-A 237 05-SEP-2000;
FEATURES Location/Qualifiers
SOURCE 1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 59;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 979 TTGGCCATCTGCTGCGCTGCCCTTC 1002
Db 1 TTGGCCATCTGCTGCGCTGCCCTTC 1002

Db 1 TTCACCCCTGCTGCTGCCCTTC 24

RESULT 177
ARI1751/c 24 bp DNA linear PAT 03-APR-1996
LOCUS 117151
DEFINITION Sequence 6 from patent US 5484886.
ACCESSION 117151
VERSION 117151.1 GI:1252059
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 24)
AUTHORS Fong,T.M. and Strader,C.D.
TITLE Human neurokinin-1 receptor
JOURNAL Patent: US 5484886-A 6 16-JUN-1996;
FEATURES Location/Qualifiers
SOURCE 1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 59;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1051 AAGTTTATCCAGAGGCTACTCTG 1074
Db 24 AAGTTCATCCAGAGGTACTCTG 1

RESULT 178
ARI09608/c 24 bp DNA linear PAT 14-FEB-2001
LOCUS Sequence 15 from patent US 6114139.
DEFINITION ARI09608
ACCESSION ARI09608
VERSION ARI09608.1 GI:12825884
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 24)
AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.
TITLE G-protein coupled receptor protein and a DNA encoding the receptor
JOURNAL Patent: US 6114139-A 15 05-SEP-2000;
FEATURES Location/Qualifiers
SOURCE 1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 20.6; DB 1; Length 24;
Best Local Similarity 70.8%; Pred. No. 63;
Matches 17; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 979 TTGGCCATCTGCTGCTGCCCTTC 1002
Db 24 TTGGCCTTCTGCTGCTGCCCTTC 1

RESULT 179
ARI09806 24 bp DNA linear PAT 14-FEB-2001
LOCUS Sequence 230 from patent US 6114139.
DEFINITION ARI09806
ACCESSION ARI09806
VERSION ARI09806.1 GI:12826082
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 24)
AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.
TITLE G-protein coupled receptor protein and a DNA encoding the receptor
JOURNAL Patent: US 6114139-A 230 05-SEP-2000;

FEATURES
source
Location/Qualifiers
1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 20.6; DB 1; Length 24;
Best Local Similarity 70.8%; Pred. No. 63;
Matches 17; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 979 TTGCGCATCTGCTGCTGCCCTTC 1002
|||||:|||||:|||||:|||||:
1 TTGCGCNTSTGCTGCTGCCCMWC 24

RESULT 180
LOCUS E12479 24 bp DNA linear PAT 27-APR-1998
DEFINITION PCR primer for selective amplification and cloning of the family of
genes encoding G protein-coupled receptors.
VERSION E12479.1 GI:3251312
KEYWORDS JP 1997000268-A/15.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 24)
AUTHORS Hinuma,K., Hosoya,M., Fujii,A., Ohtaki,T., Fukuzumi,M. and
Ooyoshi,K.
TITLE NEW G PROTEIN CONJUGATION TYPE RECEPTOR PROTEIN, ITS PRODUCTION AND
JOURNAL Patent: JP 1997000268-A 15 07-JAN-1997;
TAKEDA CHEM IND LTD

COMMENT
OC None
Artificial sequences.
PN JP 1997000268-A/15
PD 07-JAN-1997
PR 10-AUG-1995 JP 1995224544
PR 11-AUG-1994 JP 94P 189272, 11-AUG-1994 JP 94P 189273, PR
11-AUG-1994 JP 94P 189274, 30-SEP-1994 JP 94P 226356, PR
30-SEP-1994 JP 94P 236357, 02-NOV-1994 JP 94P 270017, PR
28-DEC-1994 JP 94P 326611, 20-JAN-1995 JP 95P 7177, PR
16-MAR-1995 JP 95P 57186, 19-APR-1995 JP 95P 93989, PI
HINUMA KUNIIJI, HOSOKA MASAKI, FUJII AKIRA, OHTAKI TETSUYA, PI
FUKUZUMI MASASHI, OYOSHI KAZUHIRO
PC C12N15/09, C07H21/04, C12N1/21, G01N3/53, G01N3/566//C07K14/705,
PC C07K16/28,
PC C12P21/02, C12P21/08, C12Q1/68, C12N1/21, C12R1/19, C12P21/02,
PC C12R1/19;
CC strandedness: Single;
CC topology: Linear;
FH Key Location/Qualifiers
FH source 1..24
FT /organism='Artificial sequences' FT
FT misc_feature 1..24
FT /note='degenerate primer based on conserved
amino acid
sequences of the sixth transmembrane domain of
known G
protein-coupled receptors'.
FT Location/Qualifiers
1..24
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

FEATURES
source
Location/Qualifiers
1..24
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.2%; Score 20.6; DB 1; Length 24;
Best Local Similarity 70.8%; Pred. No. 63;
Matches 17; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 979 TTGCGCATCTGCTGCTGCCCTTC 1002
|||||:|||||:|||||:|||||:
24 TTGCGCNTSTGCTGCTGCCCMWC 1

RESULT 181
LOCUS AR300918 24 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 15 from patent US 6538107.
ACCESSION AR300918
VERSION AR300918.1 GI:31688591
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Hinuma,S., Ito,Y. and Fujii,R.
TITLE G protein coupled receptor protein production, and use thereof
JOURNAL Patent: US 6538107-A 15 25-MAR-2003;
Takeda Chemical Industries, Ltd.; Osaka;
JPX;

FEATURES
source
Location/Qualifiers
1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 20.6; DB 1; Length 24;
Best Local Similarity 70.8%; Pred. No. 63;
Matches 17; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 979 TTGCGCATCTGCTGCTGCCCTTC 1002
|||||:|||||:|||||:|||||:
24 TTGCGCNTSTGCTGCTGCCCMWC 1

RESULT 182
LOCUS AR109811 23 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 235 from patent US 6114139.
ACCESSION AR109811
VERSION AR109811.1 GI:12826087
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukuzumi,S. and Ohgi,K.
TITLE G-protein coupled receptor protein and a DNA encoding the receptor
JOURNAL Patent: US 6114139-A 235 05-SEP-2000;
Location/Qualifiers
1..23
/organism="unknown"
/mol_type="unassigned DNA"

FEATURES
source
Location/Qualifiers
1..23
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 61;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 979 TTGCGCATCTGCTGCTGCCCT 1000
|||||:|||||:|||||:|||||:
1 TTGCGCATCTGCTGCTGCCCT 22

RESULT 183
LOCUS BD223567 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Gene polymorphism in human neurokinin 1 receptor gene and
utilization thereof in diagnosing and treating disease.
ACCESSION BD223567
VERSION BD223567.1 GI:33033337
KEYWORDS JP 2002521062-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 20)

AUTHORS Smith,J.C., Anand,R. and Morten,J.E.N.
TITLE Gene polymorphism in human neurokinin 1 receptor gene and
utilization thereof in diagnosing and treating disease
JOURNAL Patent: JP 2002521062-A 2 16-JUL-2002;
ASTRAZENECA AB
COMMENT OS Homo sapiens (human)
PN JP 2002521062-A/2
PD 16-JUL-2002
PF 20-JUL-1999 JP 2000562550
PR 25-JUL-1998 GB 9816192.0,22-AUG-1998 GB 9818280.1 PI
JOHN CRAIG SMITH, RAKESH ANAND, JOHN EDWARD NORRIS MORTEN PC
C12N15/09,A61K45/00,A61P11/06,A61P43/00,C12M1/00,C12Q1/68, PC
G01N33/50,
PC G01N33/53,G01N33/566,C12N15/00
CC Gene polymorphism in human neurokinin 1 receptor gene and CC
utilization
CC thereof in diagnosing and treating disease
FH Key Location/Qualifiers
FT source 1..20
FT /organism='Homo sapiens (human)'.
FEATURES
source 1..20
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 524 GCAAGTCCACACTCTTT 543
Db 1 GCAAGTCCACACTCTTT 20
RESULT 184
CS186497
LOCUS CS186497 20 bp DNA linear PAT 04-NOV-2005
DEFINITION Sequence 3 from Patent WO2005100986.
ACCESSION CS186497
VERSION CS186497.1 GI:80748369
KEYWORDS
SOURCE .
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Golz,S.
TITLE Diagnostics and therapeutics for diseases associated with
tachykinin receptor 1(tacr1)
JOURNAL Patent: WO 2005100986-A 3 27-OCT-2005;
Bayer Healthcare AG (DE)
FEATURES
source 1..20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="forward primer"
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 276 CAATCAGTTCGTGCAACGAG 295
Db 1 CAATCAGTTCGTGCAACGAG 20
RESULT 185
I17156/c
LOCUS I17156 20 bp DNA linear PAT 03-APR-1996
DEFINITION Sequence 11 from patent US 5484886.
ACCESSION I17156
VERSION I17156.1 GI:1252064

KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Fong,T.M. and Strader,C.D.
TITLE Human neurokinin-1 receptor
JOURNAL Patent: US 5484886-A 11 16-JAN-1996;
Location/Qualifiers
FEATURES
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 601 TACATGGCATCATATCATCC 620
Db 20 TACATGGCATCATATCATCC 1
RESULT 186
I17157/c
LOCUS I17157 20 bp DNA linear PAT 03-APR-1996
DEFINITION Sequence 12 from patent US 5484886.
ACCESSION I17157
VERSION I17157.1 GI:1252065
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Fong,T.M. and Strader,C.D.
TITLE Human neurokinin-1 receptor
JOURNAL Patent: US 5484886-A 12 16-JAN-1996;
Location/Qualifiers
FEATURES
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 637 TCAGCCACAGCCACCAAGT 656
Db 20 TCAGCCACAGCCACCAAGT 1
RESULT 187
I17159/c
LOCUS I17159 20 bp DNA linear PAT 03-APR-1996
DEFINITION Sequence 14 from patent US 5484886.
ACCESSION I17159
VERSION I17159.1 GI:1252067
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Fong,T.M. and Strader,C.D.
TITLE Human neurokinin-1 receptor
JOURNAL Patent: US 5484886-A 14 16-JAN-1996;
Location/Qualifiers
FEATURES
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 862 GTAGTGGAGATCAGACTATG 881
Db 20 GTAGTGGAGATCAGACTATG 1

RESULT 188
117161/c
LOCUS 117161 20 bp DNA linear PAT 03-APR-1996
DEFINITION Sequence 16 from patent US 5484886.
ACCESSION 117161
VERSION 117161.1 GI:1252069
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Fong,T.M. and Strader,C.D.
TITLE Human neurokinin-1 receptor
JOURNAL Patent: US 5484886-A 16 16-JAN-1996;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Gaps 0;
Indels 0;

Qy 1012 TTCTCTCGCCCTACATCA 1031
Db 20 TTCTCTCGCCCTACATCA 1

RESULT 189
117164
LOCUS 117164 20 bp DNA linear PAT 03-APR-1996
DEFINITION Sequence 19 from patent US 5484886.
ACCESSION 117164
VERSION 117164.1 GI:1252072
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Fong,T.M. and Strader,C.D.
TITLE Human neurokinin-1 receptor
JOURNAL Patent: US 5484886-A 19 16-JAN-1996;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Gaps 0;
Indels 0;

Qy 1000 TTCACATCTTCTCTCTCT 1019
Db 1 TTCACATCTTCTCTCTCT 20

RESULT 190
117165
LOCUS 117165 20 bp DNA linear PAT 03-APR-1996
DEFINITION Sequence 20 from patent US 5484886.
ACCESSION 117165
VERSION 117165.1 GI:1252073
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Fong,T.M. and Strader,C.D.

TITLE Human neurokinin-1 receptor
JOURNAL Patent: US 5484886-A 20 16-JAN-1996;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Gaps 0;
Indels 0;

Qy 1023 CTACATCAACCCAGATCTCT 1042
Db 1 CTACATCAACCCAGATCTCT 20

RESULT 191
AX468706
LOCUS AX468706 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 22 from Patent WO0213799.
ACCESSION AX468706
VERSION AX468706.1 GI:21901476
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Henry,J.L., Cahill,C.M. and Yashpal,K.
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway
JOURNAL Patent: WO 0213799-A 22 21-FEB-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Gaps 0;
Indels 0;

Qy 1000 TTCACATCTTCTCTCTCT 1019
Db 1 TTCACATCTTCTCTCTCT 20

RESULT 192
AX468709/c
LOCUS AX468709 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 25 from Patent WO0213799.
ACCESSION AX468709
VERSION AX468709.1 GI:21901479
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Henry,J.L., Cahill,C.M. and Yashpal,K.
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway
JOURNAL Patent: WO 0213799-A 25 21-FEB-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1012 TTCCCTCTGCGCCATACATCAA 1031
Db 20 TTCCCTCTGCGCCATACATCAA 1

RESULT 193
AX468711/c 20 bp DNA linear PAT 16-JUL-2002
LOCUS AX468711
DEFINITION Sequence 27 from Patent WO0213799.
ACCESSION AX468711
VERSION AX468711.1 GI:21901481
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 GTAGTGGGATCATCACTATG 881
Db 20 GTAGTGGGATCATCACTATG 1

RESULT 194
AX468713/c 20 bp DNA linear PAT 16-JUL-2002
LOCUS AX468713
DEFINITION Sequence 29 from Patent WO0213799.
ACCESSION AX468713
VERSION AX468713.1 GI:21901483
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 637 TCAGCCACAGCCACCAAGT 656
Db 20 TCAGCCACAGCCACCAAGT 1

RESULT 195
AX468714/c

LOCUS AX468714 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 30 from Patent WO0213799.
ACCESSION AX468714
VERSION AX468714.1 GI:21901484
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 601 TACATGGCCATCATCATCC 620
Db 20 TACATGGCCATCATCATCC 1

RESULT 196
AX468725/c 20 bp DNA linear PAT 16-JUL-2002
LOCUS AX468725
DEFINITION Sequence 41 from Patent WO0213799.
ACCESSION AX468725
VERSION AX468725.1 GI:21901495
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1000 TTCCACATCTTCTTCCTCT 1019
Db 20 TTCCACATCTTCTTCCTCT 1

RESULT 197
AX468728 20 bp DNA linear PAT 16-JUL-2002
LOCUS AX468728
DEFINITION Sequence 44 from Patent WO0213799.
ACCESSION AX468728
VERSION AX468728.1 GI:21901498
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
synthetic construct
other sequences; artificial sequences.

AUTHORS Henry, J.L., Cahill, C.M. and Yashpal, K.
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway
JOURNAL Patent: WO 0213799-A 44 21-FEB-2002;
McGILL UNIVERSITY (CA)
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1012 TTCTCTCTGCGCTACATCAA 1031
|||||
1 TTCTCTCTGCGCTACATCAA 20

RESULT 198
LOCUS AX468730 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 46 from Patent WO0213799.
ACCESSION AX468730
VERSION AX468730.1 GI:21901500
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Henry, J.L., Cahill, C.M. and Yashpal, K.
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway
JOURNAL Patent: WO 0213799-A 46 21-FEB-2002;
McGILL UNIVERSITY (CA)
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 GTAGTGGGATCACAATG 881
|||||
1 GTAGTGGGATCACAATG 20

RESULT 199
LOCUS AX468732 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 48 from Patent WO0213799.
ACCESSION AX468732
VERSION AX468732.1 GI:21901502
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Henry, J.L., Cahill, C.M. and Yashpal, K.
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway
JOURNAL Patent: WO 0213799-A 48 21-FEB-2002;
McGILL UNIVERSITY (CA)
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"

/db_xref="taxon:32630"
/note="Primer"

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 637 TCAGCCACAGCCACCAAGT 656
|||||
1 TCAGCCACAGCCACCAAGT 20

RESULT 200
LOCUS AX468733 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 49 from Patent WO0213799.
ACCESSION AX468733
VERSION AX468733.1 GI:21901503
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Henry, J.L., Cahill, C.M. and Yashpal, K.
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway
JOURNAL Patent: WO 0213799-A 49 21-FEB-2002;
McGILL UNIVERSITY (CA)
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 601 TACATGGCCATCATCATCC 620
|||||
1 TACATGGCCATCATCATCC 20

RESULT 201
LOCUS AX616473 20 bp DNA linear PAT 20-FEB-2003
DEFINITION Sequence 34 from Patent EP1262565.
ACCESSION AX616473
VERSION AX616473.1 GI:28447516
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Affouric, J.P., Nelson, D.L., Seymour, A.B. and Webb, S.M.
TITLE Genetic polymorphisms in the human neurokinin 1 receptor gene and their uses in diagnosis and treatment of diseases
JOURNAL Patent: EP 1262565-A 34 04-DEC-2002;
Pfizer Products Inc. (US)
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 GGCACGTGTAGTATGTG 374
|||||
20 GGCACGTGTAGTATGTG 1

RESULT 202
AX616485/c 20 bp DNA linear PAT 20-FEB-2003
LOCUS AX616485
DEFINITION Sequence 46 from Patent EP1262565.
ACCESSION AX616485
VERSION AX616485.1 GI:28447528
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
1 Affourtit,J.P., Nelson,D.L., Seymour,A.B. and Webb,S.M.
AUTHORS Genetic polymorphisms in the human neurokinin 1 receptor gene and
TITLE their uses in diagnosis and treatment of diseases
JOURNAL Patent: EP 1262565-A 46 04-DEC-2002;
Pflizer Products Inc. (US)
FEATURES
source location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1483 CCCTTCATGCATGCAATTC 1502
Db 20 CCCTTCATGCATGCAATTC 1

RESULT 203
AX616486 20 bp DNA linear PAT 20-FEB-2003
LOCUS AX616486
DEFINITION Sequence 47 from Patent EP1262565.
ACCESSION AX616486
VERSION AX616486.1 GI:28447529
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
1 Affourtit,J.P., Nelson,D.L., Seymour,A.B. and Webb,S.M.
AUTHORS Genetic polymorphisms in the human neurokinin 1 receptor gene and
TITLE their uses in diagnosis and treatment of diseases
JOURNAL Patent: EP 1262565-A 47 04-DEC-2002;
Pflizer Products Inc. (US)
FEATURES
source location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1417 TCCATGCTCTCTCTAGGC 1436
Db 1 TCCATGCTCTCTCTAGGC 20

RESULT 204
AX616487/c 20 bp DNA linear PAT 20-FEB-2003
LOCUS AX616487
DEFINITION Sequence 48 from Patent EP1262565.
ACCESSION AX616487
VERSION AX616487.1 GI:28447530
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct

other sequences; artificial sequences.

REFERENCE
1 Affourtit,J.P., Nelson,D.L., Seymour,A.B. and Webb,S.M.
AUTHORS Genetic polymorphisms in the human neurokinin 1 receptor gene and
TITLE their uses in diagnosis and treatment of diseases
JOURNAL Patent: EP 1262565-A 48 04-DEC-2002;
Pflizer Products Inc. (US)
FEATURES
source location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1746 GCGAGTGCATTCAGAT 1765
Db 20 GCGAGTGCATTCAGAT 1

RESULT 205
AX616488/c 21 bp DNA linear PAT 03-APR-1996
LOCUS AX616488
DEFINITION Sequence 9 from patent US 5484886.
ACCESSION AX616488
VERSION AX616488.1 GI:1252062
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
1 (bases 1 to 21)
AUTHORS Fong,T.M. and Strader,C.D.
TITLE Human neurokinin-1 receptor
JOURNAL Patent: US 5484886-A 9 16-JAN-1996;
FEATURES
source location/Qualifiers
1..21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 523 TGCAAGTCCACAACTTCTT 542
Db 21 TGCAAGTCCACAACTTCTT 2

RESULT 206
AX68716/c 21 bp DNA linear PAT 16-JUL-2002
LOCUS AX68716
DEFINITION Sequence 32 from Patent WO0213799.
ACCESSION AX68716
VERSION AX68716.1 GI:21901486
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
1 Henry,J.L., Cahill,C.M. and Yashpal,K.
AUTHORS Oligonucleotides and other modulators of the nk-1 receptor pathway
TITLE and therapeutic uses thereof
JOURNAL Patent: WO 0213799-A 32 21-FEB-2002;
McGILL UNIVERSITY (CA)
FEATURES
source location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 523 TGCAGTTCACCACTCTT 542
|||||
21 TGCAGTTCACCACTCTT 2

RESULT 207
AX468735
LOCUS AX468735 21 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 51 from Patent WO2023799.
ACCESSION AX468735
VERSION AX468735.1 GI:21901505
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Henry,J.L., Cahill,C.M. and Yashpal,K.
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway
JOURNAL Patent: WO 0213799-A 51 21-FEB-2002;
MCGILL UNIVERSITY (CA)
FEATURES
source 1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 523 TGCAGTTCACCACTCTT 542
|||||
1 TGCAGTTCACCACTCTT 20

RESULT 208
AR109816
LOCUS AR109816 23 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 240 from patent US 6114139.
ACCESSION AR109816
VERSION AR109816.1 GI:12826092
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 23)
AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.
TITLE G-protein coupled receptor protein and a DNA encoding the receptor
JOURNAL Patent: US 6114139-A 240 05-SEP-2000;
FEATURES
source 1. .23
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 19.8; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 74;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 979 TTGCCATCTGCTGCTGCCCT 1001
|||||
1 TTGCCATCTGCTGCTGCCCT 23

RESULT 209
AX463104
LOCUS AX463104 23 bp DNA linear PAT 15-JUL-2002
DEFINITION Sequence 11 from Patent WO250115.

ACCESSION AX463104
VERSION AX463104.1 GI:21886095
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Hall,M.D., Suman-Chauhan,N., McNulty,S. and Murray,J.H.
TITLE Modified tachykinin receptors
JOURNAL Patent: WO 0250115-A 11 27-JUN-2002;
WARNER LAMBERT CO (US)
FEATURES
source 1. .23
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"

Query Match 1.1%; Score 19.8; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 74;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 438 CGCGAGGCTTCATGCTGCAT 460
|||||
1 CGCGAGGCTTCATGCTGCAT 23

RESULT 210
AR109833
LOCUS AR109833 21 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 257 from patent US 6114139.
ACCESSION AR109833
VERSION AR109833.1 GI:12826109
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.
TITLE G-protein coupled receptor protein and a DNA encoding the receptor
JOURNAL Patent: US 6114139-A 257 05-SEP-2000;
FEATURES
source 1. .21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 68;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 979 TTGCCATCTGCTGCTGCC 999
|||||
1 TTGCCATCTGCTGCTGCC 21

RESULT 211
AR001364
LOCUS AR001364 24 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 7 from patent US 5739118.
ACCESSION AR001364
VERSION AR001364.1 GI:3963431
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Carrano,R.A., Wang,B. and Weiner,D.B.
TITLE Compositions and methods for delivery of genetic material
JOURNAL Patent: US 5739118-A 7 14-APR-1998;
FEATURES
source 1. .24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 99;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 885 CAGTGAGATCCCGGGGAGACTCCTC 908
DB 1 CAGTGATATCCCGGAGACTCCTC 24

RESULT 212
AR044849 24 bp DNA linear PAT 29-SEP-1999
LOCUS AR044849
DEFINITION Sequence 7 from patent US 5817637.
ACCESSION AR044849
VERSION AR044849.1 GI:5966314
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Weiner,D.B., Williams,W.V. and Wang,B.
TITLE Genetic immunization
JOURNAL Patent: US 5817637-A 7 06-OCT-1998;
FEATURES Location/Qualifiers
1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 99;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 885 CAGTGAGATCCCGGGGAGACTCCTC 908
DB 1 CAGTGATATCCCGGAGACTCCTC 24

RESULT 213
AR052235 24 bp DNA linear PAT 29-SEP-1999
LOCUS AR052235
DEFINITION Sequence 7 from patent US 5830876.
ACCESSION AR052235
VERSION AR052235.1 GI:5975599
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Weiner,D.B., Williams,W.V. and Wang,B.
TITLE Genetic immunization
JOURNAL Patent: US 5830876-A 7 03-NOV-1998;
FEATURES Location/Qualifiers
1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 99;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 885 CAGTGAGATCCCGGGGAGACTCCTC 908
DB 1 CAGTGATATCCCGGAGACTCCTC 24

RESULT 214
AR078344 24 bp DNA linear PAT 31-AUG-2000
LOCUS AR078344
DEFINITION Sequence 7 from patent US 5962428.
ACCESSION AR078344
VERSION AR078344.1 GI:10005090
KEYWORDS

SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Carrano,R.A., Wang,B. and Weiner,D.B.
TITLE Compositions and methods for delivery of genetic material
JOURNAL Patent: US 5962428-A 7 05-OCT-1999;
FEATURES Location/Qualifiers
1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 99;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 885 CAGTGAGATCCCGGGGAGACTCCTC 908
DB 1 CAGTGATATCCCGGAGACTCCTC 24

RESULT 215
AR085195 24 bp DNA linear PAT 01-SEP-2000
LOCUS AR085195
DEFINITION Sequence 7 from patent US 5981505.
ACCESSION AR085195
VERSION AR085195.1 GI:10011965
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Weiner,D.B., Williams,W.V. and Wang,B.
TITLE Compositions and methods for delivery of genetic material
JOURNAL Patent: US 5981505-A 7 09-NOV-1999;
FEATURES Location/Qualifiers
1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 99;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 885 CAGTGAGATCCCGGGGAGACTCCTC 908
DB 1 CAGTGATATCCCGGAGACTCCTC 24

RESULT 216
AR138115 24 bp DNA linear PAT 16-JUN-2001
LOCUS AR138115
DEFINITION Sequence 7 from patent US 6197755.
ACCESSION AR138115
VERSION AR138115.1 GI:14479624
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Carrano,R.A., Wang,B. and Weiner,D.B.
TITLE Compositions and methods for delivery of genetic material
JOURNAL Patent: US 6197755-A 7 06-MAR-2001;
FEATURES Location/Qualifiers
1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 99;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 885 CAGTGAGATCCCGGGGAGACTCCTC 908

Db 1 CAGTGATATCCCGGAGACTCTC 24

RESULT 217
LOCUS ARI178989/c 24 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 13 from patent US 6320022.
ACCESSION ARI178989
VERSION ARI178989.1 GI:20220127
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 24)
Cutlita, F., Martinez, A., Miller, M. Jean., Unsworth, E. J., Hook, W.,
Walsh, T., Gray, K. and Macri, C.
TITLE Adrenomedullin peptides
JOURNAL Patent: US 6320022-A 13 20-NOV-2001;
FEATURES Location/Qualifiers
Source 1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 99;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 980 TCGCCATCTGCTGCTGCTCC 1003
24 TTGTATCTGCTGCTGCTCC 1

RESULT 218
LOCUS CO898470 24 bp DNA linear PAT 08-NOV-2004
DEFINITION Sequence 7 from Patent EPI473369.
ACCESSION CO898470
VERSION CO898470.1 GI:55582783
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
AUTHORS 1
Weiner, D.B., Williams, W.V., Wang, B., Coney, L.R., Merva, M.J. and
Zurawski, V.R.
TITLE Compositions and methods for delivery of genetic material
JOURNAL Patent: EP 1473369-A 7 03-NOV-2004;
Weiner, David B. (US); WILLIAMS, William V. (US); WANG, Bin (US);
CONEY, Leslie R. (US); MERYA, Michael J. (US); ZURANSKI, Vincent R
Jr. (US)
FEATURES Location/Qualifiers
Source 1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence:
Oligonucleotide"

Query Match 1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 99;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 885 CAGTGAGATCCCGGAGACTCTC 908
1 CAGTGATATCCCGGAGACTCTC 24

RESULT 219
LOCUS CS252672 24 bp DNA linear PAT 25-JAN-2006
DEFINITION Sequence 7 from Patent EPI616578.
ACCESSION CS252672

VERSION CS252672.1 GI:85814972
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unidentified
REFERENCE unclassified sequences.
AUTHORS 1
Carriano, R.A.
TITLE Compositions and methods for delivery of genetic material
JOURNAL Patent: EP 1616578-A 7 18-JAN-2006;
Myeth (US)
FEATURES Location/Qualifiers
Source 1..24
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 99;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 885 CAGTGAGATCCCGGAGACTCTC 908
1 CAGTGATATCCCGGAGACTCTC 24

RESULT 220
LOCUS I13899 24 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 7 from patent US 5593972.
ACCESSION I13899
VERSION I13899.1 GI:1824690
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 24)
Weiner, D.B., Williams, W.V. and Wang, B.
TITLE Genetic immunization
JOURNAL Patent: US 5593972-A 7 14-JAN-1997;
FEATURES Location/Qualifiers
Source 1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 99;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 885 CAGTGAGATCCCGGAGACTCTC 908
1 CAGTGATATCCCGGAGACTCTC 24

RESULT 221
LOCUS AR241150 24 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 7 from patent US 6468962.
ACCESSION AR241150
VERSION AR241150.1 GI:27286376
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 24)
Weiner, D.B., Williams, W.V. and Wang, B.
TITLE Genetic immunization
JOURNAL Patent: US 6468962-A 7 22-OCT-2002;
The Trustees of the University of Pennsylvania and The Wistar
Institute; Philadelphia, PA
FEATURES Location/Qualifiers
Source 1..24
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 99;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 885 CAGTGAGATCCCCGGGAGACTCTC 908
|||||
1 CAGTGATATCCCGGAGACTCTC 24

Db

RESULT 222
CS128871 19 bp DNA linear PAT 02-AUG-2005
LOCUS
DEFINITION Sequence 52 from Patent WO2005063983.
ACCESSION CS128871
VERSION CS128871.1 GI:71790738
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.

REFERENCE
AUTHORS van Rompaey, L.J.
JOURNAL Patent: WO 2005063983-A 52 14-JUL-2005;
Galapagos Genomics N.V. (BE)
LOCATION/Qualifiers

FEATURES
source 1..19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Gaps 0;

Qy 1137 TGACAGGTTCCGCTGGGC 1155
|||||
1 TGACAGGTTCCGCTGGGC 19

Db

RESULT 223
CS132144 19 bp DNA linear PAT 02-AUG-2005
LOCUS
DEFINITION Sequence 53 from Patent WO2005063976.
ACCESSION CS132144
VERSION CS132144.1 GI:71790894
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS van Rompaey, L.J.
JOURNAL Methods for inducing differentiation of undifferentiated mammalian
cells into osteoblasts
Patent: WO 2005063976-A 53 14-JUL-2005;
Galapagos Genomics N.V. (BE)
LOCATION/Qualifiers

FEATURES
source 1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Gaps 0;

Qy 1137 TGACAGGTTCCGCTGGGC 1155
|||||
1 TGACAGGTTCCGCTGGGC 19

Db

RESULT 224
CS186498/c 19 bp DNA linear PAT 04-NOV-2005
LOCUS
DEFINITION Sequence 4 from Patent WO2005100986.
ACCESSION CS186498
VERSION CS186498.1 GI:80748370
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS Golz, S.
JOURNAL Diagnostics and therapeutics for diseases associated with
tachykinin receptor 1 (tacr1)
Patent: WO 2005100986-A 4 27-OCT-2005;
Bayer Healthcare AG (DE)
LOCATION/Qualifiers

FEATURES
source 1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="reverse primer"

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Gaps 0;

Qy 322 GCCTACACGGTCATTTGTG 340
|||||
19 GCCTACACGGTCATTTGTG 1

Db

RESULT 225
CS207431 19 bp DNA linear PAT 08-DEC-2005
LOCUS
DEFINITION Sequence 139 from Patent WO2005109000.
ACCESSION CS207431
VERSION CS207431.1 GI:83413738
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS Spitael, K.F.
JOURNAL Patent: WO 2005109000-A 139 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spitael, Koenraad Frederick F. (BE)
LOCATION/Qualifiers

FEATURES
source 1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Gaps 0;

Qy 528 GTTCACAACCTTTTCCC 546
|||||
1 GTTCACAACCTTTTCCC 19

Db

RESULT 226
CS207432 19 bp DNA linear PAT 08-DEC-2005
LOCUS
DEFINITION Sequence 140 from Patent WO2005109000.
ACCESSION CS207432
VERSION CS207432.1 GI:83413739
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS

AUTHORS Spititaelis, K.F.
JOURNAL Patent: WO 2005109000-A 140 17-NOV-2005;
Galapagos Genomics N.V. (BE); Spititaelis, Koenraad Frederick F. (BE)
FEATURES
source
1. .19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 799 CACATCTGTGTGACTGTGC 817
|||||
1 CACATCTGTGTGACTGTGC 19

RESULT 227
LOCUS CS207433 19 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 141 from Patent WO2005109000.
ACCESSION CS207433
VERSION CS207433.1 GI:83413740
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1 Spititaelis, K.F.
AUTHORS Patent: WO 2005109000-A 141 17-NOV-2005;
JOURNAL Galapagos Genomics N.V. (BE); Spititaelis, Koenraad Frederick F. (BE)
FEATURES
source
1. .19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1027 ATCAACCCAGATCTCTACC 1045
|||||
1 ATCAACCCAGATCTCTACC 19

RESULT 228
LOCUS CS207434 19 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 142 from Patent WO2005109000.
ACCESSION CS207434
VERSION CS207434.1 GI:83413741
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1 Spititaelis, K.F.
AUTHORS Patent: WO 2005109000-A 142 17-NOV-2005;
JOURNAL Galapagos Genomics N.V. (BE); Spititaelis, Koenraad Frederick F. (BE)
FEATURES
source
1. .19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1137 TGCAGATTCCTCTGGCC 1155
|||||
Db 1 TGCAGATTCCTCTGGCC 19

RESULT 229
LOCUS CS207722 19 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 430 from Patent WO2005109000.
ACCESSION CS207722
VERSION CS207722.1 GI:83413999
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1 Spititaelis, K.F.
AUTHORS Patent: WO 2005109000-A 430 17-NOV-2005;
JOURNAL Galapagos Genomics N.V. (BE); Spititaelis, Koenraad Frederick F. (BE)
FEATURES
source
1. .19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 857 ACACCGTAGTGGGAATCAC 875
|||||
Db 1 ACACCGTAGTGGGAATCAC 19

RESULT 230
LOCUS 117168/c 19 bp DNA linear PAT 03-APR-1996
DEFINITION Sequence 23 from patent US 5484886.
ACCESSION 117168
VERSION 117168.1 GI:1252076
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 19)
AUTHORS Fong, T.M. and Strader, C.D.
TITLE Human neurokinin-1 receptor
JOURNAL Patent: US 5484886-A 23 16-JAN-1996;
FEATURES
source
1. .19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1548 AAAAGGTCAGTATGGATT 1566
|||||
Db 19 AAAAGGTCAGTATGGATT 1

RESULT 231
LOCUS 117170 19 bp DNA linear PAT 03-APR-1996
DEFINITION Sequence 25 from patent US 5484886.
ACCESSION 117170
VERSION 117170.1 GI:1252078
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 Unclassified.
1 (bases 1 to 19)

AUTHORS Fong,T.M. and Strader,C.D.

TITLE Human neurokinin-1 receptor

JOURNAL Patent: US 5484886-A 25 16-JUN-1996;

FEATURES Location/Qualifiers

source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 19; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 61;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 GTGTACAGATAGTAGGCTT 194

Db 1 GTGTACAGATAGTAGGCTT 19

RESULT 232

AX468719

LOCUS AX468719 19 bp DNA linear PAT 16-JUL-2002

DEFINITION Sequence 35 from Patent WO0213799.

ACCESSION AX468719

VERSION AX468719.1 GI:21901489

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.1%; Score 19; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 61;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 GTGTACAGATAGTAGGCTT 194

Db 1 GTGTACAGATAGTAGGCTT 19

RESULT 233

AX468721/c

LOCUS AX468721 19 bp DNA linear PAT 16-JUL-2002

DEFINITION Sequence 37 from Patent WO0213799.

ACCESSION AX468721

VERSION AX468721.1 GI:21901491

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.1%; Score 19; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 61;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1548 AAAAGGTCAGTATGGCTT 1566

Db 19 AAAAGGTCAGTATGGCTT 1

RESULT 234

AX468738/c

LOCUS AX468738 19 bp DNA linear PAT 16-JUL-2002

DEFINITION Sequence 54 from Patent WO0213799.

ACCESSION AX468738

VERSION AX468738.1 GI:21901508

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.1%; Score 19; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 61;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 GTGTACAGATAGTAGGCTT 194

Db 19 GTGTACAGATAGTAGGCTT 1

RESULT 235

AX468740

LOCUS AX468740 19 bp DNA linear PAT 16-JUL-2002

DEFINITION Sequence 56 from Patent WO0213799.

ACCESSION AX468740

VERSION AX468740.1 GI:21901510

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.1%; Score 19; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 61;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1548 AAAAGGTCAGTATGGCTT 1566

Db 1 AAAAGGTCAGTATGGCTT 19

RESULT 236
LOCUS AR109799 22 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 223 from patent US 6114139.
ACCESSION AR109799
VERSION AR109799.1 GI:12826075
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.
TITLE G-protein coupled receptor protein and a DNA encoding the receptor
JOURNAL Patent: US 6114139-A 223 05-SEP-2000;
FEATURES
source 1..22
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 92;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 587 TGGCCTTTGATGATGACTGCG 608
DB 1 TGGCCTTTGACAGATACATGCG 22
|||||
|||||

RESULT 237
LOCUS I60476 20 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 9 from patent US 5656462.
ACCESSION I60476
VERSION I60476.1 GI:2478921
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Keller,C., Mitsuhashi,M. and Akitaya,T.
TITLE Method for synthesizing cDNA using a polynucleotide immobilized
JOURNAL Patent: US 5656462-A 9 12-AUG-1997;
FEATURES
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 84;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 562 GCCAGTATCTACTCCATGAC 581
DB 1 GCCAGCATCTACTCCATGAC 20
|||||
|||||

RESULT 238
LOCUS AR098634 20 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 12 from patent US 6077666.
ACCESSION AR098634
VERSION AR098634.1 GI:12808400
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Hadcock,J.,Richard., Ozenberger,B.,Alton. and,Pausch,M.,Henry.
TITLE Receptor identification method
JOURNAL Patent: US 6077666-A 12 20-JUN-2000;
FEATURES
Location/Qualifiers

source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 18.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 90;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 979 TTGGCATTGCTGCTGCTGCC 998
DB 1 TTGGCATTGCTGCTGCTGCC 20
|||||
|||||

RESULT 239
LOCUS I65553 20 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 12 from patent US 5668006.
ACCESSION I65553
VERSION I65553.1 GI:2482123
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Hadcock,J.,Richard., Ozenberger,B.,Alton. and Pausch,M.,Henry.
TITLE Somatostatin receptors
JOURNAL Patent: US 5668006-A 12 16-SEP-1997;
FEATURES
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 18.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 90;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 979 TTGGCATTGCTGCTGCTGCC 998
DB 1 TTGGCATTGCTGCTGCTGCC 20
|||||
|||||

RESULT 240
LOCUS I17166 18 bp DNA linear PAT 03-APR-1996
DEFINITION Sequence 21 from patent US 548486.
ACCESSION I17166
VERSION I17166.1 GI:1252074
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Fong,T.M. and Strader,C.D.
TITLE Human neurokinin-1 receptor
JOURNAL Patent: US 548486-A 21 16-JAN-1996;
FEATURES
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1038 TCTCTACCTGAAGAATT 1055
DB 1 TCTCTACCTGAAGAATT 18
|||||
|||||

RESULT 241
LOCUS AX468723 18 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 39 from Patent WO0213799.

ACCESSION AX468723
VERSION AX468723.1 GI:21901493
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1038 TCTCTACCTGAAGAAGTT 1055
Db 1 TCTCTACCTGAAGAAGTT 18

RESULT 242
AX468742/c 18 bp DNA linear PAT 16-JUL-2002
LOCUS
DEFINITION Sequence 58 from Patent WO0213799.
ACCESSION AX468742
VERSION AX468742.1 GI:21901512
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1038 TCTCTACCTGAAGAAGTT 1055
Db 1 TCTCTACCTGAAGAAGTT 1

RESULT 243
AX616471/c 18 bp DNA linear PAT 20-FEB-2003
LOCUS
DEFINITION Sequence 32 from Patent EP1262565.
ACCESSION AX616471
VERSION AX616471.1 GI:28447514
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1038 TCTCTACCTGAAGAAGTT 1055
Db 1 TCTCTACCTGAAGAAGTT 1

RESULT 244
AR109832 21 bp DNA linear PAT 14-FEB-2001
LOCUS
DEFINITION Sequence 256 from patent US 6114139.
ACCESSION AR109832
VERSION AR109832.1 GI:12826108
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 979 TTCGCATCTGCTGCTGCC 999
Db 1 TTCACCTCTGCTGCTGCC 21

RESULT 245
AR109843 21 bp DNA linear PAT 14-FEB-2001
LOCUS
DEFINITION Sequence 267 from patent US 6114139.
ACCESSION AR109843
VERSION AR109843.1 GI:12826119
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 979 TTCGCATCTGCTGCTGCC 999
Db 1 TTCATCATCTGCTGCTGCC 21

their uses in diagnosis and treatment of diseases
Patent: EP 1262565-A 32 04-DEC-2002;
Pfizer Products Inc. (US)
Location/Qualifiers

FEATURES
source
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 58 CGCCAGTTGAGCTTCAA 75
Db 18 CGCCAGTTGAGCTTCAA 1

RESULT 244
AR109832 21 bp DNA linear PAT 14-FEB-2001
LOCUS
DEFINITION Sequence 256 from patent US 6114139.
ACCESSION AR109832
VERSION AR109832.1 GI:12826108
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 979 TTCGCATCTGCTGCTGCC 999
Db 1 TTCACCTCTGCTGCTGCC 21

RESULT 245
AR109843 21 bp DNA linear PAT 14-FEB-2001
LOCUS
DEFINITION Sequence 267 from patent US 6114139.
ACCESSION AR109843
VERSION AR109843.1 GI:12826119
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 979 TTCGCATCTGCTGCTGCC 999
Db 1 TTCATCATCTGCTGCTGCC 21

RESULT 246
ARI09845 21 bp DNA linear PAT 14-FEB-2001
LOCUS Sequence 269 from patent US 6114139.
DEFINITION ARI09845
ACCESSION ARI09845
VERSION ARI09845.1 GI:12826121
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.
TITLE G-protein coupled receptor protein and a DNA encoding the receptor
JOURNAL Patent: US 6114139-A 269 05-SEP-2000;
FEATURES
source
1. .21
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 979 TTGCCCATCTGCTGCTGCC 999
DB 1 TTGCCCTCTGCTGCTGCC 21

RESULT 247
ARI09846 21 bp DNA linear PAT 14-FEB-2001
LOCUS Sequence 270 from patent US 6114139.
DEFINITION ARI09846
ACCESSION ARI09846
VERSION ARI09846.1 GI:12826122
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.
TITLE G-protein coupled receptor protein and a DNA encoding the receptor
JOURNAL Patent: US 6114139-A 270 05-SEP-2000;
FEATURES
source
1. .21
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 979 TTGCCCATCTGCTGCTGCC 999
DB 1 TTGCCCTCTGCTGCTGCC 21

RESULT 248
CO976990/c 21 bp DNA linear PAT 19-JAN-2005
LOCUS Sequence 38 from Patent WO200500875.
DEFINITION CO976990
ACCESSION CO976990
VERSION CO976990.1 GI:57975973
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Wiltamer,V., Communi,D., Detheux,M., Parmentier,M., Loison,C. and Ooms,F.D.
TITLE Compositions and methods comprising a ligand of chemerin
JOURNAL Patent: WO 200500875-A 38 06-JAN-2005;
Euroscreen S.A. (BE)

FEATURES
source
1. .21
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic primer"
1. .21
/note="Synthetic primer"

Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 669 CATCTGGCTCTGCTCTCTCT 689
DB 21 CATCTGGCTCTGCTCTCTCT 1

RESULT 249
AX720862/c 21 bp DNA linear PAT 15-APR-2003
LOCUS Sequence 42 from Patent WO03006996.
DEFINITION AX720862
ACCESSION AX720862
VERSION AX720862.1 GI:29892630
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Wiltamer,V., Communi,D., Vandenoogaerde,A., Detheux,M. and Parmentier,M.
TITLE Natural ligand of GPCR chemr23 and uses thereof
JOURNAL Patent: WO 03006996-A 42 23-JAN-2003;
Euroscreen S.A. (BE)
FEATURES
source
1. .21
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"

Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 669 CATCTGGCTCTGCTCTCTCT 689
DB 21 CATCTGGCTCTGCTCTCTCT 1

RESULT 250
AR014600/c 21 bp DNA linear PAT 05-DEC-1998
LOCUS Sequence 25 from patent US 5773691.
DEFINITION AR014600
ACCESSION AR014600
VERSION AR014600.1 GI:3972054
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Falco,S., Carl., Keeler,S., Jo. and Rice,J., Ann.
TITLE Chimeric genes and methods for increasing the lysine and threonine content of the seeds of plants
JOURNAL Patent: US 5773691-A 25 30-JUN-1998;
FEATURES
source
1. .21
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1404 CTTGAGCTTCTCTCCA 1420
|||||
Db 19 CTTGAGCTTCTCTCCA 3

RESULT 251
AR014608/c 21 bp DNA linear PAT 05-DEC-1998
LOCUS AR014608 41 from patent US 5773691.
DEFINITION AR014608
ACCESSION AR014608
VERSION AR014608.1 GI:3972062
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Falco,S.Carl., Keeler,S.Jo. and Rice,J.Ann.
TITLE Chimeric genes and methods for increasing the lysine and threonine
JOURNAL content of the seeds of plants
FEATURES Patent: US 5773691-A 41 30-JUN-1998;
source Location/Qualifiers
1..21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1404 CTTGAGCTTCTCTCCA 1420
|||||
Db 19 CTTGAGCTTCTCTCCA 3

RESULT 252
AR014610/c 21 bp DNA linear PAT 05-DEC-1998
LOCUS AR014610 43 from patent US 5773691.
DEFINITION AR014610
ACCESSION AR014610
VERSION AR014610.1 GI:3972064
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Falco,S.Carl., Keeler,S.Jo. and Rice,J.Ann.
TITLE Chimeric genes and methods for increasing the lysine and threonine
JOURNAL content of the seeds of plants
FEATURES Patent: US 5773691-A 43 30-JUN-1998;
source Location/Qualifiers
1..21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1404 CTTGAGCTTCTCTCCA 1420
|||||
Db 19 CTTGAGCTTCTCTCCA 3

RESULT 253
BD010392/c 21 bp DNA linear PAT 09-JAN-2004
LOCUS BD010392 21 from patent US 5773691.
DEFINITION BD010392
ACCESSION BD010392
VERSION BD010392.1 GI:18638765
KEYWORDS
SOURCE Unidentified

ORGANISM unidentified
unclassified sequences.
REFERENCE 1 (bases 1 to 21)
AUTHORS Falco,S.C., Ili,R.E.M. and Epelbaum,S.U.
TITLE Chimeric genes and methods for increasing the lysine content of the
JOURNAL seeds of plants
PATENT: JP 2001502923-A 24 06-MAR-2001;
COMMENT E1 DU PONT DE NEMOURS AND CO
OS Unidentified
PN JP 2001502923-A/24
PD 06-MAR-2001
PF 27-MAR-1998 JP 1998543284
PR 27-MAR-1997 US 08/824627
PI SAVERIO CARL FALCO, RAYMOND ERVIN MCDEVITT III, PI SABINE
URSULA EPELBAUM
PC C12N9/06,C12N9/12,C12N9/88,C12P13/08,C12N15/82 CC
Strandedness: Single;
CC Topology: Linear;
FH Key location/Qualifiers
FT source 1..21
/organism="unidentified".
/db_xref="taxon:32644"

FEATURES
source 1..21
/organism="unidentified"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1404 CTTGAGCTTCTCTCCA 1420
|||||
Db 19 CTTGAGCTTCTCTCCA 3

RESULT 254
BD010400/c 21 bp DNA linear PAT 09-JAN-2004
LOCUS BD010400 43 from patent US 5773691.
DEFINITION BD010400
ACCESSION BD010400
VERSION BD010400.1 GI:18638773
KEYWORDS JP 2001502923-A/32.
SOURCE Unidentified
ORGANISM Unclassified
REFERENCE 1 (bases 1 to 21)
AUTHORS Falco,S.C., Ili,R.E.M. and Epelbaum,S.U.
TITLE Chimeric genes and methods for increasing the lysine content of the
JOURNAL seeds of plants
PATENT: JP 2001502923-A 32 06-MAR-2001;
COMMENT E1 DU PONT DE NEMOURS AND CO
OS Unidentified
PN JP 2001502923-A/32
PD 06-MAR-2001
PF 27-MAR-1998 JP 1998543284
PR 27-MAR-1997 US 08/824627
PI SAVERIO CARL FALCO, RAYMOND ERVIN MCDEVITT III, PI SABINE
URSULA EPELBAUM
PC C12N9/06,C12N9/12,C12N9/88,C12P13/08,C12N15/82 CC
Strandedness: Single;
CC Topology: Linear;
FH Key location/Qualifiers
FT source 1..21
/organism="unidentified".
/db_xref="taxon:32644"

FEATURES
source 1..21
/organism="unidentified"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1404 CTTGAGCTTCCTCCCA 1420

Db 19 CTTGAGCTTCCTCCCA 3

RESULT 255

BD010402/c

LOCUS

DEFINITION BD010402 21 bp DNA linear PAT 09-JAN-2004

Chimeric genes and methods for increasing the lysine content of the

seeds of plants.

BD010402

BD010402.1 GI:18638775

JP 2001502923-A/34.

unidentified

unidentified

unclassified sequences.

1 (bases 1 to 21)

REFERENCE Falco,S.C., Ili,R.E.M. and Epelbaum,S.U.

AUTHORS Chimeric genes and methods for increasing the lysine content of the

TITLE seeds of plants

Patent: JP 2001502923-A 34 06-MAR-2001;

Ei DU PONT DE NEMOURS AND CO

OS Unidentified

PN JP 2001502923-A/34

PD 06-MAR-2001

PF 27-MAR-1998 JP 1998543284

PR 27-MAR-1997 US 08/824627

PI SAVERIO CARL FALCO,RAYMOND ERVIN MCDEVITT III, PI SABINE

URSULA EPELBAUM

PC C12N9/06,C12N9/12,C12N9/88,C12P13/08,C12N15/82 CC

Strandedness: Single;

CC Topology: Linear;

FH Key Location/Qualifiers

FT source 1..21

/organism='Unidentified'.

Location/Qualifiers

1..21

/organism='unidentified'

/mol_type='unassigned DNA'

/db_xref='taxon:32644'

Query Match 1.0%; Score 17; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1404 CTTGAGCTTCCTCCCA 1420

Db 19 CTTGAGCTTCCTCCCA 3

RESULT 256

I26729/c

LOCUS

DEFINITION I26729 21 bp DNA linear PAT 07-OCT-1996

Sequence 17 from patent US 5559223.

I26729

I26729.1 GI:1606599

unidentified

unidentified

unclassified sequences.

1 (bases 1 to 21)

REFERENCE Falco,S.C., Keeler,S.J. and Rice,J.A.

AUTHORS Synthetic storage proteins with defined structure containing

TITLE programmable levels of essential amino acids for improvement of the

nutritional value of plants

Patent: US 5559223-A 17 24-SEP-1996;

Location/Qualifiers

1..21

/organism='unknown'

/mol_type='unassigned DNA'

Query Match 1.0%; Score 17; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1404 CTTGAGCTTCCTCCCA 1420

Db 19 CTTGAGCTTCCTCCCA 3

RESULT 257

I26731/c

LOCUS

DEFINITION I26731 21 bp DNA linear PAT 07-OCT-1996

Sequence 19 from patent US 5559223.

I26731

I26731.1 GI:1606601

unidentified

unidentified

unclassified sequences.

1 (bases 1 to 21)

REFERENCE Falco,S.C., Keeler,S.J. and Rice,J.A.

AUTHORS Synthetic storage proteins with defined structure containing

TITLE programmable levels of essential amino acids for improvement of the

nutritional value of plants

Patent: US 5559223-A 19 24-SEP-1996;

Location/Qualifiers

1..21

/organism='unknown'

/mol_type='unassigned DNA'

Query Match 1.0%; Score 17; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1404 CTTGAGCTTCCTCCCA 1420

Db 19 CTTGAGCTTCCTCCCA 3

RESULT 258

I26733/c

LOCUS

DEFINITION I26733 21 bp DNA linear PAT 07-OCT-1996

Sequence 21 from patent US 5559223.

I26733

I26733.1 GI:1606603

unidentified

unidentified

unclassified sequences.

1 (bases 1 to 21)

REFERENCE Falco,S.C., Keeler,S.J. and Rice,J.A.

AUTHORS Synthetic storage proteins with defined structure containing

TITLE programmable levels of essential amino acids for improvement of the

nutritional value of plants

Patent: US 5559223-A 21 24-SEP-1996;

Location/Qualifiers

1..21

/organism='unknown'

/mol_type='unassigned DNA'

Query Match 1.0%; Score 17; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1404 CTTGAGCTTCCTCCCA 1420

Db 19 CTTGAGCTTCCTCCCA 3

RESULT 259

AR235402/c

LOCUS

DEFINITION AR235402 21 bp DNA linear PAT 20-DEC-2002

DEFINITION Sequence 25 from patent US 6459019.
ACCESSION AR235402
VERSION AR235402.1 GI:27278543
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Falco,S.C., Keeler,S.J. and Rice,J.A.
TITLE Chimeric genes and methods for increasing the lysine and threonine content of the seeds of plants
JOURNAL Patent: US 6459019-A 25 01-OCT-2002;
E.I. du Pont de Nemours and Company; Wilmington, DE
FEATURES
source 1..21
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1404 CTTGAGCTTCTCCTCA 1420
Db 19 CTTGAGCTTCTCCTCA 3

RESULT 260
LOCUS AR235410 21 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 41 from patent US 6459019.
ACCESSION AR235410
VERSION AR235410.1 GI:27278551
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Falco,S.C., Keeler,S.J. and Rice,J.A.
TITLE Chimeric genes and methods for increasing the lysine and threonine content of the seeds of plants
JOURNAL Patent: US 6459019-A 41 01-OCT-2002;
E.I. du Pont de Nemours and Company; Wilmington, DE
FEATURES
source 1..21
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1404 CTTGAGCTTCTCCTCA 1420
Db 19 CTTGAGCTTCTCCTCA 3

RESULT 261
LOCUS AR235412/c 21 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 43 from patent US 6459019.
ACCESSION AR235412
VERSION AR235412.1 GI:27278553
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Falco,S.C., Keeler,S.J. and Rice,J.A.
TITLE Chimeric genes and methods for increasing the lysine and threonine content of the seeds of plants
JOURNAL Patent: US 6459019-A 43 01-OCT-2002;
E.I. du Pont de Nemours and Company; Wilmington, DE

FEATURES
source Location/Qualifiers
1..21
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1404 CTTGAGCTTCTCCTCA 1420
Db 19 CTTGAGCTTCTCCTCA 3

RESULT 262
LOCUS BD240830 21 bp DNA linear PAT 17-JUL-2003
DEFINITION Isoforms of human calcium sensing receptor.
ACCESSION BD240830
VERSION BD240830.1 GI:33050600
KEYWORDS JP 2002521052-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 21)
AUTHORS Yu,K.T., Labaudiniere,R.F. and Thrower,L.W.
TITLE Isoforms of human calcium sensing receptor
JOURNAL Patent: JP 2002521052-A 2 16-JUL-2002;
AVENTIS PHARMACEUTICALS PRODUCTS INC
COMMENT OS Homo sapiens (human)
PN JP 2002521052-A/2
PD 16-JUL-2002
PF 28-JUL-1999 JP 2000562397
PR 30-JUL-1998 US 60/094702
PI KIN T YU,RICHARD F LABAUDINIERE,LARRY W THROWER PC
C12N15/09,A61K31/7088,A61K35/74,A61K38/00,A61K45/00,PC
A61K48/00,A61K31/7088,A61K35/74,A61K38/00,A61K45/00,PC
PC A61P3/14,A61P5/18,A61P9/12,A61P19/10,A61P35/00,A61P43/00,PC
C07K14/705,
PC C07K16/28,C12N1/19,C12N1/21,C12N5/10,C12P21/08,C12Q1/02,G01N33/PC
15,
G01N33/50//C12N5/10,C12R1:91,C12N15/00,C12N5/00,A61K37/02,PC
C12N5/00,C12R1:91)
CC Isoforms of human calcium sensing receptor
FH Key Location/Qualifiers
FT source 1..21
/organism="Homo sapiens (human)".
FEATURES
source 1..21
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 1.0%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 656 TGGTCATCTGTCATCTGG 675
Db 21 TTGTCACTCTGTGTATCTGG 2

RESULT 263
LOCUS AR209863 21 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 7 from patent US 6387619.
ACCESSION AR209863
VERSION AR209863.1 GI:21511944
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Gottschling, D.E. and Singer, M.S.
TITLE Telomerase compositions and methods
JOURNAL Patent: US 6387619-A 7 14-MAY-2002;
FEATURES Location/Qualifiers
SOURCE 1..21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 921 CGACCAAGTCTGCGCAAGC 940
|||||
21 CGACCAAGTCTATGCAAGC 2

RESULT 264
LOCUS 185799 21 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 7 from patent US 5698686.
ACCESSION 185799
VERSION 185799.1 GI:3205517
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Gottschling, D.E. and Singer, M.S.
TITLE Yeast telomerase compositions
JOURNAL Patent: US 5698686-A 7 16-DEC-1997;
FEATURES Location/Qualifiers
SOURCE 1..21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 921 CGACCAAGTCTGCGCAAGC 940
|||||
21 CGACCAAGTCTATGCAAGC 2

RESULT 265
LOCUS 117147 18 bp DNA linear PAT 03-APR-1996
DEFINITION Sequence 2 from patent US 5484886.
ACCESSION 117147
VERSION 117147.1 GI:1252055
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Fong, T.M. and Strader, C.D.
TITLE Human neurokinin-1 receptor
JOURNAL Patent: US 5484886-A 2 16-JAN-1996;
FEATURES Location/Qualifiers
SOURCE 1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 448 TCATGCGTGCATTCAT 465
|||||

Db 1 TCATGCGTGCATTCAT 18

RESULT 266
LOCUS AR190721/c 18 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 6209 from patent US 6346398.
ACCESSION AR190721
VERSION AR190721.1 GI:20236686
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 6209 12-FEB-2002;
FEATURES Location/Qualifiers
SOURCE 1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 624 CCAGCCCGCGCTGCAGC 641
|||||
18 CCAGCCCGCGCTGCAGC 1

RESULT 267
LOCUS AR325569/c 18 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 2971 from patent US 6566127.
ACCESSION AR325569
VERSION AR325569.1 GI:33711377
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 2971 20-MAY-2003;
FEATURES Location/Qualifiers
SOURCE 1..18
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.9%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 624 CCAGCCCGCGCTGCAGC 641
|||||
18 CCAGCCCGCGCTGCAGC 1

RESULT 268
LOCUS AR599029/c 18 bp RNA linear PAT 15-DEC-2004
DEFINITION Sequence 2971 from patent US 6818447.
ACCESSION AR599029
VERSION AR599029.1 GI:56650043
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)

AUTHORS Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6818447-A 2971 16-NOV-2004;
Sirma Therapeutics, Inc.; Boulder, CO
FEATURES
source
1. .18
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.9%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 624 CCAGCCCCGGCTGCAGC 641
Db 18 CCAGCCGGCGCTGCAGC 1

RESULT 269
CQ778932 19 bp DNA linear PAT 11-MAR-2004
LOCUS Sequence 4 from Patent WO2004015422.
DEFINITION CQ778932
ACCESSION CQ778932
VERSION CQ778932.1 GI:45381605
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
AUTHORS 1
TITLE Golz, S., Brueggemeier, U. and Summer, H.
JOURNAL Diagnostics and therapeutics for diseases associated with
ovariancancer g-protein coupled receptor 1 (ogr-1)
Patent: WO 2004015422-A 4 19-FEB-2004;
Bayer Healthcare AG (DE)
FEATURES
source
Location/Qualifiers
1. .19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 985 ATCTGCTGCTGCCCTTC 1002
Db 19 ATCTGCTGCTGCCCTTC 2

RESULT 270
AX958828 20 bp DNA linear PAT 14-JAN-2004
LOCUS AX958828
DEFINITION Sequence 3 from Patent WO03100059.
ACCESSION AX958828
VERSION AX958828.1 GI:40879621
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.
REFERENCE
AUTHORS 1
TITLE Macaulay, V.M. and Schall, M.W.
JOURNAL Molecular targeting of the igf-1 receptor
Patent: WO 03100059-A 3 04-DEC-2003;
ISIS INNOVATION LIMITED (GB)
FEATURES
source
Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Antisense oligonucleotide"

Query Match 0.9%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1409 GCTTCTCTCCATGTGC 1426
Db 3 GCTTCTCTCCATGTGC 20

RESULT 271
CQ755471 20 bp DNA linear PAT 01-MAR-2004
LOCUS CQ755471
DEFINITION Sequence 3 from Patent WO2003100093.
ACCESSION CQ755471
VERSION CQ755471.1 GI:44846276
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.
REFERENCE
AUTHORS 1
TITLE Schall, M. and Macaulay, V.M.
JOURNAL Method of selecting targets for gene silencing by rna interference
Patent: WO 2003100093-A 3 04-DEC-2003;
Isis Innovation Limited (GB)
FEATURES
source
Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Antisense oligonucleotide"

Query Match 0.9%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1409 GCTTCTCTCCATGTGC 1426
Db 3 GCTTCTCTCCATGTGC 20

RESULT 272
AR475720 20 bp DNA linear PAT 20-FEB-2004
LOCUS AR475720
DEFINITION Sequence 87 from patent US 6692960.
ACCESSION AR475720
VERSION AR475720.1 GI:42715203
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
AUTHORS 1 (bases 1 to 20)
TITLE Bennett, C.F. and Freier, S.M.
JOURNAL Antisense modulation of sphingosine-1-phosphate lyase expression
Patent: US 6692960-A 87 17-FEB-2004;
Isis Pharmaceuticals, Inc.; Carlsbad, CA
FEATURES
source
Location/Qualifiers
1. .20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.9%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 963 TGTGCTGTGTGCACCTT 980
Db 18 TGTGCTGTGTGCACCTT 1

RESULT 273
AX218029 17 bp RNA linear PAT 07-SEP-2001
LOCUS AX218029

DEFINITION Sequence 3471 from Patent WO0159103.
ACCESSION AX218029
VERSION AX218029.1 GI:15528090
KEYWORDS
SOURCE
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
AUTHORS 1 Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 3471 16-AUG-2001;
RIBZYNE PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
source 1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 801 CATCTGTGACTGTG 816
DB 2 CATCTGTGACTGTG 17
|||||
|||||

RESULT 274
LOCUS CQ815064 19 bp DNA linear PAT 24-MAY-2004
CQ815064/c
DEFINITION Sequence 10 from Patent WO2004039978.
ACCESSION CQ815064
VERSION CQ815064.1 GI:47604155
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
AUTHORS 1 Meder, W., Wendland, M., John, H., Richter, R., Meyer, M. and
Forsmann, W.G.
TITLE Hf-chondroosteomodulin, production, and use for the treatment or
diagnosis of bone diseases, cartilage diseases, obesity,
inflammatory diseases, and skin diseases
JOURNAL Patent: WO 2004039978-A 10 13-MAY-2004;
IPF Pharmaceuticals GmbH (DE)
FEATURES
source 1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der k netlichen Sequenz: Primer
MDEZ014"

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 671 TTGGGTCCTGCTCTCCT 689
DB 19 TCTGGGTCTCTGCTTTCTT 1
|||||
|||||

RESULT 275
LOCUS CQ815066 19 bp DNA linear PAT 24-MAY-2004
CQ815066/c
DEFINITION Sequence 12 from Patent WO2004039978.
ACCESSION CQ815066
VERSION CQ815066.1 GI:47604157
KEYWORDS
SOURCE synthetic construct

ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
AUTHORS 1 Meder, W., Wendland, M., John, H., Richter, R., Meyer, M. and
Forsmann, W.G.
TITLE Hf-chondroosteomodulin, production, and use for the treatment or
diagnosis of bone diseases, cartilage diseases, obesity,
inflammatory diseases, and skin diseases
JOURNAL Patent: WO 2004039978-A 12 13-MAY-2004;
IPF Pharmaceuticals GmbH (DE)
FEATURES
source 1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der k netlichen Sequenz: Primer
HDEZ-a-0114"

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 671 TTGGGTCCTGCTCTCCT 689
DB 19 TCTGGGTCTCTGCTTTCTT 1
|||||
|||||

RESULT 276
LOCUS DQ6ADRB2B 19 bp DNA linear STS 09-APR-1996
DQ6ADRB2B/c
DEFINITION Canis familiaris Adrenergic Receptor Beta 2 (ADRB2) STS DNA, 3'
primer, sequence tagged site.
ACCESSION L77385
VERSION L77385.1 GI:1256663
KEYWORDS STS; Adrenergic Receptor Beta 2; PCR identification; PCR primer;
sequence tagged site; universal mammalian STS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Mammalia; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
REFERENCE
AUTHORS 1 (bases 1 to 19)
Venter, P.J., Brouillette, J.A., Yuzbasyan-Gurkan, V. and Brewer, G.J.
TITLE Gene-specific universal mammalian sequence-tagged sites:
application to the canine genome
JOURNAL Unpublished (1996)
COMMENT Original source text: Canis familiaris DNA.
Gene-specific universal mammalian sequence-tagged site for ADRB2.
Primer for the 3' end is in exon 1. Human product is 360 bp. Canine
product is 360 bp. PCR conditions: 1 min, 94 C, 2 min, 57 C, 3 min,
94 C, 35 cycles.
FEATURES
source 1..19
/organism="Canis familiaris"
/mol_type="genomic DNA"
/db_xref="taxon:9615"
1..19
/experiment="experimental evidence, no additional details
recorded"
/note="PCR primer binding site"

STS
primer_bind 1..19

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 979 TTGGCATTCTGCTGCTGC 997
DB 19 TTACCCCTCTGCTGCTGC 1
|||||
|||||

RESULT 277
LOCUS ARI90056/c

LOCUS AR190056 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 5544 from patent US 6346398.
ACCESSION AR190056
VERSION AR190056.1 GI:20236021
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 5544 12-FEB-2002;
FEATURES
Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No.1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 716 CAACCAAGAGACCATG 732
Db 17 CAACCAAGAGACCATG 1
RESULT 278
AR325033 17 bp RNA linear PAT 17-AUG-2003
LOCUS AR325033
DEFINITION Sequence 2435 from patent US 6566127.
ACCESSION AR325033
VERSION AR325033.1 GI:33710841
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 2435 20-MAY-2003;
FEATURES
Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned RNA"
Query Match 0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No.1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 716 CAACCAAGAGACCATG 732
Db 17 CAACCAAGAGACCATG 1
RESULT 279
AR598493 17 bp RNA linear PAT 15-DEC-2004
LOCUS AR598493
DEFINITION Sequence 2435 from patent US 6818447.
ACCESSION AR598493
VERSION AR598493.1 GI:56649507
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6818447-A 2435 16-NOV-2004;
Sirma Therapeutics, Inc.; Boulder, CO

FEATURES
Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned RNA"
Query Match 0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No.1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 716 CAACCAAGAGACCATG 732
Db 17 CAACCAAGAGACCATG 1
RESULT 280
AX216399 17 bp RNA linear PAT 07-SEP-2001
LOCUS AX216399
DEFINITION Sequence 1841 from Patent WO0159103.
ACCESSION AX216399
VERSION AX216399.1 GI:15526460
KEYWORDS
SOURCE
ORGANISM synthetic construct
REFERENCE
1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 1841 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
Location/Qualifiers
1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
Query Match 0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No.1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 619 CCCCTCAGCCCGGCT 635
Db 1 CCCCGCAGCCCGGCT 17
RESULT 281
AR109819 18 bp DNA linear PAT 14-FEB-2001
LOCUS AR109819
DEFINITION Sequence 243 from patent US 6114139.
ACCESSION AR109819
VERSION AR109819.1 GI:12826095
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 18)
AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.
TITLE G-protein coupled receptor protein and a DNA encoding the receptor
JOURNAL Patent: US 6114139-A 243 05-SEP-2000;
FEATURES
Location/Qualifiers
1..18
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No.1.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 427 AACCTGGCCTTGCGGA 443
Db 1 AACCTGGCCTTGCGGA 17

RESULT 282
AR698481/c
LOCUS AR698481 18 bp DNA linear PAT 14-SEP-2005
DEFINITION Sequence 19 from patent US 6919176.
ACCESSION AR698481
VERSION AR698481.1 GI:75203030
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Yang, J. and An, S.
TITLE Polypeptides and nucleic acids associated with cancer
JOURNAL Patent: US 6919176-A 19 19-JUL-2005;
Amgen Inc.; Thousand Oaks, CA
FEATURES
source location/Qualifiers
1. 18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 986 TCTGCTGCTGCTGCTTC 1002
Db 18 TCTGCTGCTGCTGCTTC 2

RESULT 283
CQ876950/c
LOCUS CQ876950 19 bp DNA linear PAT 04-OCT-2004
DEFINITION Sequence 3 from Patent WO2004078981.
ACCESSION CQ876950
VERSION CQ876950.1 GI:53790337
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Blyor, Y., Auge-Goullion, C., Hamelin, M.H. and Brillet, B.
TITLE Hyperactive, non-phosphorylated, mutant transposases of mariner
JOURNAL mobile genetic elements
Patent: WO 2004078981-A 3 16-SEP-2004;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR);
Universite Francois Rabelais de Tours (FR)
FEATURES
source location/Qualifiers
1. 19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description de la s quence artificielle: Amorce
site consensus d'initiation de la traduction - Vecteur
pBad18"

Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 891 GATCCCCGGGACTCCT 907
Db 19 GATCCCCGGGACTCCT 3

RESULT 284
CS096561
LOCUS CS096561 19 bp RNA linear PAT 03-JUN-2005
DEFINITION Sequence 62 from Patent WO2005045038.
ACCESSION CS096561
VERSION CS096561.1 GI:66953025
KEYWORDS

SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Richards, I., Polisky, B. and Mcswigen, J.
TITLE RNA interference mediated inhibition of GPRA and AA1 gene
JOURNAL expression using short Nucleic Acid (siNA)
Patent: WO 2005045038-A 62 19-MAY-2005;
Sirna Therapeutics, Inc. (US)
FEATURES
source location/Qualifiers
1. 19
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: Target
Sequence/siNA sense region"

Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1110 CAACCCCATCATCTACT 1126
Db 3 CAACCCCATCATCTACT 19

RESULT 285
CS096648/c
LOCUS CS096648 19 bp RNA linear PAT 03-JUN-2005
DEFINITION Sequence 149 from Patent WO2005045038.
ACCESSION CS096648
VERSION CS096648.1 GI:66953112
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Richards, I., Polisky, B. and Mcswigen, J.
TITLE RNA interference mediated inhibition of GPRA and AA1 gene
JOURNAL expression using short Nucleic Acid (siNA)
Patent: WO 2005045038-A 149 19-MAY-2005;
Sirna Therapeutics, Inc. (US)
FEATURES
source location/Qualifiers
1. 19
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: siNA antisense
region"

Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1110 CAACCCCATCATCTACT 1126
Db 17 CAACCCCATCATCTACT 1

RESULT 286
DD203034
LOCUS DD203034 19 bp DNA linear PAT 19-JAN-2006
DEFINITION RNA interference Mediated Inhibition of Vascular Endothelial Growth
Factor and Vascular Endothelial Growth Factor Receptor Gene
Expression Using Short Interfering RNA.
ACCESSION DD203034
VERSION DD203034.1 GI:85659126
KEYWORDS JP 2005517436-A/1515.
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 19)
AUTHORS Beigelman, L., Mcswigen, J. and Pavco, P.

TITLE RNA Interference Mediated Inhibition of Vascular Endothelial Growth Factor and Vascular Endothelial Growth Factor Receptor Gene Expression Using Short Interfering RNA
JOURNAL Patent: JP 200517436-A 1515 16-JUN-2005;
OS Sirna Therapeutics Inc
COMMENT OS Artificial Sequence
PN JP 200517436-A/1515
PD 16-JUN-2005
PR 15-JAN-2003 US 60/440129, 27-NOV-2002 US 10/306747, PR 04-NOV-2002 US 10/287949, 09-SEP-2002 US 60/409293, PR 05-SEP-2002 US 60/408378, 29-AUG-2002 US 60/406784, PR 20-FEB-2002 US 60/358580, 29-MAY-2002 US T/US02/17674, PR 11-MAR-2002 US 60/363124, 06-JUN-2002 US 60/386782, PR 03-JUL-2002 US 60/393796, 29-JUL-2002 US 60/399348 PI
Beigelman, James mcswigen, Pamela pavco CC Description of Artificial Sequence: Target Sequence/siRNA CC sense region
CC The type of this sequence is wrong in the original data. It is automatically modified by the JPO.
FH Location/Qualifiers
FEATURES
source 1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 0.8%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 139 AGGCGCCAGCCACGGA 155
Db 2 AGGCGCCAGCCACCGGA 18
RESULT 287
DD203281/c 19 bp RNA linear PAT 19-JAN-2006
LOCUS DD203281
DEFINITION RNA Interference Mediated Inhibition of Vascular Endothelial Growth Factor and Vascular Endothelial Growth Factor Receptor Gene Expression Using Short Interfering RNA.
ACCESSION DD203281
VERSION DD203281.1 GI:85660056
KEYWORDS JP 200517436-A/1762.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 19)
Beigelman, J., Mcswigen, J. and Pavco, P.
AUTHORS RNA Interference Mediated Inhibition of Vascular Endothelial Growth Factor and Vascular Endothelial Growth Factor Receptor Gene Expression Using Short Interfering RNA
JOURNAL Patent: JP 200517436-A 1762 16-JUN-2005;
OS Sirna Therapeutics Inc
COMMENT OS Artificial Sequence
PN JP 200517436-A/1762
PD 16-JUN-2005
PR 15-JAN-2003 US 60/440129, 27-NOV-2002 US 10/306747, PR 04-NOV-2002 US 10/287949, 09-SEP-2002 US 60/409293, PR 05-SEP-2002 US 60/408378, 29-AUG-2002 US T/US02/17674, PR 20-FEB-2002 US 60/358580, 29-MAY-2002 US 60/386782, PR 11-MAR-2002 US 60/363124, 06-JUN-2002 US 60/386782, PR 03-JUL-2002 US 60/393796, 29-JUL-2002 US 60/399348 PI
Beigelman, James mcswigen, Pamela pavco CC Description of Artificial Sequence: siRNA antisense region FH Key
FH Location/Qualifiers
FEATURES
source 1..19
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"

Query Match 0.8%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 139 AGGCGCCAGCCACGGA 155
Db 18 AGGCGCCAGCCACCGGA 2
RESULT 288
CO622226 17 bp DNA linear PAT 02-FEB-2004
LOCUS CO622226
DEFINITION Sequence 6966 from Patent WO0192524.
ACCESSION CO622226
VERSION CO622226.1 GI:41672444
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 6966 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.8%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 28 CAGTGCATCCGAAG 42
Db 3 CAGTGCATCCGAAG 17
RESULT 289
CO622227 17 bp DNA linear PAT 02-FEB-2004
LOCUS CO622227
DEFINITION Sequence 6967 from Patent WO0192524.
ACCESSION CO622227
VERSION CO622227.1 GI:41672445
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 6967 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Db 2 CAGTGCATCCAGAAG 16

RESULT 290
LOCUS C0622228
DEFINITION Sequence 6968 from Patent WO0192524.
ACCESSION C0622228
VERSION C0622228.1 GI:41672446
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Gu.Y., Ji.Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 6968 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
source location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.8%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred.No.1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 CAGTGCATCCAGAAG 42
|||||
1 CAGTGCATCCAGAAG 15

Db 1 CAGTGCATCCAGAAG 15

RESULT 291
LOCUS AR463289 17 bp DNA
DEFINITION Sequence 6966 from patent US 6686188.
ACCESSION AR463289
VERSION AR463289.1 GI:42698346
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu.Y., Ji.Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 6966 03-FEB-2004;
Amer sham PLC; Buckinghamshire;
GBX;

FEATURES
source location/Qualifiers
1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.8%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred.No.1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 CAGTGCATCCAGAAG 42
|||||
3 CAGTGCATCCAGAAG 17

Db 3 CAGTGCATCCAGAAG 17

RESULT 292
LOCUS AR463290 17 bp DNA
DEFINITION Sequence 6967 from patent US 6686188.
ACCESSION AR463290

VERSION AR463290.1 GI:42698347
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu.Y., Ji.Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 6967 03-FEB-2004;
Amer sham PLC; Buckinghamshire;
GBX;

FEATURES
source location/Qualifiers
1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.8%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred.No.1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 CAGTGCATCCAGAAG 42
|||||
2 CAGTGCATCCAGAAG 16

Db 2 CAGTGCATCCAGAAG 16

RESULT 293
LOCUS AR463291 17 bp DNA
DEFINITION Sequence 6968 from patent US 6686188.
ACCESSION AR463291
VERSION AR463291.1 GI:42698348
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu.Y., Ji.Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 6968 03-FEB-2004;
Amer sham PLC; Buckinghamshire;
GBX;

FEATURES
source location/Qualifiers
1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.8%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred.No.1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 CAGTGCATCCAGAAG 42
|||||
1 CAGTGCATCCAGAAG 15

Db 1 CAGTGCATCCAGAAG 15

RESULT 294
LOCUS AX047386/c 17 bp DNA
DEFINITION Sequence 2 from Patent WO0066402.
ACCESSION AX047386
VERSION AX047386.1 GI:11876617
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS van den Ende,W., van Laere,A., de Roover,V. and Michiels,A.
TITLE Manipulation of fructan catabolism in plants
JOURNAL Patent: WO 0068402-A 2 16-NOV-2000;

FEATURES K.U. Leuven Research & Development (BE)
source Location/Qualifiers
1..17
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="sense primer HFQp"

Query Match 0.8%; Score 15; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 1.7e+02;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1208 GGCCTGAATGAATCC 1224
Db 17 GGYTGAAATGAAACC 1

RESULT 295
AX217961 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 3403 from Patent WO0159103.
ACCESSION AX217961
VERSION AX217961.1 GI:15528022
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Blatt, L., McSwigen, J. and Chowitra, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
PATENT: WO 0159103-A 3403 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwigen, James (US) ; Chowitra, Bharat M. (US)
LOCATION/Qualifiers
1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

FEATURES source
Query Match 0.8%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 802 ATCTGTGACTGTG 816
Db 1 ATCTGTGACTGTG 15

RESULT 296
CQ931585/c 18 bp DNA linear PAT 23-NOV-2004
LOCUS CQ931585
DEFINITION Sequence 6618 from Patent WO2004083403.
ACCESSION CQ931585
VERSION CQ931585.1 GI:56220975
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE 1
AUTHORS Cargill, M., Begovich, A.B. and Alexander, H.C.
TITLE Genetic polymorphisms associated with rheumatoid arthritis, methods
JOURNAL of detection and uses thereof
PATENT: WO 2004083403-A 6618 30-SEP-2004;
Applera Corporation (US)
LOCATION/Qualifiers
1..18
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

FEATURES source

Query Match 0.8%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 677 TCCTGGCTCTCTGC 691
Db 15 TCCTGGCTCTCTGC 1

RESULT 297
AR257450 18 bp mRNA linear PAT 20-DEC-2002
LOCUS AR257450
DEFINITION Sequence 5 from patent US 6486310.
ACCESSION AR257450
VERSION AR257450.1 GI:27307461
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 18)
AUTHORS O'Malley, K.L. and Todd, R.D.
TITLE Gene encoding the rat dopamine D4 receptor
JOURNAL Patent: US 6486310-A 5 26-NOV-2002;
Washington University; St. Louis, MO
LOCATION/Qualifiers
1..18
/organism="unknown"
/mol_type="mRNA"

FEATURES source
Query Match 0.8%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 988 TGCTGGCTGCCCTTC 1002
Db 1 TGCTGGCTGCCCTTC 15

RESULT 298
A90829/c 18 bp DNA linear PAT 22-JAN-2000
LOCUS A90829
DEFINITION Sequence 8 from Patent WO9830687.
ACCESSION A90829
VERSION A90829.1 GI:6739239
KEYWORDS
SOURCE
ORGANISM
unidentified
unclassified
unclassified sequences.

REFERENCE 1 (bases 1 to 18)
AUTHORS Poustka, A. and Mollenhauer, J.
TITLE PROTEIN CONTAINING AN SRCK DOMAIN
JOURNAL Patent: WO 9830687-A 8 16-JUL-1998;
DEUTSCHES KREBSFORSCH (DE); POUSTKA ANNEMARIE (DE)
LOCATION/Qualifiers
1..18
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

FEATURES source
Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1263 CAGCGCGCTGAGACAC 1280
Db 18 CAGCTGCGCTGAGACAC 1

RESULT 299
AR054536/c 18 bp DNA linear PAT 29-SEP-1999
LOCUS AR054536
DEFINITION Sequence 45 from patent US 5637441.

ACCESSION AR054536
VERSION AR054536.1 GI:5980113
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Hjelte, B. and Jensen, S.
TITLE Hantavirus-associated respiratory distress virus antigens
JOURNAL Patent: US 5837441-A 45 17-NOV-1998;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 129 CCTGAGCCCCGAGCCCA 146
DB 18 CCTGAGCCCCGAGCCCA 1

RESULT 300
ARI38040/c 18 bp DNA linear PAT 16-JUN-2001
LOCUS ARI38040 Sequence 50 from patent US 6197584.
ACCESSION ARI38040
VERSION ARI38040.1 GI:14479549
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Bennett, C. Frank, and Cowser, L. M.
TITLE Antisense modulation of CD40 expression
JOURNAL Patent: US 6197584-A 50 06-MAR-2001;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1406 TCAGCTTCTCTCCCATG 1423
DB 18 TCAGCTTCTCTCCCATG 1

RESULT 301
BD064969/c 18 bp DNA linear PAT 27-AUG-2002
LOCUS BD064969 Protein containing an SRCR domain.
ACCESSION BD064969
VERSION BD064969.1 GI:22610572
KEYWORDS JP 2001509667-A/7.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Mollenhauer, J. and Poustka, A.
TITLE Protein containing an SRCR domain
JOURNAL Patent: JP 2001509667-A 7 24-JUL-2001;
COMMENT DEUTSCHES KREBSFORSCHUNGSZENTRUM STIFTUNG DES OFFENTLICHEN RECHTS
OS Artificial Sequence
PN JP 2001509667-A/7
PD 24-JUL-2001
PF 09-JAN-1998 JP 1998530469
PR 09-JAN-1997 DE 197 00 519.5, 18-JUL-1997 DE 197 30 997.6 PI
JAN MOLLENHAUER, ANNEMARIE POUSTKA

PC C12N15/12, C12N15/70, C12N1/21, C12Q1/68, C07K14/47, C07K16/18, PC
A61K38/17,
PC A61K48/00, G01N33/50
CC Description of Artificial Sequence: primer sequence for CC
amplifying a DNA
CC encoding a protein containing SRCR domain.
FH Key Location/Qualifiers
FT source 1..18
/organism="Artificial Sequence".
FEATURES Location/Qualifiers
source 1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 243 CTCGCCAAACATCTCCAC 260
DB 1 CTCGCCAAACATCTCTC 18

RESULT 303
BD226591/c 18 bp DNA linear PAT 17-JUL-2003
LOCUS BD226591

PC C12N15/12, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
00', C12P1/02, C12Q1/02, A61K48/00, A61K39/395, A61K45/00, A61P11/00 CC
Description of Artificial Sequence: Artificially Synthesized CC
Primer
CC Sequence Location/Qualifiers
FH Key 1..18
FT source /organism="Artificial Sequence".
FEATURES Location/Qualifiers
source 1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 243 CTCGCCAAACATCTCCAC 260
DB 1 CTCGCCAAACATCTCTC 18

RESULT 303
BD226591/c 18 bp DNA linear PAT 17-JUL-2003
LOCUS BD226591

BD170368 18 bp DNA linear PAT 17-JAN-2003
LOCUS BD170368 Novel human chloride channel.
ACCESSION BD170368
VERSION BD170368.1 GI:27876180
KEYWORDS WO 0244369-A/5
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 18)
AUTHORS Furukawa, T. and Ogura, T.
TITLE Novel human chloride channel
JOURNAL Patent: WO 0244369-A 5 06-JUN-2002;
COMMENT BANYU PHARMACEUTICAL CO LTD, TETSUSHI FURUKAWA, TAKEHIKO OGURA
OS Artificial Sequence
PN WO 0244369-A/5
PD 06-JUN-2002
PF 30-NOV-2001 WO 2001JP010499
PR 30-NOV-2000 JP 00P 365103
PT TETSUSHI FURUKAWA, TAKEHIKO OGURA
PC C12N15/12, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
00', C12P1/02, C12Q1/02, A61K48/00, A61K39/395, A61K45/00, A61P11/00 CC
Description of Artificial Sequence: Artificially Synthesized CC
Primer
CC Sequence Location/Qualifiers
FH Key 1..18
FT source /organism="Artificial Sequence".
FEATURES Location/Qualifiers
source 1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 243 CTCGCCAAACATCTCCAC 260
DB 1 CTCGCCAAACATCTCTC 18

RESULT 303
BD226591/c 18 bp DNA linear PAT 17-JUL-2003
LOCUS BD226591

DEFINITION Antisense modulation of CD40 expression.
ACCESSION BD226591
VERSION BD226591.1 GI:33036361
KEYWORDS JP 2002513593-A/50.
SOURCE unclassified
ORGANISM unclassified
REFERENCE unclassified sequences.
AUTHORS 1 (bases 1 to 18)
TITLE Bennett,C.F. and Cowseert,L.M.
JOURNAL Antisense modulation of CD40 expression
PATENT: JP 2002513593-A 50 14-MAY-2002;
ISIS PHARMACEUTICALS INC
COMMENT OS Unidentified
PN JP 2002513593-A/50
PD 14-MAY-2002
PF 22-APR-1999 JP 2000547271
PR 01-MAY-1998 US 09/071433
PI C FRANK BENNETT, LEX M COMSERT
PC C12N15/09,A61K9/10,A61K45/00,A61K48/00,A61P1/00,A61P11/06, PC
A61P17/06,
PC A61P29/00,A61P35/00,A61P37/02,A61P37/06,A61P43/00,C12P19/34,
PC C12Q1/68,
PC C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC Antisense modulation of CD40 expression
FH Key Location/Qualifiers
FT source 1..18
FT Location/Qualifiers
1..18
/organism="Unidentified".
FEATURES
source 1..18
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1406 TCAGCTTCTCTCCCATG 1423
DB 18 TCGGCTTCTCTCCCATG 1
|||||
|||||

RESULT 304
BD250496/c 18 bp DNA linear PAT 17-JUL-2003
LOCUS Identification of genetic targets for modulation by
DEFINITION oligonucleotides and generation of oligonucleotides for gene
modulation.
ACCESSION BD250496
VERSION BD250496.1 GI:33060266
KEYWORDS JP 2002511276-A/50.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Cowseert,L.M., Baker,B.F., Mcneil,J., Freier,S.M., Saemor,H.M.,
TITLE Brooks,D.G., Ohasi,C., Wyatt,J.R., Borchers,A.H. and Vikkars,T.A.
JOURNAL Identification of genetic targets for modulation by
PATENT: JP 2002511276-A 50 16-APR-2002;
ISIS PHARMACEUTICALS INC
COMMENT OS Artificial Sequence
PN JP 2002511276-A/50
PD 16-APR-2002
PF 13-APR-1999 JP 2000543647
PR 13-APR-1998 US 60/081483, 28-APR-1998 US 09/067638 PT
LEX M COMSERT, BRENDA F BAKER, JOHN MCNEILL, SUSAN M FREIER, HENRI PI
M SASMOR,
PI DOUGLAS G BROOKS, CARA OHASI, JACQUELINE R WYATT, ALEXANDER H PI
BORCHERS,

PI TIMOTHY A VIKKARS
PC C12N15/09,C07B61/00,C07B61/00,C12Q1/68,G06F17/30,G06F17/50, PC
C12N15/00
CC Antisense Oligonucleotide
FH Key Location/Qualifiers
FT source 1..18
FT Location/Qualifiers
1..18
/organism="Artificial Sequence".
FEATURES
source 1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1406 TCAGCTTCTCTCCCATG 1423
DB 18 TCGGCTTCTCTCCCATG 1
|||||
|||||

RESULT 305
AR193175/c 18 bp DNA linear PAT 20-APR-2002
LOCUS AR193175
DEFINITION Sequence 9 from patent US 6346606.
ACCESSION AR193175
VERSION AR193175.1 GI:20239140
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Mollenhauer,J. and Poustka,A.
TITLE Protein containing a scavenger receptor cysteine rich domain
JOURNAL Patent: US 6346606-A 9 12-FEB-2002;
FEATURES Location/Qualifiers
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1263 CAGCCGCTGAGACAC 1280
DB 18 CAGCTGCTGACACAC 1
|||||
|||||

RESULT 306
AX146659 18 bp DNA linear PAT 31-MAY-2001
LOCUS AX146659
DEFINITION Sequence 1 from Patent WO0134834.
ACCESSION AX146659
VERSION AX146659.1 GI:14285052
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Jeffers,H., Jorgensen,M. and Skakkebaek,K.N.E.
TITLE Endogenous gene expression assay
JOURNAL Patent: WO 0134834-A 1 17-MAY-2001;
Rigshospitalet (DK)
FEATURES Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer sequence"

Query Match 0.8%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 105 CCTCTGCTGCTCTTAG 122
|||||
Db 1 CCTCTGCTGCTCTTAG 18

RESULT 307
AX686022 18 bp DNA linear PAT 29-MAR-2003
LOCUS
DEFINITION Sequence 66 from Patent WO02064791.
ACCESSION AX686022
VERSION AX686022.1 GI:29371875
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

1
Alababrook II, J.P., Anderson, D.W., Burgess, C.E., Boldog, F.L.,
Caeman, S.J., Colman, S.D., Edinger, S.R., Ellerman, K., Gerlach, V.,
Gorman, L., Grose, W.M., Guo, X., Herrmann, J.L., Kekuda, R.,
Lepley, D.M., Li, L., Macdougall, J.R., Miller, I., Pena, C.E.,
Peyman, J.A., Rastelli, L., Rieger, D.K., Shinkens, R.A., Smithson, G.,
Spytek, K.A., Stone, D.J., Tchernev, V.T., Vernet, C.A., Voss, E.Z.,
Zerhagen, B.D., Zhong, H. and Zhong, M.
Proteins and nucleic acids encoding same
Patent: WO 02064791-A 66 22-AUG-2002;
Curagen Corporation (US)

FEATURES
source
1. 18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide primer"

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 315 GGCAGCTGCTACACGGT 332
|||||
Db 1 GGCAGCTGCTACACGGT 18

RESULT 308
AX468698 16 bp DNA linear PAT 16-JUL-2002
LOCUS
DEFINITION Sequence 14 from Patent WO0213799.
ACCESSION AX468698
VERSION AX468698.1 GI:21901468
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

1
Henry, J.L., Cahill, C.M. and Yashpal, K.
Oligonucleotides and other modulators of the nk-1 receptor pathway
and therapeutic uses thereof
Patent: WO 0213799-A 14 21-FEB-2002;
MCGILL UNIVERSITY (CA)
Location/Qualifiers
1. 16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"

Query Match 0.8%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 207 CGAATGATACGTC 222

Db 16 CAATGATACGTC 1
|||||

RESULT 309
DD184677/c 17 bp DNA linear PAT 19-JAN-2006
LOCUS
DEFINITION Probe sets and methods for identifying HLA-B allele.
ACCESSION DD184677
VERSION DD184677.1 GI:85637624
KEYWORDS JP 2005185172-A/103.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
OS Homo sapiens
PN JP 2005185172-A/103
PD 14-JUL-2005
PF 25-DEC-2003 JP 2003430554
PI mamoru tsukada
CC
FH Key Location/Qualifiers.
1. 17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

FEATURES
source
1. 17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 438 GCGGAGGCTTCATG 453
|||||
Db 17 GCGGAGGCTTCATG 2

RESULT 310
DD188299/c 17 bp DNA linear PAT 19-JAN-2006
LOCUS
DEFINITION Probe set and method for identification of allele of HLA.
ACCESSION DD188299
VERSION DD188299.1 GI:85646382
KEYWORDS WO 2005063985-A/740.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
OS Homo sapiens
PN WO 2005063985-A/740
PD 14-JUL-2005
PF 24-DEC-2004 WO 2004JP019763
PR 25-DEC-2003 JP 03P 430556, 25-DEC-2003 JP 03P 430555, PR
25-DEC-2003 JP 03P 430559, 25-DEC-2003 JP 03P 430553, PR
25-DEC-2003 JP 03P 430558, 25-DEC-2003 JP 03P 430557, PR
25-DEC-2003 JP 03P 430554
PI mamoru tsukada
CC
FH Key Location/Qualifiers.
1. 17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

FEATURES
source
1. 17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Chiquet-Ehrismann, R. and Scherberich, A.
TITLE Tenascin-w compositions and uses thereof
JOURNAL Patent: WO 03080663-A 22 OCT-2003;
Novartis Forschungsförderung Zweigleiderlaassung (CH)
Location/Qualifiers

FEATURES
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence:
oligonucleotide"

Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1276 ACCACCATCTCCACAG 1291
|||
16 ACCACCTCTCCACAG 1

RESULT 316
LOCUS BD217386 18 bp DNA linear PAT 17-JUL-2003
DEFINITION Antisense modulation of TNFR1 expression.
ACCESSION BD217386
VERSION BD217386.1 GI:33027156
KEYWORDS JP 2002519015-A/9.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS Baker, B.F. and Cowse, L.M.
TITLE Antisense modulation of TNFR1 expression
JOURNAL Patent: JP 2002519015-A 9 OCT-2002;
ISIS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002519015-A/9
PD 02-JUL-2002
PR 17-JUN-1999 JP 2000557265
PI 26-JUN-1998 US 09/106038
PI BRENDA F BAKER, LEX M COWSE
PC C12N15/09, A61K31/7105, A61K31/711, A61K48/00, A61P29/00, A61P43/00, PC
C1201/68
PC C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC Antisense modulation of TNFR1 expression
FH Key Location/Qualifiers
FT source 1..18
Location/Qualifiers
1..18
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

QY 105 CCCTCGTCTGCTTT 120
|||
3 CCTCTCTCTGCTTT 18

RESULT 317
CQ799859

LOCUS CQ799859 18 bp DNA linear PAT 28-APR-2004
DEFINITION Sequence 509 from Patent WO2004031413.
ACCESSION CQ799859
VERSION CQ799859.1 GI:4684806
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Nakamura, Y., Daigo, Y. and Nakatsu, S.
TITLE Method for diagnosing non-small cell lung cancers
JOURNAL Patent: WO 2004031413-A 509 15-APR-2004;
Oncotherapy Science, Inc. (JP); Japan as represented by the
president of the university of Tokyo (JP)
Location/Qualifiers

FEATURES
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Artificially synthesized S-oligonucleotide sequence
for antisense method"

Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1277 CCACCATCTCCACAGT 1292
|||
3 CCACCATCTCCACAGT 18

RESULT 318
LOCUS AR190767 18 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 6255 from patent US 6346398.
ACCESSION AR190767
VERSION AR190767.1 GI:20236732
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Pavco, P., McSwiggan, J., Srincomb, D. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions
JOURNAL related to levels of vascular endothelial growth factor receptor
PATENT: US 6346398-A 6255 12-FEB-2002;
Location/Qualifiers
1..18
/organism="unknown"
/mol_type="unassigned DNA"

QY 662 TCTGTGTCATCTGGGT 677
|||
18 TCTGTGTCATCTGAGT 3

RESULT 319
LOCUS AR299235 18 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 10970 from patent US 6537751.
ACCESSION AR299235
VERSION AR299235.1 GI:3168519
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Cohen, D., Chumakov, I. and Blumenfeld, M.
TITLE Biallelic markers for use in constructing a high density

disequilibrium map of the human genome
Patent: US 6537751-A 10970 25-MAR-2003;
Genset S.A.;;

FEATURES

source Location/Qualifiers
1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1404 CTTGAGCTTCTCCTCC 1419

Db 2 CTTGATCTTCTCTCTC 17

RESULT 320
AR325611/c 18 bp RNA linear PAT 17-AUG-2003

LOCUS AR325611
DEFINITION Sequence 3013 from patent US 6566127.
ACCESSION AR325611
VERSION AR325611.1 GI:33711419
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)
Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
AUTHORS Method and reagent for the treatment of diseases or conditions
TITLE related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 3013 20-MAY-2003;
FEATURES Ribozyme Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO
source Location/Qualifiers
1..18
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 662 TCTGTGTCATCTGGGT 677

Db 18 TCTGTGTCATCTGAGT 3

RESULT 321
181946 18 bp DNA linear PAT 10-JUN-1998
LOCUS 181946
DEFINITION Sequence 44 from patent US 5712094.
ACCESSION 181946
VERSION 181946.1 GI:3210243
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)
Seidel,H.,Martin., Lamb,I.,Peter. and Chan,S.-S.Tian.
AUTHORS Methods for detecting modulators of cytokine action
TITLE Patent: US 5712094-A 44 27-JAN-1998;
JOURNAL Location/Qualifiers
FEATURES 1..18
source /organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1717 TCCATTTCTGGAAGTG 1732

Db 1717 TCCATTTCTGGAAGTG 1732

Db 3 TCCATTTCTGGAAGTG 18

RESULT 322
AR442143/c 18 bp DNA linear PAT 20-FEB-2004
LOCUS AR442143
DEFINITION Sequence 42 from patent US 6670124.
ACCESSION AR442143
VERSION AR442143.1 GI:42669400
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)
Chow,R. and Tonal,R.
AUTHORS High throughput methods of HLA typing
TITLE Patent: US 6670124-A 42 30-DEC-2003;
JOURNAL StemCyle, Inc.; Arcadia, CA
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 438 CGCGAGGCTCTCATG 453

Db 18 CGCGAGGCTCTCATG 3

RESULT 323
AR599071/c 18 bp RNA linear PAT 15-DEC-2004
LOCUS AR599071
DEFINITION Sequence 3013 from patent US 6818447.
ACCESSION AR599071
VERSION AR599071.1 GI:56650085
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)
Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
AUTHORS Method and reagent for the treatment of diseases or conditions
TITLE related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6818447-A 3013 16-NOV-2004;
FEATURES Sinna Therapeutics, Inc.; Boulder, CO
source Location/Qualifiers
1..18
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 662 TCTGTGTCATCTGGGT 677

Db 18 TCTGTGTCATCTGAGT 3

RESULT 324
AX115374 18 bp DNA linear PAT 11-MAY-2001
LOCUS AX115374
DEFINITION Sequence 497 from Patent WO0129262.
ACCESSION AX115374
VERSION AX115374.1 GI:14032316
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 other sequences; artificial sequences.

AUTHORS Picoult-Newburg, L. and Pohl, M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 497 26-APR-2001;
Orchid Biosciences, Inc. (US)

FEATURES
source
1. 18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1223 CCACCCGGTATCTCCA 1238
Db 18 CCACCCGGTCTCTCCA 3

RESULT 325
AX468696/c 18 bp DNA linear PAT 16-JUL-2002
LOCUS AX468696
DEFINITION Sequence 12 from Patent WO0213799.
ACCESSION AX468696
VERSION AX468696.1 GI:21901466
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Henry, J.L., Cahill, C.M. and Yashpal, K.
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway
JOURNAL Patent: WO 0213799-A 12 21-FEB-2002;
MCGILL UNIVERSITY (CA)

FEATURES
source
1. 18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 207 CGAATGATTAACCTC 222
Db 16 CAAATGATTAACCTC 1

RESULT 326
AR407912 14 bp RNA linear PAT 18-DEC-2003
LOCUS AR407912
DEFINITION Sequence 5 from patent US 6632057.
ACCESSION AR407912
VERSION AR407912.1 GI:40157899
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 14)
AUTHORS Fauchet, C.R.J.
TITLE Fixing unit with an end imprint in a threaded terminal portion
JOURNAL Patent: US 6632057-A 5 14-OCT-2003;
GRT Aerospace; Paris;
PRX;

FEATURES
source
1. 14
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 689 TGCTGACCTTCCCC 702
Db 1 TGCTGACCTTCCCC 14

RESULT 327
E09069 15 bp DNA linear PAT 29-SEP-1997
LOCUS E09069
DEFINITION DNA encoding N-terminal fragment of recombinant bile
salt-activating lipase.
ACCESSION E09069
VERSION E09069.1 GI:22025695
KEYWORDS JP 199511891-A/11.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 15)
AUTHORS Murasugi, A. and Asami, Y.
TITLE EXPRESSION OF RECOMBINANT BILE SALT ACTIVATED LIPASE IN HIGH YIELD
JOURNAL Patent: JP 199511891-A 11 02-MAY-1995;
MEIJI MILK PROD CO LTD
OS None
COMMENT

OC Artificial sequences.
PN JP 199511891-A/11
PD 02-MAY-1995
PF 30-SEP-1993 JP 1993245079
PI MURASUGI AKIRA, ASAMI YUKIO
PC C12N9/20, C12N1/19, C12N15/09, (C12N9/20, C12R1/84), (C12N1/19, PC
C12R1/84);
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key
FT source 1. 15
Location/Qualifiers
/organism="Artificial sequences".

FEATURES
source
1. 15
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1133 TCAATGACAGGTTTC 1146
Db 1 TCAATGACAGGTTTC 14

RESULT 328
AX468699/c 15 bp DNA linear PAT 16-JUL-2002
LOCUS AX468699
DEFINITION Sequence 15 from Patent WO0213799.
ACCESSION AX468699
VERSION AX468699.1 GI:21901469
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 15)
AUTHORS Henry, J.L., Cahill, C.M. and Yashpal, K.
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway
JOURNAL Patent: WO 0213799-A 15 21-FEB-2002;
MCGILL UNIVERSITY (CA)

FEATURES
source
1. 15
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned RNA"

source

1. .15
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 209 AAATGATACGTC 222
| | | | | | | | | | | | | | | |
Db 14 AAATGATACGTC 1

RESULT 329

AR043296 16 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 84 from patent US 5814457.
ACCESSION AR043296
VERSION AR043296.1 GI:5964304
KEYWORDS
SOURCE
ORGANISM Unknown.
UNCLASSIFIED.

REFERENCE 1 (bases 1 to 16)
AUTHORS Kern,S.E. and Hahn,S.A.
TITLE DPC4 polypeptide
JOURNAL Patent: US 5814457-A 84 29-SEP-1998;
FEATURES
Location/Qualifiers
1. .16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 730 ATGCCACGACGAGT 743
| | | | | | | | | | | | | | | |
Db 2 ATGCCACGACGAGT 15

RESULT 330

AR074951 16 bp DNA linear PAT 28-AUG-2000
LOCUS AR074951
DEFINITION Sequence 84 from patent US 5955292.
ACCESSION AR074951
VERSION AR074951.1 GI:10001703
KEYWORDS
SOURCE
ORGANISM Unknown.
UNCLASSIFIED.

REFERENCE 1 (bases 1 to 16)
AUTHORS Kern,S.E. and Hahn,S.A.
TITLE Tumor suppressor gene, DPC4
JOURNAL Patent: US 5955292-A 84 21-SEP-1999;
FEATURES
Location/Qualifiers
1. .16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 730 ATGCCACGACGAGT 743
| | | | | | | | | | | | | | | |
Db 2 ATGCCACGACGAGT 15

RESULT 331

182147

LOCUS 182147 16 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 84 from patent US 5712097.
ACCESSION 182147
VERSION 182147.1 GI:3210444
KEYWORDS
SOURCE
ORGANISM Unknown.
UNCLASSIFIED.

REFERENCE 1 (bases 1 to 16)
AUTHORS Kern,S.E. and Hahn,S.A.
TITLE Tumor suppressor gene, DPC4
JOURNAL Patent: US 5712097-A 84 27-JAN-1998;
FEATURES
Location/Qualifiers
1. .16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 730 ATGCCACGACGAGT 743
| | | | | | | | | | | | | | | |
Db 2 ATGCCACGACGAGT 15

RESULT 332

AR075054 17 bp DNA linear PAT 28-AUG-2000
LOCUS AR075054
DEFINITION Sequence 14 from patent US 5955306.
ACCESSION AR075054
VERSION AR075054.1 GI:10001806
KEYWORDS
SOURCE
ORGANISM Unknown.
UNCLASSIFIED.

REFERENCE 1 (bases 1 to 17)
AUTHORS Gimeno,C.J. and Errada,P.R.
TITLE Genes encoding proteins that interact with the tub protein
JOURNAL Patent: US 5955306-A 14 21-SEP-1999;
FEATURES
Location/Qualifiers
1. .17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 571 TACTCATGACGCG 584
| | | | | | | | | | | | | | | |
Db 3 TACTCATGACGCG 16

RESULT 333

AR141872 17 bp DNA linear PAT 08-AUG-2001
LOCUS AR141872
DEFINITION Sequence 14 from patent US 6147192.
ACCESSION AR141872
VERSION AR141872.1 GI:15101388
KEYWORDS
SOURCE
ORGANISM Unknown.
UNCLASSIFIED.

REFERENCE 1 (bases 1 to 17)
AUTHORS Gimeno,C.J. and Errada,P.R.
TITLE Tub interactor (TI) polypeptides and uses therefor
JOURNAL Patent: US 6147192-A 14 14-NOV-2000;
FEATURES
Location/Qualifiers
1. .17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 571 TACTCATGACGCG 584
|||||
Db 3 TACTCATGACGCG 16

RESULT 334
LOCUS C0622225 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 6965 from Patent WO0192524.
ACCESSION C0622225
VERSION C0622225.1 GI:41672443
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS Gu.Y., Ji.Y., Penn.S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNML Patent: WO 0192524-A 6965 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 CAGTGCATCCAGAA 41
|||||
Db 4 CAGTGCATCCAGAA 17

RESULT 335
LOCUS C0622229 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 6969 from Patent WO0192524.
ACCESSION C0622229
VERSION C0622229.1 GI:41672447
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS Gu.Y., Ji.Y., Penn.S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNML Patent: WO 0192524-A 6969 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 AGTGCATCCAGAG 42
|||||
Db 1 AGTGCATCCAGAG 14

RESULT 336
LOCUS C0931584/c 17 bp DNA linear PAT 23-NOV-2004
DEFINITION Sequence 6617 from Patent WO2004083403.
ACCESSION C0931584
VERSION C0931584.1 GI:56220974
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS Cargill,M., Begovich,A.B. and Alexander,H.C.
TITLE Genetic polymorphisms associated with rheumatoid arthritis, methods
JOURNML of detection and uses thereof
Patent: WO 2004083403-A 6617 30-SEP-2004;
Applera Corporation (US)
FEATURES
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 677 TCCTGGCTTCCTG 690
|||||
Db 14 TCCTGGCTTCCTG 1

RESULT 337
LOCUS AR404183 17 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 22 from patent US 6627739.
ACCESSION AR404183
VERSION AR404183.1 GI:40152223
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 17)
Anderson,J.P., Basl,G., Doan,M.T., Frigon,N., John,V., Power,M.,
Sinha,S., Tatsuno,G., Tung,J., Wang,S. and McConlogue,L.
TITLE .beta.-secretase enzyme compositions and methods
JOURNML Patent: US 6627739-A 22 30-SEP-2003;
Elian Pharmaceuticals, Inc.; South San Francisco, CA
FEATURES
source 1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.4e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1306 GAGGAGGAGCCAGGA 1322
|||||
Db 1 GAYGARGAGCCGAGGA 17

RESULT 338
LOCUS AR463288 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 6965 from patent US 6666186.
ACCESSION AR463288
VERSION AR463288.1 GI:42698345
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu.Y., Ji.Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 6965 03-FEB-2004;
Amer sham PLC; Buckinghamshire;
GBX;
FEATURES
source
1. 17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 28 CAGTGCATCCAGAA 41
|||||
4 CAGTGCATCCAGAA 17

Db

RESULT 339
AR463292 17 bp DNA linear PAT 20-FEB-2004
LOCUS AR463292
DEFINITION Sequence 6969 from patent US 6686188.
ACCESSION AR463292
VERSION AR463292.1 GI:42698349
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu.Y., Ji.Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 6969 03-FEB-2004;
Amer sham PLC; Buckinghamshire;
GBX;
FEATURES
source
1. 17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 29 AGTGCATCCAGAG 42
|||||
1 AGTGCATCCAGAG 14

Db

RESULT 340
AX218126 17 bp RNA linear PAT 07-SEP-2001
LOCUS AX218126
DEFINITION Sequence 3568 from Patent WO0159103.
ACCESSION AX218126
VERSION AX218126.1 GI:15528187
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt,U., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 3568 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)

FEATURES
source
Location/Qualifiers
1. 17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 803 TCTGTGACTGTTG 816
|||||
1 TCTGTGACTGTTG 14

Db

RESULT 341
AR046956 17 bp DNA linear PAT 29-SEP-1999
LOCUS AR046956
DEFINITION Sequence 1749 from patent US 5817796.
ACCESSION AR046956
VERSION AR046956.1 GI:5968421
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myb ribozymes having 2'-5',-linked adenylate residues
JOURNAL Patent: US 5817796-A 1749 06-OCT-1998;
FEATURES
source
1. 17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 441 GGAGCGCTCCATGGCTG 457
|||||
1 GGAGCGCTCCATGGCTG 17

Db

RESULT 342
BD067403/c 17 bp RNA linear PAT 27-AUG-2002
LOCUS BD067403/c
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors.
ACCESSION BD067403
VERSION BD067403.1 GI:22613006
KEYWORDS JP 2001511003-A/243.
SOURCE JP 2001511003-A/243.
ORGANISM unidentified
unclassified
unclassified sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Akhtar,S., Fell,P. and McSwiggen,J.A.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors
JOURNAL Patent: JP 2001511003-A 243 07-AUG-2001;
RIBOZYME PHARMACEUTICALS INC,ASTON UNIV
COMMENT OS Unidentified
PN JP 2001511003-A/243
PD 07-AUG-2001
PF 14-JAN-1998 JP 1998532913
PR 31-JAN-1997 US 60/036476,04-DEC-1997 US 08/985162 PI
SAGHIR AKHTAR, PATRICIA FELL,JAMES A MCSWIGGEN PC
CL2N9/00, C07K14/71
CC Strandedness: Single;
CC Topology: linear;
CC Enzymatic nucleic acid treatment of diseases or conditions related to
CC levels of epidermal growth factor receptors

ORGANISM	Homo sapiens
REFERENCE	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
TITLE	Homnidae; Homo.
JOURNAL	1 (bases 1 to 17)
COMMENT	Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswigen,J.A. Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response Patent: JP 2002509721-A 3895 02-APR-2002; RIBOZYME PHARMACEUTICALS INC OS Homo sapiens (human) PN JP 2002509721-A/3895 PD 02-APR-2002 PR 24-MAR-1999 JP 2000541291 PI 27-MAR-1998 US 60/079678 PI PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT, PI JAMES A MCSWIGEN
FEATURES	location/Qualifiers 1..17 /organism="Homo sapiens" /mol_type="genomic RNA" /db_xref="taxon:9606"
source	CC Method and reagent for treating diseases or conditions CC CC participating in vasculogenic response FH key location/Qualifiers FT source 1..17 FT location/Qualifiers 1..17 /organism="Homo sapiens (human)".
Query Match	0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity	88.2%; Pred. No. 2.5e+02;
Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	1720 ATTTCCTGGAAGTGAAGTCTT 1736
Db	17 ACTTCTGGAAGTGAAT 1
RESULT 345	
LOCUS	COG618016 17 bp DNA linear PAT 02-FEB-2004
DEFINITION	Sequence 2756 from Patent WO0192524.
ACCESSION	COG618016
VERSION	COG618016.1 GI:41668234
KEYWORDS	
SOURCE	
ORGANISM	Homo sapiens (human)
REFERENCE	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
TITLE	Homnidae; Homo.
JOURNAL	1 (bases 1 to 17)
COMMENT	Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E. Myostatin-like gene expressed in human heart and muscle Patent: WO 0192524-A 2756 06-DEC-2001; Aeomica, Inc. (US) location/Qualifiers 1..17 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
FEATURES	location/Qualifiers 1..17 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
source	CC Method and reagent for treating diseases or conditions CC CC participating in vasculogenic response FH key location/Qualifiers FT source 1..17 FT location/Qualifiers 1..17 /organism="Homo sapiens (human)".
Query Match	0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity	88.2%; Pred. No. 2.5e+02;
Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	1196 GCGACTATGAGGGGCTG 1212
Db	1196 GCGACTATGAGGGGCTG 1212

Db 1 GCGAGTATGAGGAGCTG 17

RESULT 346
LOCUS DD185435 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Probe sets for detection of HLA-C allele and methods thereof.
ACCESSION DD185435
VERSION DD185435.1 GI:185638904
KEYWORDS JP 2005185174-A/180.
SOURCE synthetic construct
ORGANISM Homo sapiens (human)
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 7674 06-DEC-2001;
Aecomica, Inc. (US)
FEATURES
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1404 CTTGAGCTTCTCTCCA 1420
Db 17 CTTGCTCTCTCTCCA 1

RESULT 347
LOCUS DD184601 17 bp DNA linear PAT 19-JAN-2006
DEFINITION Probe sets and methods for identifying HLA-B allele.
ACCESSION DD184601
VERSION DD184601.1 GI:85637235
KEYWORDS JP 2005185172-A/27.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Tsukada,M.
TITLE Probe sets and methods for identifying HLA-B allele
JOURNAL Patent: JP 2005185172-A 27 14-JUL-2005;
CANON INC
COMMENT OS Homo sapiens
PN JP 2005185172-A/27
PD 14-JUL-2005
PF 25-DEC-2003 JP 2003430554
PI mamoru tsukada
CC

FEATURES
source FH Key Location/Qualifiers.
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 138 CAGGCGCCAGCCACAGG 154
Db 1 CAAGCGCCAGGCACAGG 17

RESULT 348
LOCUS DD185435 17 bp DNA linear PAT 19-JAN-2006
DEFINITION Probe sets for detection of HLA-C allele and methods thereof.
ACCESSION DD185435
VERSION DD185435.1 GI:185638904
KEYWORDS JP 2005185174-A/180.
SOURCE synthetic construct
ORGANISM Homo sapiens (human)
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Tsukada,M.
TITLE Probe sets for detection of HLA-C allele and methods thereof
JOURNAL Patent: JP 2005185174-A 180 14-JUL-2005;
Canon Inc
COMMENT OS artificial sequence
PN JP 2005185174-A/180
PD 14-JUL-2005
PF 25-DEC-2003 JP 2003430556
PI mamoru tsukada
CC probe for detection
FEATURES
source FH Key Location/Qualifiers.
1..17
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 138 CAGGCGCCAGCCACAGG 154
Db 1 CAAGCGCCAGGCACAGG 17

RESULT 349
LOCUS DD188223 17 bp DNA linear PAT 19-JAN-2006
DEFINITION Probe set and method for identification of allele of HLA.
ACCESSION DD188223
VERSION DD188223.1 GI:85646306
KEYWORDS WO 2005063985-A/664.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Tsukada,M.
TITLE Probe set and method for identification of allele of HLA
JOURNAL Patent: WO 2005063985-A 664 14-JUL-2005;
CANON INC
COMMENT OS Homo sapiens
PN WO 2005063985-A/664
PD 14-JUL-2005
PF 24-DEC-2004 WO 2004JP019763
PR 25-DEC-2003 JP 03P 430556,25-DEC-2003 JP 03P 430553, PR
25-DEC-2003 JP 03P 430558,25-DEC-2003 JP 03P 430557, PR
25-DEC-2003 JP 03P 430554
PI mamoru tsukada
CC

FEATURES
source FH Key Location/Qualifiers.
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORGANISM	Unknown. Unclassified
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REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 5545 12-FEB-2002;
FEATURES Location/Qualifiers
SOURCE 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 714 CTCACCCAGAGACCA 730
DB 17 CACACCCAGAGACCA 1

RESULT 355
AR190206/c 17 bp DNA linear PAT 20-APR-2002
LOCUS AR190206 Sequence 5694 from patent US 6346398.
DEFINITION AR190206
ACCESSION AR190206.1 GI:20236171
VERSION
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 5694 12-FEB-2002;
FEATURES Location/Qualifiers
SOURCE 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1505 TTCATCTGGAACCATCA 1521
DB 17 TTCATCTGATCCATGA 1

RESULT 356
AR196300/c 17 bp DNA linear PAT 20-APR-2002
LOCUS AR196300 Sequence 765 from patent US 6350934.
DEFINITION AR196300
ACCESSION AR196300
VERSION AR196300.1 GI:20245737
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Zwick, M.G., Edington, B.E., McSwiggen, J.A., Merlo, P., Ann Owens, G., L., Skokut, T.A., Young, S.A., Folkerts, O. and Merlo, D.J.
TITLE Nucleic acid encoding delta-9 desaturase
JOURNAL Patent: US 6350934-A 765 26-FEB-2002;
FEATURES Location/Qualifiers
SOURCE 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 636 GTCAGCCACAGCCACCA 652

DB 17 GTCAGCCAGAGCCACCA 1

RESULT 357
AR324312/c 17 bp RNA linear PAT 17-AUG-2003
LOCUS AR324312 Sequence 1714 from patent US 6566127.
DEFINITION AR324312
ACCESSION AR324312
VERSION AR324312.1 GI:33710120
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1714 20-MAY-2003;
FEATURES Ribozyme Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO Location/Qualifiers
SOURCE 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 714 CTCACCCAGAGACCA 730
DB 17 CACACCCAGAGACCA 1

RESULT 358
AR324484/c 17 bp RNA linear PAT 17-AUG-2003
LOCUS AR324484 Sequence 1886 from patent US 6566127.
DEFINITION AR324484
ACCESSION AR324484
VERSION AR324484.1 GI:33710292
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1886 20-MAY-2003;
FEATURES Ribozyme Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO Location/Qualifiers
SOURCE 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1505 TTCATCTGGAACCATCA 1521
DB 17 TTCATCTGATCCATGA 1

RESULT 359
AR328943/c 17 bp RNA linear PAT 17-AUG-2003
LOCUS AR328943 Sequence 6345 from patent US 6566127.
DEFINITION AR328943
ACCESSION AR328943
VERSION AR328943.1 GI:33714751
KEYWORDS
SOURCE
ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 17)
 AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
 TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
 JOURNAL Patent: US 6566127-A 6345 20-MAY-2003;
 FEATURES Rhozyme Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO
 source 1..17
 /organism="unknown"
 /mol_type="unassigned RNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 713 ACTCAACACAGAGACC 729
 Db 17 ACACACACAGAGACC 1

RESULT 360
 LOCUS 154008 17 bp DNA linear PAT 07-OCT-1997
 DEFINITION Sequence 1749 from patent US 5646042.
 ACCESSION 154008
 VERSION 154008.1 GI:2475211
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 17)
 AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
 TITLE C-myc targeted ribozymes
 JOURNAL Patent: US 5646042-A 1749 08-JUL-1997;
 FEATURES location/Qualifiers
 source 1..17
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 441 GGAGCGCTCCATGCGCTG 457
 Db 1 GGAGCGCTCCATGCGCTG 17

RESULT 361
 LOCUS 160477 17 bp DNA linear PAT 07-OCT-1997
 DEFINITION Sequence 10 from patent US 5656462.
 ACCESSION 160477
 VERSION 160477.1 GI:2478922
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 17)
 AUTHORS Keller,C., Mitsuhashi,M. and Akitaya,T.
 TITLE Method for synthesizing cDNA using a polynucleotide immobilized support
 JOURNAL Patent: US 5656462-A 10 12-AUG-1997;
 FEATURES location/Qualifiers
 source 1..17
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 983 CCATCTGCTGGCGCCC 999
 Db 17 CCATCTGCTGGCGCCC 1

RESULT 362
 LOCUS AR401903 17 bp DNA linear PAT 18-DEC-2003
 DEFINITION Sequence 243 from patent US 6623962.
 ACCESSION AR401903
 VERSION AR401903.1 GI:40149353
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 17)
 AUTHORS Ahltaar,S., Fell,P. and McSwiggen,J.A.
 TITLE Enzymatic nucleic acid treatment of diseases of conditions related to levels of epidermal growth factor receptors
 JOURNAL Patent: US 6623962-A 243 23-SEP-2003;
 FEATURES Sirta Therapeutics, Inc. and Aston University; Boulder, CO
 location/Qualifiers
 source 1..17
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1313 AGCGAGAGAGAGCGCCC 1329
 Db 17 AGCGAGAGAGAGCGCCC 1

RESULT 363
 LOCUS AR459079 17 bp DNA linear PAT 20-FEB-2004
 DEFINITION Sequence 2756 from patent US 6686188.
 ACCESSION AR459079
 VERSION AR459079.1 GI:42694136
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 17)
 AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
 TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
 JOURNAL Patent: US 6686188-A 2756 03-FEB-2004;
 FEATURES Amerisham PLC; Buckinghamshire;
 location/Qualifiers
 source 1..17
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1196 GCGAGTATGAGGAGCTG 1212
 Db 1 GCGAGTATGAGGAGCTG 17

RESULT 364
 LOCUS AR463997 17 bp DNA linear PAT 20-FEB-2004
 DEFINITION Sequence 7674 from patent US 6686188.
 ACCESSION AR463997
 VERSION AR463997.1 GI:42699054

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu.Y., Ji.Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 7674 03-FEB-2004;
Amer sham PLC; Buckinghamshire;
GBX;
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1404 CTCGAGCTTCTCTCCA 1420
Db 17 CTTCTGCTTCTTCTCCA 1
RESULT 365
AR597772/c AR597772 17 bp RNA linear PAT 15-DEC-2004
LOCUS Sequence 1714 from patent US 6818447.
DEFINITION AR597772
ACCESSION AR597772
VERSION AR597772.1 GI:56648786
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwigen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6818447-A 1714 16-NOV-2004;
Sirma Therapeutics, Inc.; Boulder, CO
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned RNA"
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 714 CTCACACACAGAGACCA 730
Db 17 CACAACACAGAGACCA 1
RESULT 366
AR597944/c AR597944 17 bp RNA linear PAT 15-DEC-2004
LOCUS Sequence 1886 from patent US 6818447.
DEFINITION AR597944
ACCESSION AR597944
VERSION AR597944.1 GI:56648958
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwigen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6818447-A 1886 16-NOV-2004;
Sirma Therapeutics, Inc.; Boulder, CO
FEATURES
Location/Qualifiers

source 1..17
/organism="unknown"
/mol_type="unassigned RNA"
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1505 TTCATCTGGAAACCATCA 1521
Db 17 TTCATCTGGATCCATCA 1
RESULT 367
AX216138 AX216138 17 bp RNA linear PAT 07-SEP-2001
LOCUS Sequence 1580 from Patent WO0159103.
DEFINITION AX216138
ACCESSION AX216138
VERSION AX216138.1 GI:15526181
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., McSwigen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 1580 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwigen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source Location/Qualifiers
1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 545 CCATCGCCGCTGTCTTC 561
Db 1 CCATCCCGCGCTGTCTGC 17
RESULT 368
AX216915 AX216915 17 bp RNA linear PAT 07-SEP-2001
LOCUS Sequence 2357 from Patent WO0159103.
DEFINITION AX216915
ACCESSION AX216915
VERSION AX216915.1 GI:15526976
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., McSwigen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 2357 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwigen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source Location/Qualifiers
1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Qy 1003 CACATCTTCTCTCCT 1019
Db 17 CTCTCTTCTCTCCT 1

RESULT 369
LOCUS AX216921 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 2363 from Patent WO0159103.
ACCESSION AX216921
VERSION AX216921.1 GI:15526982
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 Blact, L., Mcawigen, J. and Chowitra, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
PATENT: WO 0159103-A 2363 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blact, Lawrence (US) ;
Mcswigen, James (US) ; Chowitra, Bharat M. (US)
FEATURES
source location/Qualifiers
1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1306 GAGGAGAGCCAGAGA 1322
Db 1 GAGGAGAGAGAGAGA 17

RESULT 370
LOCUS AX226878 17 bp RNA linear PAT 10-SEP-2001
DEFINITION Sequence 250 from Patent WO0157206.
ACCESSION AX226878
VERSION AX226878.1 GI:15556019
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Fattaey, A.R., Jarvis, T., Mcswigen, J., Bocher, R.N. and Holman, P.S.
TITLE Method and reagent for the inhibition of checkpoint kinase-1 (chk
1) enzyme
PATENT: WO 0157206-A 250 09-AUG-2001;
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
FEATURES
source location/Qualifiers
1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1369 TCTTCAGAGAGTGCATC 1385
Db 17 TCTTCAGAGAGTGTCTC 1

RESULT 371
LOCUS AX475125 17 bp DNA linear PAT 12-AUG-2002

DEFINITION Sequence 346 from Patent WO0224750.
ACCESSION AX475125
VERSION AX475125.1 GI:22214410
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Zhang, J.
TITLE Human kidney tumor overexpressed membrane protein 1
JOURNAL Patent: WO 0224750-A 346 28-MAR-2002;
Aeomica, Inc. (US)
FEATURES
source location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1402 AGCTTCAGCTTCTCTC 1418
Db 1 AGCTTCAGTTCCTCTC 17

RESULT 372
LOCUS AX502961 17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 4268 from Patent EP1229046.
ACCESSION AX502961
VERSION AX502961.1 GI:2385254
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Zhan, J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 4268 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
source location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1089 GGCCATGAGCTCCACCA 1105
Db 17 GGCCATGAGCTGCCCA 1

RESULT 373
LOCUS AX531944 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1453 from Patent EP1239051.
ACCESSION AX531944
VERSION AX531944.1 GI:25255658
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1453 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1444 CCTTGGCAGGTGCAGC 1460
Db 17 CCTTTGCAGGTCCAGC 1
RESULT 374
AX673572 17 bp DNA linear PAT 27-MAR-2003
LOCUS Sequence 2017 from Patent WO03004526.
DEFINITION AX673572
ACCESSION AX673572.1 GI:29331920
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Tejeraman,A., Amson,R. and Tuijinder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and their use as
medicines
JOURNAL Patent: WO 03004526-A 2017 16-JAN-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1665 GAGCCTGFAAATAAAA 1681
Db 1 GATCCTTAATAATAAAA 17
RESULT 375
AX674304 17 bp DNA linear PAT 27-MAR-2003
LOCUS Sequence 2749 from Patent WO03004526.
DEFINITION AX674304
ACCESSION AX674304.1 GI:29332652
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Tejeraman,A., Amson,R. and Tuijinder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and their use as
medicines
JOURNAL Patent: WO 03004526-A 2749 16-JAN-2003;
Molecular Engines Laboratories (FR)

FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 806 GTGTGACTGTGCTGATC 822
Db 17 GTGTGCTGTGTCAGATC 1
RESULT 376
AX688110 17 bp DNA linear PAT 31-MAR-2003
LOCUS Sequence 842 from Patent EP1281758.
DEFINITION AX688110
ACCESSION AX688110.1 GI:29410808
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
JOURNAL Patent: EP 1281758-A 842 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 429 CCTGACCTTCGCGGAGG 445
Db 1 CCTGACCTTCCTCGAGG 17
RESULT 377
AX692036 17 bp DNA linear PAT 31-MAR-2003
LOCUS Sequence 4768 from Patent EP1281758.
DEFINITION AX692036
ACCESSION AX692036.1 GI:29414980
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
JOURNAL Patent: EP 1281758-A 4768 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.8%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 684 TCTCTGCTGCTGCTTCC 700
| | | | |
| | | | |
Db 1 TCTTCTCTGCTGCTTCC 17

RESULT 378
AX722337 17 bp DNA linear PAT 08-MAY-2003
LOCUS Sequence 24 from Patent WO03025176.
DEFINITION AX722337
ACCESSION AX722337
VERSION AX722337.1 GI:30422838
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murineae; Mus.

REFERENCE
AUTHORS Telerman, A., Amson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 24 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source Location/Qualifiers
1.17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 891 GATCCCGGGGACTCTCT 907
| | | | |
| | | | |
Db 1 GATCCCGGGGACTCTCT 17

RESULT 379
AX729053 17 bp DNA linear PAT 08-MAY-2003
LOCUS Sequence 687 from Patent WO03025175.
DEFINITION AX729053
ACCESSION AX729053
VERSION AX729053.1 GI:30508396
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
AUTHORS Telerman, A., Amson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 687 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source Location/Qualifiers
1.17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 788 AGAAGTGATCCAGATC 804
| | | | |
| | | | |

Db 17 AGAAGTGATCCAGATC 1

RESULT 380
AX730414 17 bp DNA linear PAT 08-MAY-2003
LOCUS Sequence 2048 from Patent WO03025175.
DEFINITION AX730414
ACCESSION AX730414
VERSION AX730414.1 GI:30509757
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
AUTHORS Telerman, A., Amson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 2048 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source Location/Qualifiers
1.17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 806 GTGTGACTGTGCTGATC 822
| | | | |
| | | | |
Db 17 GTGTGACTGTGCTGATC 1

RESULT 381
AX738266 17 bp DNA linear PAT 08-MAY-2003
LOCUS Sequence 3856 from Patent WO03025177.
DEFINITION AX738266
ACCESSION AX738266
VERSION AX738266.1 GI:30517554
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
AUTHORS Telerman, A., Amson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 3856 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source Location/Qualifiers
1.17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 806 GTGTGACTGTGCTGATC 822
| | | | |
| | | | |
Db 17 GTGTGACTGTGCTGATC 1

RESULT 382
AX744431

LOCUS AX744431 17 bp DNA linear PAT 14-MAY-2003
DEFINITION Sequence 396 from Patent WO03031621.
ACCESSION AX744431
VERSION AX744431.1 GI:30723098
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
AUTHORS Zhang, J.
TITLE A human G protein coupled receptor
JOURNAL Patent: WO 03031621-A 396 17-APR-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source 1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1536 CTGGACTTGCAGAAAG 1552
Db 1 CTGGACTGCGCAATAG 17

RESULT 383
LOCUS AX744432 17 bp DNA linear PAT 14-MAY-2003
DEFINITION Sequence 397 from Patent WO03031621.
ACCESSION AX744432
VERSION AX744432.1 GI:30723099
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
AUTHORS Zhang, J.
TITLE A human G protein coupled receptor
JOURNAL Patent: WO 03031621-A 397 17-APR-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source 1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1537 TGGGACTTGCAGAAAG 1553
Db 1 TGGGACTGCGCAATAG 17

RESULT 384
LOCUS AX745037 17 bp DNA linear PAT 14-MAY-2003
DEFINITION Sequence 1002 from Patent WO03031621.
ACCESSION AX745037
VERSION AX745037.1 GI:30723704
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE
AUTHORS Zhang, J.
TITLE A human G protein coupled receptor
JOURNAL Patent: WO 03031621-A 1002 17-APR-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source 1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 455 CTGCATTCAATACATG 471
Db 1 CTGCATTCAATACATG 17

RESULT 385
LOCUS AX760000 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 3321 from Patent WO03040369.
ACCESSION AX760000
VERSION AX760000.1 GI:32254616
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
AUTHORS Telerman, A., Anson, R. and Tuijinder, M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 3321 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 375 GATCATCTTAGCCACA 391
Db 1 GATCATCAAGCCACA 17

RESULT 386
LOCUS AX782045 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 376 from Patent WO03050284.
ACCESSION AX782045
VERSION AX782045.1 GI:32949894
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
AUTHORS Guo, J.
TITLE Human prostate cancer candidate protein 1
JOURNAL Patent: WO 03050284-A 376 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
Location/Qualifiers

source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 786 TGAGAAAGTGTACACACA 802
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1 TGAGAAAGTGTCCACA 17

RESULT 387
AX783524 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 1855 from Patent WO03050284.
ACCESSION AX783524
VERSION AX783524.1 GI:32951373
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS Guo,J.
TITLE Human prostate cancer candidate protein 1
JOURNML Patent: WO 03050284-A 1855 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
LOCATION/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 987 CTGCTGCTGCTGCTTCC 1003
|||||
1 CTGCTGCTGCTCTCTCC 17

RESULT 388
AX783713 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 2044 from Patent WO03050284.
ACCESSION AX783713
VERSION AX783713.1 GI:32951562
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS Guo,J.
TITLE Human prostate cancer candidate protein 1
JOURNML Patent: WO 03050284-A 2044 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
LOCATION/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 255 CTCACATACACCTCCG 271
|||||
Db 17 CTCCTCTACACACCG 1

RESULT 389
AR109816/c 23 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 240 from patent US 6114139.
ACCESSION AR109816
VERSION AR109816.1 GI:12826092
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 23)
AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukushima,S. and Ohgi,K.
TITLE G-protein coupled receptor protein and a DNA encoding the receptor
JOURNML Patent: US 6114139-A 240 05-SEP-2000;
FEATURES
LOCATION/Qualifiers
1..23
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 13.6; DB 1; Length 23;
Best Local Similarity 80.0%; Pred. No. 4.5e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1307 AGGAGAGCCAGAGACGCG 1326
|||||
Db 23 AGGGGAGCCAGCAGACGCG 4

RESULT 390
A09447/c 15 bp DNA linear PAT 09-NOV-1993
DEFINITION Oligonucleotide (es).
ACCESSION A09447
VERSION A09447.1 GI:490550
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS Ueda,I., Niwa,M., Satoh,Y., Satoh,S. and Yamada,H.
TITLE Process for production of somatostatin
JOURNML Patent: EP 019758-A 53 15-OCT-1986;
FUJISAWA PHARMACEUTICAL CO., LTD
FEATURES
LOCATION/Qualifiers
1..15
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 759 ATGGCCAGAGCATCC 773
|||||
Db 15 ATGACGAGAGCATCC 1

RESULT 391
A10650/c 15 bp DNA linear PAT 02-DEC-1993
DEFINITION Oligonucleotide (es).
ACCESSION A10650
VERSION A10650.1 GI:490776
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE	1 (bases 1 to 15)			
AUTHORS	Ueda,I., Niwa,M., Saito,Y., Sato,S., Ono,H. and Kitaguchi,T.			
TITLE	Process for production of gamma-interferon			
JOURNAL	Patent: EP 0176916-A 35 09-APR-1986;			
FEATURES	FUJISAWA PHARMACEUTICAL CO., LTD			
SOURCE	location/Qualifiers			
	1..15			
	/organism="synthetic construct"			
	/mol_type="unassigned DNA"			
	/db_xref="taxon:32630"			
Query Match	0.8%;	Score 13.4;	DB 1;	Length 15;
Best Local Similarity	93.3%;	Pred. No.2.2e+02;		
Matches	14;	Conservative	0;	Mismatches 1;
				Indels 0;
				Gaps 0;
OY	759	ATGGCCAGAGCATCC	773	
	11			
	15	ATGACCGAGCATCC	1	
RESULT 392				
A11598/c				
LOCUS	A11598	15 bp	DNA	linear
DEFINITION	oligonucleotide 'es'.			
ACCESSION	A11598			
VERSION	A11598.1	GI:491138		
KEYWORDS	.			
SOURCE	synthetic construct			
ORGANISM	synthetic construct			
REFERENCE	other sequences; artificial sequences.			
AUTHORS	1 (bases 1 to 15)			
TITLE	Ueda,I., Niwa,M., Saito,Y., Sato,S., Ono,H. and Kitaguchi,T.			
JOURNAL	59 Valine insulin-like growth factor I and process for production thereof			
FEATURES	Patent: EP 0158992-A 94 23-OCT-1985;			
SOURCE	FUJISAWA PHARMACEUTICAL CO., LTD			
	1..15	location/Qualifiers		
	/organism="synthetic construct"			
	/mol_type="unassigned DNA"			
	/db_xref="taxon:32630"			
Query Match	0.8%;	Score 13.4;	DB 1;	Length 15;
Best Local Similarity	93.3%;	Pred. No.2.2e+02;		
Matches	14;	Conservative	0;	Mismatches 1;
				Indels 0;
				Gaps 0;
OY	759	ATGGCCAGAGCATCC	773	
	11			
	15	ATGACCGAGCATCC	1	
RESULT 393				
A35118/c				
LOCUS	A35118	15 bp	DNA	linear
DEFINITION	Synthetic IGF-I gene oligo.			
ACCESSION	A35118			
VERSION	A35118.1	GI:1926777		
KEYWORDS	.			
SOURCE	synthetic construct			
ORGANISM	synthetic construct			
REFERENCE	other sequences; artificial sequences.			
AUTHORS	1 (bases 1 to 15)			
TITLE	Ueda,I., Niwa,M., Saito,S., Saitoh,Y. and Kusunoki,C.			
JOURNAL	Process for production of insulin-like growth factor I and plasmid for production thereof			
FEATURES	Patent: EP 0219814-A 68 29-APR-1987;			
SOURCE	FUJISAWA PHARMACEUTICAL CO., LTD			
	1..15	location/Qualifiers		
	/organism="synthetic construct"			
	/mol_type="unassigned DNA"			
	/db_xref="taxon:32630"			

Query Match	0.8%	Score 13.4	DB 1	Length 15
Best Local Similarity	93.3%	Pred. No. 2.2e+02		
Matches	14	Conservative 0	Mismatches 1	Indels 0
Qy	759	ATGCCAGAGCATCC	773	
Db	15	ATGCACAGAGCATCC	1	
RESULT 394				
LOCUS	AR133675	15 bp	DNA	linear
DEFINITION	Sequence 2100 from patent US 6194150.			PAT 16-MAY-2001
ACCESSION	AR133675			
VERSION	AR133675.1	GI:14122580		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 15)			
AUTHORS	Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.			
TITLE	Nucleic acid based inhibition of CD40			
JOURNAL	Patent: US 6194150-A 2100 27-FEB-2001;			
FEATURES	Location/Qualifiers			
source	1..15			
	/organism="unknown"			
	/mol_type="unassigned DNA"			
Query Match	0.8%	Score 13.4	DB 1	Length 15
Best Local Similarity	93.3%	Pred. No. 2.2e+02		
Matches	14	Conservative 0	Mismatches 1	Indels 0
Qy	1409	GCTTCTCCTCCATG	1423	
Db	1	GCTTCTCCTCCATG	15	
RESULT 395				
LOCUS	AR133676	15 bp	DNA	linear
DEFINITION	Sequence 2101 from patent US 6194150.			PAT 16-MAY-2001
ACCESSION	AR133676			
VERSION	AR133676.1	GI:14122581		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 15)			
AUTHORS	Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.			
TITLE	Nucleic acid based inhibition of CD40			
JOURNAL	Patent: US 6194150-A 2101 27-FEB-2001;			
FEATURES	Location/Qualifiers			
source	1..15			
	/organism="unknown"			
	/mol_type="unassigned DNA"			
Query Match	0.8%	Score 13.4	DB 1	Length 15
Best Local Similarity	93.3%	Pred. No. 2.2e+02		
Matches	14	Conservative 0	Mismatches 1	Indels 0
Qy	1411	TTCTCTTCATGTG	1425	
Db	1	TTCTCTTCATGTG	15	
RESULT 396				
LOCUS	DD184741	15 bp	DNA	linear
DEFINITION	Probe sets and methods for identifying HLA-B allele.			PAT 19-JAN-2006
ACCESSION	DD184741.1	GI:85637688		
VERSION	DD184741.1	GI:85637688		
KEYWORDS	JP 2005185172-A/167.			
SOURCE	Homo sapiens (human)			

```

ORGANISM      Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Homiidae; Homo.
REFERENCE      1 (bases 1 to 15)
AUTHORS        Tsukada,M.
TITLE          Probe sets and methods for identifying HLA-B allele
JOURNAL        Patent: JP 2005185172-A 167 14-JUL-2005;
COMMENT        OS Homo sapiens
                PN JP 2005185172-A/167
                PD 14-JUL-2005
                PF 25-DEC-2003 JP 2003430554
                PI mamoru tsukada
                CC
FEATURES       FH Key Location/Qualifiers.
                source      1..15
                        /organism="Homo sapiens"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"
Query Match    0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 132 GAGCCCGAGCGCCA 146
    |||||
Db 1 GAGCCCGAGCGCCA 15

RESULT 397
LOCUS          DD188363 15 bp DNA linear PAT 19-JAN-2006
DEFINITION     Probe set and method for identification of allele of HLA.
ACCESSION      DD188363
VERSION        DD188363.1 GI:85646715
KEYWORDS       WO 2005063985-A/804.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Homiidae; Homo.
REFERENCE      1 (bases 1 to 15)
AUTHORS        Tsukada,M.
TITLE          Probe set and method for identification of allele of HLA
JOURNAL        Patent: WO 2005063985-A 804 14-JUL-2005;
COMMENT        OS Homo sapiens
                PN WO 2005063985-A/804
                PD 14-JUL-2005
                PR 24-DEC-2004 WO 2004JP019763
                PR 25-DEC-2003 JP 03P 430556, 25-DEC-2003 JP 03P 430555, PR
                25-DEC-2003 JP 03P 430558, 25-DEC-2003 JP 03P 430553, PR
                25-DEC-2003 JP 03P 430558, 25-DEC-2003 JP 03P 430557, PR
                25-DEC-2003 JP 03P 430554
                PI mamoru tsukada
                CC
FEATURES       FH Key Location/Qualifiers.
                source      1..15
                        /organism="Homo sapiens"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"
Query Match    0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 132 GAGCCCGAGCGCCA 146
    |||||
Db 1 GAGCCCGAGCGCCA 15

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RESULT 398
LOCUS          BD184657/c 16 bp DNA linear PAT 17-JUN-2003
DEFINITION     Method and detector for identifying subtypes of human papilloma
                viruses.
ACCESSION      BD184657
VERSION        BD184657.1 GI:31876857
KEYWORDS       JP 2002360271-A/636.
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1 (bases 1 to 16)
AUTHORS        Ling,C., Lin,R., Yoo,Z., Huang,X., Lee,B., Lee,S., Lin,Y.,
                Huang,C., Hsu,H., Shi,C., Yeh,C., Gao,Y. and Pan,C.
TITLE          Method and detector for identifying subtypes of human papilloma
JOURNAL        Patent: JP 2002360271-A 636 17-DEC-2002;
                KING CAR FOOD INDUSTRIAL CO LTD
COMMENT        OS Artificial Sequence
                PN JP 2002360271-A/636
                PD 17-DEC-2002
                PF 28-NOV-2001 JP 2001362595
                PR 04-MAY-2001 TW 90110785
                PI CHING-YEE LING, RUBY-WEN LIN, ZHOU-MENG YOO, XIN-HSUAN HUANG, BO-
                PI HAENG LEE,
                PI SHENG-HSIUNG LEE, YI-JU LIN, CI-CHUNG HUANG, HAN-CHANG HSU, CHA-
                PI MEN SHI,
                PI CHIH-XIN YEH, YI-FENG CAO, CHIH-LONG PAN
                PC C12N15/09, C12N15/09, C12M1/34, C12Q1/04, C12Q1/42, C12Q1/68 PC
                C12Q1/70, G01N21/64,
                PC G01N33/53, G01N33/574, G01N33/58, G01N37/00// (C12M1/34, C12R1:93),
                PC (C12Q1/70, C12R1:93), C12N15/00, C12N15/00
                CC Oligonucleotide MW711 for identifying HPV MW7. FH Key
                Location/Qualifiers
                FT source      1..16
                        /organism='Artificial Sequence'.
FEATURES       FH Key Location/Qualifiers.
                source      1..16
                        /organism="synthetic construct"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:326310"
Query Match    0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 601 TACATGGCATCATTA 615
    |||||
Db 16 TACATGGCATCATTA 2

RESULT 399
LOCUS          AX742804/c 16 bp DNA linear PAT 12-MAY-2003
DEFINITION     Sequence 607 from Patent EP1302550.
ACCESSION      AX742804
VERSION        AX742804.1 GI:30576793
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Lin,C.Y., Lin,R.W., You,C.M., Huang,H.H., Lee,B.H., Lee,H.H.,
                Lin,Y.J., Fan,C.C., Hsu,H.C., Shih,C.W., Yeh,C.H., Kao,Y.F.,
                Pan,C.L. and Chan,P.
TITLE          Method and detector for identifying subtypes of human papilloma
JOURNAL        Patent: EP 1302550-A 607 16-APR-2003;
                King Car Food Industrial Co., Ltd. (TW)
COMMENT        OS Artificial Sequence
                PN King Car Food Industrial Co., Ltd. (TW)
                PD 16-APR-2003
                PF 16-APR-2003
                PI King Car Food Industrial Co., Ltd. (TW)
                CC
FEATURES       FH Key Location/Qualifiers.
                source      1..16
                        /organism="synthetic construct"
                        /mol_type="genomic DNA"

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/db_xref="taxon:32630"
/note="Oligonucleotide for Identifying HPV MM7"

Query Match 0.7%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 601 TACATGCCATCATTA 615
|||||
16 TACAGGCCATCATTA 2

Db

RESULT 400

A35619 15 bp DNA linear PAT 02-DEC-1996
LOCUS Synthetic human IFN-alpha 2 gene oligo.
ACCESSION A35619
VERSION A35619.1 GI:1927001
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 15)
AUTHORS Camble,R. and Edge,M.D.
TITLE Analogous interferon polypeptides, process for their preparation
and pharmaceutical compositions containing them
JOURNAL Patent: EP 0194006-A 64 10-SEP-1986;
IMPERIAL CHEMICAL INDUSTRIES PLC
LOCATION/Qualifiers
1. .15
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 278 ATCAGTTCGTGCA 290
|||||
1 ATCAGTTCGTGCA 13

Db

RESULT 401

A35677 15 bp DNA linear PAT 02-DEC-1996
LOCUS Synthetic human IFN-alpha 2 gene oligo.
ACCESSION A35677
VERSION A35677.1 GI:1927059
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 15)
AUTHORS Camble,R. and Edge,M.D.
TITLE Analogous interferon polypeptides, process for their preparation
and pharmaceutical compositions containing them
JOURNAL Patent: EP 0194006-A 122 10-SEP-1986;
IMPERIAL CHEMICAL INDUSTRIES PLC
LOCATION/Qualifiers
1. .15
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 278 ATCAGTTCGTGCA 290
|||||
1 ATCAGTTCGTGCA 13

Db

RESULT 402

AR037371 15 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 16 from patent US 5801156.
DEFINITION AR037371
ACCESSION AR037371
VERSION AR037371.1 GI:5955227
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Robinson,G.S. and Smith,L.Elaine.Hodgson.
TITLE Inhibition of neovascularization using VEGF-specific
oligonucleotides
JOURNAL Patent: US 5801156-A 16 01-SEP-1998;
FEATURES
1. .15
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1011 CTTCTCTCTGCC 1023
|||||
1 CTTCTCTCTGCC 13

Db

RESULT 403

AR043852 15 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 16 from patent US 5814620.
DEFINITION AR043852
ACCESSION AR043852
VERSION AR043852.1 GI:5964860
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Robinson,G.S. and Smith,L.Elaine.Hodgson.
TITLE Inhibition of neovascularization using vegf-specific
oligonucleotides
JOURNAL Patent: US 5814620-A 16 29-SEP-1998;
FEATURES
1. .15
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1011 CTTCTCTCTGCC 1023
|||||
1 CTTCTCTCTGCC 13

Db

RESULT 404

CO848325 15 bp DNA linear PAT 19-AUG-2004
LOCUS Sequence 16 from Patent EP143110.
DEFINITION CO848325
ACCESSION CO848325
VERSION CO848325.1 GI:51469826
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Robinson,G.S.
TITLE Human VEGF-specific antisense oligonucleotides
JOURNAL Patent: EP 143110-A 16 04-AUG-2004;

HYBRIDON, INC. (US)
Location/Qualifiers

FEATURES
source
1. .15
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: Synthetic oligonucleotide"

Query Match
0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1011 CTTCCTCTGCCC 1023
Db 1 CTTCCTCTGCCC 13

RESULT 405
LOCUS 147003 15 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 16 from patent US 5639736.
ACCESSION 147003
VERSION 147003.1 GI:2470968
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Robinson,G.S.
TITLE Human VEGF-specific oligonucleotides
JOURNAL Patent: US 5639736-A 16 17-JUN-1997;
FEATURES Location/Qualifiers
source
1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1011 CTTCCTCTGCCC 1023
Db 1 CTTCCTCTGCCC 13

RESULT 406
LOCUS 147651 15 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 16 from patent US 5639872.
ACCESSION 147651
VERSION 147651.1 GI:2471616
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Robinson,G.S.
TITLE Human VEGF-specific oligonucleotides
JOURNAL Patent: US 5639872-A 16 17-JUN-1997;
FEATURES Location/Qualifiers
source
1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1011 CTTCCTCTGCCC 1023
Db 1 CTTCCTCTGCCC 13

RESULT 407
LOCUS 163152 15 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 16 from patent US 5661135.
ACCESSION 163152
VERSION 163152.1 GI:2480860
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Robinson,G.S.
TITLE Human VEGF-specific oligonucleotides
JOURNAL Patent: US 5661135-A 16 26-AUG-1997;
FEATURES Location/Qualifiers
source
1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1011 CTTCCTCTGCCC 1023
Db 1 CTTCCTCTGCCC 13

RESULT 408
LOCUS 181409 15 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 16 from patent US 5710136.
ACCESSION 181409
VERSION 181409.1 GI:3209706
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Robinson,G.S. and Smith,L.Elaine,Hodgson.
TITLE Inhibition of neovascularization using VEGF-specific oligonucleotides
JOURNAL Patent: US 5710136-A 16 20-JAN-1998;
FEATURES Location/Qualifiers
source
1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1011 CTTCCTCTGCCC 1023
Db 1 CTTCCTCTGCCC 13

RESULT 409
LOCUS 193800 15 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 16 from patent US 5731294.
ACCESSION 193800
VERSION 193800.1 GI:3938270
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Robinson,G.S. and Hodgson Smith,L.Elaine.
TITLE Inhibition of neovascularization using VEGF-specific oligonucleotides
JOURNAL Patent: US 5731294-A 16 24-MAR-1998;

FEATURES
source
Location/Qualifiers
1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1011 CTTCTCTCTGCC 1023
1 CTTCTCTCTGCC 13

Db

RESULT 410
LOCUS CQ881957 16 bp DNA linear PAT 11-OCT-2004
DEFINITION Sequence 9 from Patent WO2004083441.
ACCESSION CQ881957
VERSION CQ881957.1 GI:54034727
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.

REFERENCE
1 Kleinschmidt J., Mueller O., Trepel M., Kaul F. and Leder C.
Random peptide library displayed on aav vectors
Patent: WO 2004083441-A 9 30-SEP-2004;
Deutsches Krebsforschungszentrum Stiftung des oeffentlichen n Rechts
(DB); Albert-Ludwigs-Universitaet Freiburg (DE)
Location/Qualifiers
1..16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Second strand primer"

FEATURES
source

Query Match 0.7%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1261 GTCAGCCGCTGG 1273
4 GTCAGCCGCTGG 16

Db

RESULT 411
LOCUS CQ800306 30 bp DNA linear PAT 28-APR-2004
DEFINITION Sequence 5 from Patent WO2004030695.
ACCESSION CQ800306
VERSION CQ800306.1 GI:46849172
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE
1 Gibbins J.M., Lowry P.J., Graham G.J. and Page N.M.
Treatment of vascular diseases
Patent: WO 2004030695-A 5 15-APR-2004;
University of Reading (GB)
Location/Qualifiers
1..30
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

FEATURES
source

Query Match 0.7%; Score 13; DB 1; Length 30;
Best Local Similarity 65.5%; Pred. No. 5.9e+02;
Matches 19; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 11 CACCGCGGCAAGCGGAGTGATCCAG 39

Db
1 CCCTGGGGAAGGCCAGAGAGGCCAG 29

RESULT 412
LOCUS AR131573 16 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 66 from patent US 6194149.
ACCESSION AR131573
VERSION AR131573.1 GI:14120476
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.

REFERENCE
1 (bases 1 to 16)
Neri B., Dong F., Lyamichev V., Brow M., Ann D. and Fors L.
Target-dependent reactions using structure-bridging
oligonucleotides
Patent: US 6194149-A 66 27-FEB-2001;
Location/Qualifiers
1..16
/organism="unknown"
/mol_type="unassigned DNA"

FEATURES
source

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1436 CCACAGGCGCTTTGGC 1451
16 CCACAGGCGCTTTGGC 1

Db

RESULT 413
LOCUS AX927925 16 bp DNA linear PAT 19-DEC-2003
DEFINITION Sequence 11 from Patent WO03085110.
ACCESSION AX927925
VERSION AX927925.1 GI:40250727
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE
1 Thue C.A., h G.A.M. and Kristjansen P.E.
Oligomeric compounds for the modulation hif-1alpha expression
Patent: WO 03085110-A 11 16-OCT-2003;
Cureon A/S (DK)
Location/Qualifiers
1..16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence:antisense
oligonucleotide to human HIF-1a"

FEATURES
source

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 73 CAAAAGAGTGCTGCC 88
1 CAAAAGAGTGCTGCC 16

Db

RESULT 414
LOCUS BD084991/c 16 bp DNA linear PAT 27-AUG-2002
DEFINITION Target-dependent reactions using structure-bridging
oligonucleotides.
ACCESSION BD084991
VERSION BD084991.1 GI:22630601
KEYWORDS JP 2001523111-A/66.

SOURCE unidentified
ORGANISM unidentified
REFERENCE unclassified sequences.
AUTHORS 1 (bases 1 to 16)
TITLE Target-dependent reactions using structure-bridging oligonucleotides
JOURNAL Patent: JP 2001523111-A 66 20-NOV-2001;
THIRD WAVE TECHNOLOGIES INC
COMMENT OS Unidentified
PN JP 2001523111-A/66
PD 20-NOV-2001
PF 05-MAY-1998 JP 1998548047
PR 05-MAY-1997 US 08/851588, 19-SEP-1997 US 08/934097 PR
03-MAR-1998 US 09/034205
PI FANG DONG, VICTOR I LYMICHEV, JAMES R PRUDENT, LANCE FORS, BRUCE
PI P NERI,
PI MARY ANN D BROW, TODD A ANDERSON, JAMES E DAHLBERG PC
C07H21/04, C07H21/02, C12Q1/68
CC Strandedness: Single;
CC Topology: Linear;
CC /desc = 'DNA'
FH Key Location/Qualifiers
FT source 1..16 Location/Qualifiers
FEATURES
source 1..16 Location/Qualifiers
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1436 CCACAGGGCTTTGGC 1451
DB 16 CCACAGGGCTTTGGC 1

RESULT 415
BD104692
LOCUS BD104692 16 bp DNA linear PAT 27-AUG-2002
DEFINITION Kit and method for determining HLA type.
ACCESSION BD104692.1 GI:22650266
VERSION WO 0192572-A/796.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 16)
AUTHORS Inoko, H., Kagiya, T., Ichihara, T., Matsumura, Y., Moriya, S. and Nishida, M.
TITLE Kit and method for determining HLA type
JOURNAL Patent: WO 0192572-A 796 06-DEC-2001;
NISHINO INDUSTRIES INC, SYSTEM RESEARCH INC, HIDEOTOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA, SHOGO MORIYA, MICHIO NISHIDA
COMMENT OS Artificial Sequence
PN WO 0192572-A/796
PD 06-DEC-2001
PF 01-JUN-2001 WO 2001JP004662
PR 01-JUN-2000 JP 00P 164798
PI HIDEOTOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA,
PI SHOGO MORIYA, MICHIO NISHIDA
PC C12Q1/68, C12M1/00, C12N15/09, G01N33/53
CC Description of Artificial Sequence: capture
FH Key Location/Qualifiers
FT source 1..16 Location/Qualifiers
FEATURES
source 1..16 Location/Qualifiers
/organism='Artificial Sequence'.

SOURCE 1..16
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 170 GGGGTGTGTACAGAT 185
DB 1 GGGGTGTGTACAGAT 16

RESULT 416
BD104794
LOCUS BD104794 16 bp DNA linear PAT 27-AUG-2002
DEFINITION Kit and method for determining HLA type.
ACCESSION BD104794.1 GI:22650368
VERSION WO 0192572-A/898.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 16)
AUTHORS Inoko, H., Kagiya, T., Ichihara, T., Matsumura, Y., Moriya, S. and Nishida, M.
TITLE Kit and method for determining HLA type
JOURNAL Patent: WO 0192572-A 898 06-DEC-2001;
NISHINO INDUSTRIES INC, SYSTEM RESEARCH INC, HIDEOTOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA, SHOGO MORIYA, MICHIO NISHIDA
COMMENT OS Artificial Sequence
PN WO 0192572-A/898
PD 06-DEC-2001
PF 01-JUN-2001 WO 2001JP004662
PR 01-JUN-2000 JP 00P 164798
PI HIDEOTOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA,
PI SHOGO MORIYA, MICHIO NISHIDA
PC C12Q1/68, C12M1/00, C12N15/09, G01N33/53
CC Description of Artificial Sequence: capture
FH Key Location/Qualifiers
FT source 1..16 Location/Qualifiers
FEATURES
source 1..16 Location/Qualifiers
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 170 GGGGTGTGTACAGAT 185
DB 1 GGGGTGTGTACAGAT 16

RESULT 417
BD106365
LOCUS BD106365 16 bp DNA linear PAT 18-SEP-2002
DEFINITION Novel LDI-receptor.
ACCESSION BD106365.1 GI:23201183
VERSION JP 2002501376-A/380.
KEYWORDS Chlamydia sp.
SOURCE Chlamydia sp.
ORGANISM Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
REFERENCE 1 (bases 1 to 16)
AUTHORS Todd, J.A., Hess, J.W., Caskey, C.T., Cox, R.D., Gerhold, D., Hammond, H. and Hey, P.

TITLE Novel LDL-receptor
JOURNAL Patent: JP 2002501376-A 380 15-JAN-2002;
THE WELLCOME TRUST LTD AS TRUSTEE TO THE WELLCOME TRUST, MERCK & CO
INC
COMMENT JP 2002501376-A/380
PD 15-JAN-2002
PF 15-APR-1998 JP 1998543635
PR 15-APR-1997 US 60/043553, 05-JUN-1997 US 60/048740 PI
JOHN ANDREW TODD, JOHN WILFRED HESS, CHARLES
THOMAS CASKEY, ROGER
PI DAVID COX,
PI DAVID GERHOLD, HOLLY HAMMOND, PATRICIA HEY
PC C12N15/12, C12N15/11, C12Q1/68, C07K14/705, C07K16/28, A61K38/17,
PC A61K39/395,
PC A61K48/00
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers.
FEATURES
source Location/Qualifiers
1. .16
/organism="Chlamydia sp."
/mol_type="genomic DNA"
/db_xref="taxon:35827"
Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3e+02; Mismatches 0; Gaps 0;
Matches 14; Conservative 0; Indels 2; Indels 0; Gaps 0;
OY 13 CCGCGGCGAGCGGCGC 28
DB 1 CCGCGGCGAGCGGCGC 16
RESULT 418
LOCUS BD233314 16 bp DNA linear PAT 17-JUN-2003
DEFINITION Method of detecting mutation selected by drug in HIV protease gene.
ACCESSION BD233314 GI:33043084
VERSION BD233314.1
KEYWORDS JP 2002518065-A/410.
SOURCE Aids-associated retrovirus
ORGANISM Aids-associated retrovirus
Virus; Retro-transcribing viruses; Retroviridae.
REFERENCE 1 (bases 1 to 16)
AUTHORS Stuyver, L.
TITLE Method of detecting mutation selected by drug in HIV protease gene
JOURNAL Patent: JP 2002518065-A 410 25-JUN-2002;
INNOGENETICS NV
COMMENT OS Aids-associated retrovirus
PN JP 2002518065-A/410
PD 25-JUN-2002
PF 22-JUN-1999 JP 2000556068
PR 24-JUN-1998 EP 98870143.9
PI LIEVEN STUYVER
PC C12N15/09, C12Q1/68, C12Q1/70, C12N15/00
CC Method of detecting mutation selected by drug in HIV protease
CC gene
FH Key Location/Qualifiers
FT source 1. .16
/organism="Aids-associated retrovirus".
FEATURES
source Location/Qualifiers
1. .16
/organism="Aids-associated retrovirus"
/mol_type="genomic DNA"
/db_xref="taxon:11966"
Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 14; Conservative 0; Indels 2; Indels 0; Gaps 0;
OY 1586 TGAGTCAAAAATCTC 1601
DB 16 TGAGTCAACAATTC 1

RESULT 419
LOCUS CQ808460/c 16 bp DNA linear PAT 10-MAY-2004
DEFINITION Sequence 1910 from Patent WO2004035803.
ACCESSION CQ808460
VERSION CQ808460.1 GI:47113854
KEYWORDS
SOURCE
ORGANISM synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Roekens, J., Harbeck, N., Koenig, T., Maier, S., Martens, J., Model, F.,
Nimmrich, I., Rujan, T., Schmitt, A., Schmitt, M., Look, M. P. and
Marx, A.
TITLE Method and nucleic acids for the improved treatment of breast cell
proliferative disorders
JOURNAL Patent: WO 2004035803-A 1910 29-APR-2004;
EpiGenomics AG (DE)
FEATURES
source Location/Qualifiers
1. .16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for TGB3"
Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 14; Conservative 0; Indels 2; Indels 0; Gaps 0;
OY 1001 TTCACATCTTCCT 1016
DB 16 TTCACATCTTCATCT 1
RESULT 420
LOCUS CQ828744 16 bp DNA linear PAT 05-JUL-2004
DEFINITION Sequence 462 from Patent WO2004053120.
ACCESSION CQ828744
VERSION CQ828744.1 GI:49732227
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Weihe, E., Bieller, A. and Schaefer, M. K.
TITLE Regulatory elements in the 5' region of the vrl gene
JOURNAL Patent: WO 2004053120-A 462 24-JUN-2004;
Gruententhal GmbH (DE)
FEATURES
source Location/Qualifiers
1. .16
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"
/note="V\$TH1E47 01"
Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 14; Conservative 0; Indels 2; Indels 0; Gaps 0;
OY 1534 CACTGGGACTTGCAA 1549
DB 1 CACTGGGCTGCGCAA 16
RESULT 421
LOCUS CS124427 16 bp DNA linear PAT 21-JUL-2005
DEFINITION Sequence 113 from Patent WO2005059172.

ACCESSION CS124427
VERSION CS124427.1 GI:71057582
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Homo sapiens
TITLE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
JOURNAL
FEATURES
source
Location/Qualifiers
1.16
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 640 GCCACAGCCACCAAG 655
DB 1 GCCACAGCCACCAAG 16

RESULT 422
DD186098
LOCUS DD186098 16 bp DNA linear PAT 19-JAN-2006
DEFINITION Probe sets for detection of HLA-A allele and methods thereof.
ACCESSION DD186098.1 GI:85641213
VERSION JP 2005185176-A/498.
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
AUTHORS 1 (bases 1 to 16)
TITLE Taukada,M.
JOURNAL Probe sets for detection of HLA-A allele and methods thereof
Patent: JP 2005185176-A 498 14-JUL-2005;
Canon Inc

COMMENT
OS artificial sequence
PN JP 2005185176-A/498
PD 14-JUL-2005
PF 25-DEC-2003 JP 2003430558
PI mamoru tsukada
CC probe for detection
FH Key Location/Qualifiers
1.16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

FEATURES
source
Location/Qualifiers
1.16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1299 GGGCCACGAGGAG 1314
DB 1 GGGCCATAGGCGAG 16

RESULT 423
DD188057
LOCUS DD188057 16 bp DNA linear PAT 19-JAN-2006
DEFINITION Probe set and method for identification of allele of HLA.
ACCESSION DD188057
VERSION DD188057.1 GI:85645665
KEYWORDS WO 2005063985-A/498.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Homo sapiens
TITLE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
JOURNAL
FEATURES
source
Location/Qualifiers
1.16
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1299 GGGCCACGAGGAG 1314
DB 1 GGGCCATAGGCGAG 16

RESULT 424
E39143/C
LOCUS E39143 16 bp DNA linear PAT 18-JUN-2001
DEFINITION Improved PCR method for primer elongation pre-amplification.
ACCESSION E39143
VERSION E39143.1 GI:13017705
KEYWORDS JP 1999318498-A/9.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
AUTHORS 1 (bases 1 to 16)
TITLE Unufuganku,D. and Joseph,R.
JOURNAL Improved PCR method for primer elongation pre-amplification
Patent: JP 1999318498-A 9 24-NOV-1999;
ROCHE DIAGNOSTICS GMBH

COMMENT
OS Artificial Sequence
PN JP 1999318498-A/9
PD 24-NOV-1999
PF 26-MAR-1998 JP 1999084967
PI URUFUGANKU DIETOMAIYA,JOSEPH RUSHOFFU
PC C1201/68,C12N15/09,C12N15/00
CC
FH Key Location/Qualifiers
1.16
/organism="Artificial Sequence".
FT source
1.16
/organism="Artificial Sequence".
1.16
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES
source
Location/Qualifiers
1.16
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1061 AGCAGGTCTACTGCG 1076

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 CCGCGGCGAGCGCGGC 28
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 Db 1 CCGCGGCGAGCGTGGGC 16

RESULT 430
 AR328448 16 bp RNA linear PAT 17-AUG-2003
 LOCUS Sequence 5850 from patent US 6566127.
 AR328448
 ACCESSION AR328448.1 GI:33714256
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Unkown.
 Unclassified.

REFERENCE 1 (bases 1 to 16)
 AUTHORS Payco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
 TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
 JOURNAL Patent: US 6566127-A 5850 20-MAY-2003;
 Ribozyme Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO

FEATURES
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 1..16
 /organism="unkown"
 /mol_type="unassigned RNA"

Query Match 0.7%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1594 AAAATCTCAATCTTC 1609
 |||||
 Db 16 AAAATCAAAATCTTC 1

RESULT 431
 AR328461 16 bp RNA linear PAT 17-AUG-2003
 LOCUS Sequence 5863 from patent US 6566127.
 AR328461
 ACCESSION AR328461.1 GI:33714269
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Unkown.
 Unclassified.

REFERENCE 1 (bases 1 to 16)
 AUTHORS Payco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
 TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
 JOURNAL Patent: US 6566127-A 5863 20-MAY-2003;
 Ribozyme Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO

FEATURES
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 /organism="unkown"
 /mol_type="unassigned RNA"

Query Match 0.7%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 389 ACAAAAGATGAGAC 404
 |||||
 Db 1 ACAATGATGAGAC 16

RESULT 432
 AR435791 16 bp RNA linear PAT 18-DEC-2003
 LOCUS Sequence 50 from patent US 6656731.
 AR435791
 ACCESSION AR435791.1 GI:40198875
 VERSION

KEYWORDS
 SOURCE
 ORGANISM
 Unkown.
 Unclassified.

REFERENCE 1 (bases 1 to 16)
 AUTHORS Eckstein, F., Ludwig, J. and Beigelman, L.
 TITLE Nucleic acid catalysts with endonuclease activity
 JOURNAL Patent: US 6656731-A 50 02-DEC-2003;
 Max Planck Gesellschaft zur Forderung der Wissenschaften E.V. and
 Stira Therapeutics; Munich;
 DEX;

FEATURES
 source
 1..16
 /organism="unkown"
 /mol_type="unassigned RNA"

Query Match 0.7%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 527 AGTTCCAACTCTT 542
 |||||
 Db 16 AATTCATACTCTT 1

RESULT 433
 AR488737 16 bp DNA linear PAT 15-MAY-2004
 LOCUS Sequence 66 from patent US 6709815.
 AR488737
 ACCESSION AR488737.1 GI:47254935
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Unkown.
 Unclassified.

REFERENCE 1 (bases 1 to 16)
 AUTHORS Dong, F., Lyamichov, V.I., Prudent, J.R., Fors, L., Neri, B.P.,
 Brow, M.A.D., Anderson, T.A. and Dahlberg, J.E.
 TITLE Target-dependent reactions using structure-bridging
 JOURNAL oligonucleotides
 Patent: US 6709815-A 66 23-MAR-2004;
 Third Wave Technologies, Inc.; Madison, WI

FEATURES
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 1..16
 /organism="unkown"
 /mol_type="genomic DNA"

Query Match 0.7%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1436 CCACAGGCGCTTGGC 1451
 |||||
 Db 16 CCACAGGCGCTTGGC 1

RESULT 434
 AR589824 16 bp DNA linear PAT 15-DEC-2004
 LOCUS Sequence 410 from patent US 6803187.
 AR589824
 ACCESSION AR589824.1 GI:56637132
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Unkown.
 Unclassified.

REFERENCE 1 (bases 1 to 16)
 AUTHORS Stuyver, L.
 TITLE Method for detection of drug-selected mutations in the HIV protease
 JOURNAL gene
 Patent: US 6803187-A 410 12-OCT-2004;
 Innogenetics N.V.; Ghent;
 EPX;

FEATURES
source
Location/Qualifiers
1..16
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 87.5%; Score 12.8; DB 1; Length 16;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db
16 TGAGTCACAAATTC 1

RESULT 435
AX007868/C
LOCUS AX007868 16 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 410 from Patent WO967428.
ACCESSION AX007868
VERSION AX007868.1 GI:9995565
KEYWORDS
SOURCE Aids-associated retrovirus
ORGANISM Aids-associated retrovirus
REFERENCE 1
AUTHORS Stuyver, L.
TITLE Method for detection of drug-selected mutations in the hiv protease gene
JOURNAL Patent: WO 967428-A 410 29-DEC-1999;
INNOGENETICS NV (BE); STUYVER LIEVEN (BE)
LOCATION/Qualifiers
1..16
/organism="Aids-associated retrovirus"
/mol_type="unassigned DNA"
/db_xref="taxon:11966"

Query Match
Best Local Similarity 87.5%; Score 12.8; DB 1; Length 16;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db
16 TGAGTCACAAATTC 1

RESULT 436
AX011286/C
LOCUS AX011286 16 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 9 from Patent EP0957177.
ACCESSION AX011286
VERSION AX011286.1 GI:9997837
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Dietmaier, W.D. and Rueschoff, J.P.
TITLE Improved method for primer extension preamplification-pcr
JOURNAL Patent: EP 0957177-A 9 17-NOV-1999;
ROCHE DIAGNOSTICS GMBH (DE)
LOCATION/Qualifiers
1..16
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 87.5%; Score 12.8; DB 1; Length 16;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db
161 AGCAGGTCTACTGCG 1076

Db
16 ATCAGGTCTACTGTC 1

RESULT 437
AX419729/C
LOCUS AX419729 16 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 66 from Patent WO0198537.
ACCESSION AX419729
VERSION AX419729.1 GI:21524096
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Iyamichev, V., Allawi, H., Dong, F., Neri, B.P. and Vener, I.T.
TITLE Nucleic acid accessible hybridization sites
JOURNAL Patent: WO 0198537-A 66 27-DEC-2001;
THIRD WAVE TECHNOLOGIES, INC. (US)
LOCATION/Qualifiers
1..16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 87.5%; Score 12.8; DB 1; Length 16;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db
16 CCACAGGCGCTTTCG 1

RESULT 438
I17159
LOCUS I17159 20 bp DNA linear PAT 03-APR-1996
DEFINITION Sequence 14 from patent US 548486.
ACCESSION I17159
VERSION I17159.1 GI:1252067
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Fong, T.M. and Strader, C.D.
TITLE Human neurokinin-1 receptor
JOURNAL Patent: US 548486-A 14 16-JAN-1996;
LOCATION/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 78.9%; Score 12.6; DB 1; Length 20;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db
1 CATAGTGTAATCCACTA 19

RESULT 439
AX468711
LOCUS AX468711 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 27 from Patent WO0213799.
ACCESSION AX468711
VERSION AX468711.1 GI:21901481
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
other sequences; artificial sequences.

AUTHORS Henry, J.L., Cahill, C.M. and Yashpal, K.
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway
JOURNAL Patent: WO 0213799-A 27 21-FEB-2002;
McGILL UNIVERSITY (CA)
FEATURES
source
1. 20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 0.7%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 4.7e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 861 CGTAGTGGGATCCACTA 879
Db 1 CATAGTGTGATCCCACTA 19

RESULT 440
AX468730 20 bp DNA linear PAT 16-JUL-2002
LOCUS AX468730
DEFINITION Sequence 46 from Patent WO0213799.
ACCESSION AX468730
VERSION AX468730.1 GI:21901500
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS Henry, J.L., Cahill, C.M. and Yashpal, K.
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway
JOURNAL Patent: WO 0213799-A 46 21-FEB-2002;
McGILL UNIVERSITY (CA)
FEATURES
source
1. 20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 0.7%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 4.7e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 861 CGTAGTGGGATCCACTA 879
Db 20 CATAGTGTGATCCCACTA 2

RESULT 441
A06948 14 bp DNA linear PAT 14-OCT-1993
LOCUS A06948
DEFINITION Nucleotide sequence 6 from patent number EP0246864.
ACCESSION A06948
VERSION A06948.1 GI:489034
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 14)
Car, F.J.
REFERENCE
AUTHORS Hybridisation probes
TITLE Patent: EP 0246864-A 6 25-NOV-1987;
JOURNAL IMPERIAL CHEMICAL INDUSTRIES PLC
FEATURES
source
1. 14
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1752 GCTCATTTCCAGAT 1765
Db 14 GCTCATTTCCAGAT 1

RESULT 442
A89425 14 bp DNA linear PAT 22-JAN-2000
LOCUS A89425
DEFINITION Sequence 1573 from Patent WO9833904.
ACCESSION A89425
VERSION A89425.1 GI:6737995
KEYWORDS
SOURCE
ORGANISM
unidentified
unclassified
unclassified sequences.

REFERENCE
AUTHORS Brysck, W. and Schlingensiepen, K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1573 06-AUG-1998;
BIOGEN IKB (DE); BRYSCHE WOLFGANG (DE)
FEATURES
source
1. 14
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1145 TCCGCTGGGCTTC 1158
Db 1 TCCGCTGGGCTTC 14

RESULT 443
AR027912 14 bp DNA linear PAT 29-SEP-1999
LOCUS AR027912
DEFINITION Sequence 1 from patent US 5858351.
ACCESSION AR027912
VERSION AR027912.1 GI:5939885
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
1 (bases 1 to 14)
Podsakoff, G.M., Kessler, P.D., Byrne, B.J. and Kurtzman, G.J.
REFERENCE
AUTHORS Methods for delivering DNA to muscle cells using recombinant
TITLE adeno-associated virus vectors
JOURNAL Patent: US 5858351-A 1 12-JAN-1999;
FEATURES
source
1. 14
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 315 GGCAGCTGCCTACA 328
Db 1 GGCAGCTGCCTGCA 14

RESULT 444
AR063256 14 bp DNA linear PAT 29-SEP-1999
LOCUS AR063256
DEFINITION Sequence 2 from patent US 5846528.

ACCESSION AR063256
VERSION AR063256.1 GI:5992564
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Podsakoff,G.M., and Kurtzman,G.J.
TITLE Treating anemia using recombinant adeno-associated virus virions
JOURNAL Patent: US 5846528-A 2 08-DEC-1998;
FEATURES
source 1. .14
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 315 GGCAGCTGCCTACA 328
Db 1 GGCAGCTGCCTGCA 14

RESULT 445
LOCUS AR073886 14 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 1 from patent US 5952221.
ACCESSION AR073886
VERSION AR073886.1 GI:10000646
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kurtzman,G.J., Colosi,P.C., Yoshida,J., Mizuno,M. and Okada,H.
TITLE Adeno-associated virus vectors comprising a first and second
nucleic acid sequence
JOURNAL Patent: US 5952221-A 1 14-SEP-1999;
FEATURES
source 1. .14
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 315 GGCAGCTGCCTACA 328
Db 1 GGCAGCTGCCTGCA 14

RESULT 446
LOCUS AR078208 14 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 1 from patent US 5962313.
ACCESSION AR078208
VERSION AR078208.1 GI:10004954
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Podsakoff,G.M., Keesler,P.D., Byrne,B.J. and Kurtzman,G.J.
TITLE Adeno-associated virus vectors comprising a gene encoding a
lysosomal enzyme
JOURNAL Patent: US 5962313-A 1 05-OCT-1999;
FEATURES
source 1. .14
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 315 GGCAGCTGCCTACA 328
Db 1 GGCAGCTGCCTGCA 14

RESULT 447
LOCUS AR095650 14 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 1 from patent US 6004797.
ACCESSION AR095650
VERSION AR095650.1 GI:10023714
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Colosi,P.C.
TITLE Adenovirus helper-free recombinant AAV virion production
JOURNAL Patent: US 6004797-A 1 21-DEC-1999;
FEATURES
source 1. .14
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 315 GGCAGCTGCCTACA 328
Db 1 GGCAGCTGCCTGCA 14

RESULT 448
LOCUS AR118998 14 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 124 from patent US 6150092.
ACCESSION AR118998
VERSION AR118998.1 GI:14100908
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Uchida,K., Uchida,T., Tanaka,Y., Matsuda,Y. and Kondo,S.
TITLE Antisense nucleic acid compound targeted to VEGF
JOURNAL Patent: US 6150092-A 124 21-NOV-2000;
FEATURES
source 1. .14
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 468 AGTGTGAGACTTCA 481
Db 14 AGTGTGAGATTCA 1

RESULT 449
LOCUS AR145148 14 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6211163.
ACCESSION AR145148
VERSION AR145148.1 GI:15107015
KEYWORDS

SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Podsakoff,G.M., Kessler,P.D., Byrne,B.J. and Kurtzman,G.J.
TITLE Methods for delivering DNA to the bloodstream using recombinant adeno-associated virus vectors
JOURNAL Patent: US 6211163-A 1 03-APR-2001;
FEATURES Location/Qualifiers
source 1..14
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 315 GGCAGCTGCCTGCA 328
Db 1 GGCAGCTGCCTGCA 14

RESULT 450
LOCUS ARI48600 14 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 17 from patent US 6225291.
ACCESSION ARI48600
VERSION ARI48600.1 GI:15112690
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Lewin,A.S., Hauswirth,W.W. and Drenser,K.
TITLE Rod opsin mRNA-specific ribozyme compositions and methods for the treatment of retinal diseases
JOURNAL Patent: US 6225291-A 17 01-MAY-2001;
FEATURES Location/Qualifiers
source 1..14
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1375 CGAAGTACTCCAA 1388
Db 14 CGAAGTACTCCGA 1

RESULT 451
LOCUS ARI79014 14 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2 from patent US 6325998.
ACCESSION ARI79014
VERSION ARI79014.1 GI:20220569
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Podsakoff,G.M. and Kurtzman,G.J.
TITLE Methods of treating disease using recombinant adeno-associated virus vitrons administered to muscle
JOURNAL Patent: US 6325998-A 2 04-DEC-2001;
FEATURES Location/Qualifiers
source 1..14
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.5e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 315 GGCAGCTGCCTGCA 328
Db 1 GGCAGCTGCCTGCA 14

RESULT 452
LOCUS AX934402 14 bp DNA linear PAT 05-JAN-2004
DEFINITION Sequence 5 from Patent EPI359223.
ACCESSION AX934402
VERSION AX934402.1 GI:40641665
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Natsoulis,G.
TITLE Recombinant AAV preparation substantially free of wt aav virus
JOURNAL Patent: EP 1359223-A 5 05-NOV-2003;
FEATURES Location/Qualifiers
source 1..14
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 315 GGCAGCTGCCTGCA 328
Db 1 GGCAGCTGCCTGCA 14

RESULT 453
LOCUS BD064896 14 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for detecting the extent of binding of transcriptional regulatory protein to oligodNA.
ACCESSION BD064896
VERSION BD064896.1 GI:22610499
KEYWORDS JP 2001275678-A/108.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 14)
AUTHORS Kishimoto,T., Niwa,S., Mori,Y., Sachiyo, Mimaki, Fukushima,R. and Nishikawa,K.
TITLE Method for detecting the extent of binding of transcriptional regulatory protein to oligodNA
JOURNAL Patent: JP 2001275678-A 108 09-OCT-2001;
COMMENT SUMITOMO ELECTRIC INDUSTRIES LTD
OS Artificial Sequence
PN JP 2001275678-A/108
PD 09-OCT-2001
PF 31-MAR-2000 JP 2000096306
PI TOSHIHIKO KISHIMOTO,SHINICHIRO NIWA,YUKO MORI,SACHIYO PI
MIMAKI,REI FUKUSHIMA,
PI KAZUOKO NISHIKAWA
PC C12N15/09,C12N5/10,C12Q1/00,C12Q1/68,C12N15/00,C12N5/00 CC
SYNTHETIC DNA
FT Key source 1..14
Location/Qualifiers
FT Location/Qualifiers
/organism="Artificial Sequence".
1..14
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1491 GCATGGAATTC 1504
14 GCACGGAATTC 1

Db

RESULT 454
BD066938 14 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066938
VERSION BD066938.1 GI:22612541
KEYWORDS JP 2001511000-A/1573.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1573 07-AUG-2001;
BIOLOGISTIK GEBIELTSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/1573
PD 07-AUG-2001
PR 30-JAN-1998 JP 1998532533
PI 31-JAN-1997 EP 97101531.8
PC KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11.C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
Location/Qualifiers
FT source 1. .14
/organism='Unknown'.
1. .14
Location/Qualifiers
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

FEATURES
source

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1145 TCCGCTGGGCTTC 1158
1 TCCCTCTGGGCTTC 14

Db

RESULT 455
BD082683/c 14 bp RNA linear PAT 27-AUG-2002
LOCUS BD082683
DEFINITION Material and method for ribozyme treatment of disease.
ACCESSION BD082683
VERSION BD082683.1 GI:22628293
KEYWORDS JP 2001523959-A/17.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 14)
AUTHORS Lewin,A.S., Hauswirth,W.W. and Drenser,K.
TITLE Material and method for ribozyme treatment of disease
JOURNAL Patent: JP 2001523959-A 17 27-NOV-2001;
UNIVERSITY OF FLORIDA
OS Artificial Sequence
PN JP 2001523959-A/17
PD 27-NOV-2001
PR 21-APR-1998 JP 1998546254
PI 21-APR-1997 US 60/044492.09-MAY-1997 US 60/046147 PI
ALFRED S LEWIN,WILLIAM W HAUSWIRTH,KIMBERLY DRENSER PC
C12N15/11.C12N9/00,A61K31/70,C12N15/86
CC Description of Artificial Sequence:SYNTHETIC OLIGONUCLEOTIDE

FEATURES FH Key Location/Qualifiers.
source

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1375 CGAAGTACTCCAA 1388
14 CGAAGTACTCCGA 1

Db

RESULT 456
BD209328 14 bp RNA linear PAT 17-JUL-2003
LOCUS BD209328
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.
ACCESSION BD209328
VERSION BD209328.1 GI:33019098
KEYWORDS JP 2002512791-A/2918.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Blatt,L., Mcsviggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection
JOURNAL Patent: JP 2002512791-A 2918 08-MAY-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/2918
PD 08-MAY-2002
PR 26-APR-1999 JP 2000545991
PI 27-APR-1998 US 60/083217.18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608.23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI
PAVCO,
PI DENNIS MACEJAK
PC C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC A61K37/66,
PC C12N15/00
CC Enzymatic nucleic acid treatment of diseases or conditions CC
related to
CC hepatitis C virus infection.
FH Key Location/Qualifiers
FT source 1. .14
/organism='Hepatitis virus (hepatitis C virus)'.
1. .14
Location/Qualifiers
/organism='unidentified'
/mol_type='genomic RNA'
/db_xref='taxon:32644'

FEATURES
source

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 685 CTCCTGCTGGCCTT 698
1 CTCCTGCTGGCCTT 14

Db

RESULT 457
BD235049 14 bp DNA linear PAT 17-JUL-2003
LOCUS BD235049
DEFINITION A method for stimulating the immune system.
ACCESSION BD235049
VERSION BD235049.1 GI:33044819

KEYWORDS JP 2002517434-A/153.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingsensiepen, K.H., Schlingsensiepen, R. and Brysch, W.
TITLE A method for stimulating the immune system
JOURNAL Patent: JP 2002517434-A 153 18-JUN-2002;
BIOGOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Homo sapiens (human)
PN JP 2002517434-A/153
PD 18-JUN-2002
PF 10-JUN-1998 JP 2000553044
PR 10-JUN-1998 EP 98110709.7, 25-JUL-1998 EP 98113974.4 PI
KARL HERMANN SCHLINGSENSIEPEN, REIMAR SCHLINGSENSIEPEN, WOLFGANG PI
BRYSCH
PC A61K45/06, A61K31/7088, A61K38/00, A61K39/395, A61K39/395, A61P31/
PC 00, A61P35/00
PC A61P35/02, A61P37/02, C12N15/09, A61K37/02, C12N15/00 CC A
method for stimulating the immune system
FH Key Location/Qualifiers
FT source 1..14
FT Location/Qualifiers
source 1..14
/organism="Homo sapiens (human)".
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1008 CTCTCTCTCTCTGC 1021
Db 1 CTCCTCTCTCTGC 14

RESULT 458
LOCUS CS062891 14 bp DNA linear PAT 19-APR-2005
DEFINITION Sequence 1 from Patent EP1522588.
ACCESSION CS062891
VERSION CS062891.1 GI:62750877
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Colosi, P.C.
TITLE Accessory functions for use in recombinant AAV virion production
JOURNAL Patent: EP 1522588-A 1 13-APR-2005;
Avigen, Inc. (US)
FEATURES Location/Qualifiers
source 1..14
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 315 GGCAGCTGCTTACA 328
Db 1 GGCAGCTGCTTACA 14

RESULT 459
LOCUS CS123773 14 bp DNA linear PAT 16-JUL-2005

DEFINITION Sequence 124 from Patent WO2005059133.
ACCESSION CS123773
VERSION CS123773.1 GI:70912266
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Schlingsensiepen, K.H.
TITLE Combination therapy associating a tgf-beta antagonist with a
chemotherapeutic agent
JOURNAL Patent: WO 2005059133-A 124 30-JUN-2005;
Antisense Pharma GmbH (DE)
FEATURES Location/Qualifiers
source 1..14
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Description of Artificial Sequence: human VEGF
antisense oligonucleotide"

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1008 CTCTCTCTCTGC 1021
Db 1 CTCCTCTCTCTGC 14

RESULT 460
LOCUS AR181054 14 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1 from patent US 6335011.
ACCESSION AR181054
VERSION AR181054.1 GI:20223268
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1
AUTHORS Podaskoff, G.M., Kessler, P.D., Byrne, B.J. and Kurtzman, G.J.
TITLE Methods for delivering DNA to muscle cells using recombinant
adenovirus-associated virus virions to treat lysosomal storage disease
JOURNAL Patent: US 6335011-A 1 01-JAN-2002;
FEATURES Location/Qualifiers
source 1..14
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 315 GGCAGCTGCTTACA 328
Db 1 GGCAGCTGCTTACA 14

RESULT 461
LOCUS AR255917 14 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 1 from patent US 6482633.
ACCESSION AR255917
VERSION AR255917.1 GI:27305176
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Colosi, P.C.
TITLE Accessory functions for use in recombinant AAV virion production
JOURNAL Patent: US 6482633-A 1 19-NOV-2002;

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FEATURES
  source
    Avigen, Inc.; Alameda, CA
    Location/Qualifiers
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      /organism="unknown"
      /mol_type="genomic DNA"

Query Match
  0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY
  315 GGCAGCTGCCTACA 328
  1 GGCAGCTGCCTGCA 14

RESULT 462
LOCUS AR381782 14 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6610290.
ACCESSION AR381782
VERSION AR381782.1 GI:4009043
KEYWORDS
  .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
  1 (bases 1 to 14)
  Podsakoff,G.M., Kessler,P.D., Byrne,B.J. and Kurtzman,G.J.
  Adeno associated virus vectors for the treatment of a
  cardiomyopathy
  Patent: US 6610290-A 1 26-AUG-2003;
JOURNAL Avigen, Inc. and Johns Hopkins University; Alameda, CA

FEATURES
  source
    1..14
    /organism="unknown"
    /mol_type="genomic DNA"

Query Match
  0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY
  315 GGCAGCTGCCTACA 328
  1 GGCAGCTGCCTGCA 14

Db

RESULT 463
LOCUS AR407913 14 bp RNA linear PAT 18-DEC-2003
DEFINITION Sequence 6 from patent US 6632057.
ACCESSION AR407913
VERSION AR407913.1 GI:40157900
KEYWORDS
  .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
  1 (bases 1 to 14)
  Fauchet,C.R.J.
  Fixing unit with an end imprint in a threaded terminal portion
  Patent: US 6632057-A 6 14-OCT-2003;
JOURNAL GFI Aerospace; Paris;

FEATURES
  source
    Location/Qualifiers
      1..14
      /organism="unknown"
      /mol_type="unassigned RNA"

Query Match
  0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY
  689 TGCTGCGCTTCCCC 702
  1 TGCTGCTTCCCC 14

Db
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RESULT 464
LOCUS AR658576 14 bp DNA linear PAT 13-JUN-2005
DEFINITION Sequence 1 from patent US 6697063.
ACCESSION AR658576
VERSION AR658576.1 GI:67593355
KEYWORDS
  .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
  1 (bases 1 to 14)
  Colosi,P.C.
  Accessory functions for use in recombinant AAV virion production
  Patent: US 6897063-A 1 24-MAY-2005;
JOURNAL Avigen, Inc.; Alameda, CA

FEATURES
  source
    Location/Qualifiers
      1..14
      /organism="unknown"
      /mol_type="genomic DNA"

Query Match
  0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY
  315 GGCAGCTGCCTACA 328
  1 GGCAGCTGCCTGCA 14

Db

RESULT 465
LOCUS AR775644 14 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 1573 from patent US 6972171.
ACCESSION AR775644
VERSION AR775644.1 GI:83352908
KEYWORDS
  .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
  1 (bases 1 to 14)
  Schlengersiepen,K.-H. and Brysch,W.
  Antisense oligonucleotide preparation method
  Patent: US 6972171-A 1573 06-DEC-2005;
JOURNAL Diagnostik Ges. fur Biomolekulare Diagnostik mbH; Gottingen;
EPX;

FEATURES
  source
    Location/Qualifiers
      1..14
      /organism="unknown"
      /mol_type="genomic DNA"

Query Match
  0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY
  1145 TCCGCTCGGCTTC 1158
  1 TCCCTCGGCTTC 14

Db

RESULT 466
LOCUS AX009120 14 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 153 from patent WO9963975.
ACCESSION AX009120
VERSION AX009120.1 GI:9996494
KEYWORDS
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Homidae; Homo.
```

REFERENCE 1
AUTHORS Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,K.
TITLE A method for stimulating the immune system
JOURNAL Patent: WO 963975-A 153 16-DEC-1999;
BIOGOSTRIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES
source 1.14
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1008 CTTCTTCCTCCTGC 1021
Db 1 CTCCTCTCTCTGC 14

RESULT 467
A88048/c
LOCUS A88048 15 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 196 from Patent WO9833904.
ACCESSION A88048
VERSION A88048.1 GI:6736618
KEYWORDS
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE 1 (bases 1 to 15)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 196 06-AUG-1998;
BIOGOSTRIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
source 1.15
/organism="unassigned DNA"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 936 CAAGCGCAAGTGG 949
Db 14 CAAGCGCAAGTGG 1

RESULT 468
A90015/c
LOCUS A90015 15 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 196 from Patent EP0856579.
ACCESSION A90015
VERSION A90015.1 GI:6738529
KEYWORDS
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE 1 (bases 1 to 15)
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 196 05-AUG-1998;
BIOGOSTRIK GES (DE)
FEATURES
source 1.15
/organism="unassigned DNA"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.7%; Score 12.4; DB 1; Length 15;

Best Local Similarity 92.9%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 936 CAAGCGCAAGTGG 949
Db 14 CAAGCGCAAGTGG 1

RESULT 469
AR086102/c
LOCUS AR086102 15 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 13 from patent US 5985554.
ACCESSION AR086102
VERSION AR086102.1 GI:10012868
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Tanimura,H. and Hosoya,M.
TITLE Method of probing the function of proteins or peptides encoded by
JOURNAL partially sequenced cDNAs by inhibiting protein synthesis with
antiseuse oligonucleotides
Patent: US 5985554-A 13 16-NOV-1999;
FEATURES
source 1.15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 910 GACCGTACCACGA 923
Db 14 GACCGTACCACGA 1

RESULT 470
AR126545/c
LOCUS AR126545 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 2 from patent US 6180347.
ACCESSION AR126545
VERSION AR126545.1 GI:14113138
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Iida,Y., Koshimoto,H., Kondo,S. and Tsuji,A.
TITLE Method for monitoring transcriptional synthesis of RNA
JOURNAL Patent: US 6180347-A 2 30-JAN-2001;
FEATURES
source 1.15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1155 CTTCAAGCATGCCT 1168
Db 14 CTTCAAGTATGCCT 1

RESULT 471
AR13372/c
LOCUS AR13372 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 797 from patent US 6194150.
ACCESSION AR13372
VERSION AR13372.1 GI:14121277
KEYWORDS

SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.
TITLE Nucleic acid based inhibition of CD40
JOURNAL Patent: US 6194150-A 797 27-FEB-2001;
FEATURES Location/Qualifiers
source 1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 296 CCTGGCAAAATTGTC 309
DB 15 CCTGGCAAAATTGTC 2

RESULT 472
ARI32373/c 15 bp DNA linear PAT 16-MAY-2001
LOCUS ARI32373
DEFINITION Sequence 798 from patent US 6194150.
ACCESSION ARI32373
VERSION ARI32373.1 GI:14121278
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.
TITLE Nucleic acid based inhibition of CD40
JOURNAL Patent: US 6194150-A 798 27-FEB-2001;
FEATURES Location/Qualifiers
source 1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 296 CCTGGCAAAATTGTC 309
DB 14 CCTGGCAAAATTGTC 1

RESULT 473
ARI33674 15 bp DNA linear PAT 16-MAY-2001
LOCUS ARI33674
DEFINITION Sequence 2099 from patent US 6194150.
ACCESSION ARI33674
VERSION ARI33674.1 GI:14122579
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.
TITLE Nucleic acid based inhibition of CD40
JOURNAL Patent: US 6194150-A 2099 27-FEB-2001;
FEATURES Location/Qualifiers
source 1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1409 GCTTCTCTCCCAAT 1422

DB 2 GCTTCTCTCCCAAT 15

RESULT 474
ARI33870 15 bp DNA linear PAT 16-MAY-2001
LOCUS ARI33870
DEFINITION Sequence 2295 from patent US 6194150.
ACCESSION ARI33870
VERSION ARI33870.1 GI:14122775
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.
TITLE Nucleic acid based inhibition of CD40
JOURNAL Patent: US 6194150-A 2295 27-FEB-2001;
FEATURES Location/Qualifiers
source 1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1409 GCTTCTCTCCCAAT 1422
DB 2 GCTTCTCTCCCAAT 15

RESULT 475
ARI33871 15 bp DNA linear PAT 16-MAY-2001
LOCUS ARI33871
DEFINITION Sequence 2296 from patent US 6194150.
ACCESSION ARI33871
VERSION ARI33871.1 GI:14122776
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.
TITLE Nucleic acid based inhibition of CD40
JOURNAL Patent: US 6194150-A 2296 27-FEB-2001;
FEATURES Location/Qualifiers
source 1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1409 GCTTCTCTCCCAAT 1422
DB 1 GCTTCTCTCCCAAT 14

RESULT 476
BD065561/c 15 bp DNA linear PAT 27-AUG-2002
LOCUS BD065561
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065561
VERSION BD065561.1 GI:22611164
KEYWORDS JP 2001511000-A/196.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 15)
AUTHORS Schlingensiefen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method

JOURNAL Patent: JP 2001511000-A 196 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FÜR BIOMOLEKULARE DIAGNOSTIK MBH

COMMENT OS Unknown
PN JP 2001511000-A/196
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH
PC C12N15/11, C07H21/04, A61K31/70
CC An antisense oligonucleotide preparation method FH Key
Location/Qualifiers

FEATURES FT source 1. .15
/organism='Unknown'.
Location/Qualifiers
1. .15
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 936 CAAGCCAGCTGG 949
Db 14 CAAGCCAGCTGG 1

RESULT 477
LOCUS CQ875812/c 15 bp DNA linear PAT 04-OCT-2004
DEFINITION Sequence 6 from Patent EP1462527.
ACCESSION CQ875812
VERSION CQ875812.1 GI:53789557
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Costello, C., Ma, N., Schreiber, S. and Seeger, D.
TITLE Novel markers for inflammatory bowel disease
JOURNAL Patent: EP 1462527-A 6 29-SEP-2004;
CONARIS research institute AG (DE)
Location/Qualifiers

FEATURES source 1. .15
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 134 GCCCCAGCGCCAG 147
Db 14 GCCCCAGCGCCAG 1

RESULT 478
LOCUS CQ889695/c 15 bp DNA linear PAT 19-OCT-2004
DEFINITION Sequence 6 from Patent WO2004085677.
ACCESSION CQ889695
VERSION CQ889695.1 GI:54305544
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Costello, C., Ma, N., Schreiber, S. and Seeger, D.
TITLE Novel markers for inflammatory bowel disease
JOURNAL Patent: WO 2004085677-A 6 07-OCT-2004;
CONARIS research institute AG (DE)

FEATURES Location/Qualifiers
source 1. .15
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 134 GCCCCAGCGCCAG 147
Db 14 GCCCCAGCGCCAG 1

RESULT 479
LOCUS CS052672 15 bp DNA linear PAT 23-MAR-2005
DEFINITION Sequence 13 from Patent WO2005021796.
ACCESSION CS052672
VERSION CS052672.1 GI:61891467
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Aerssens, J., Athanasiou, M., Brain, C., Cohen, N., Dain, B.,
Denton, R.R., Judson, R.S., Ozdemir, V. and Reed, C.R.
TITLE Chn2 genetic markers associated with galantamine response
JOURNAL Patent: WO 2005021796-A 13 10-MAR-2005;
Genaisance Pharmaceuticals, Inc. (US)
Location/Qualifiers

FEATURES source 1. .15
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ASO Reverse Primer for Detecting Alleles at P56 in
Haplotypes Comprising Preferred Embodiments of Response
Markers I and Response Markers II"
14
/note="r is 'g' or 'a'"

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 671 TCTGGTCTCTGCT 684
Db 2 TCTGGTCTCTGCT 15

RESULT 480
LOCUS CS125878/c 15 bp DNA linear PAT 21-JUL-2005
DEFINITION Sequence 22 from Patent WO2005061545.
ACCESSION CS125878
VERSION CS125878.1 GI:71058918
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1
AUTHORS Husain, I.
TITLE Noga antibodies for the treatment of alzheimer disease
JOURNAL Patent: WO 2005061545-A 22 07-JUL-2005;
Glaxo Group Limited (GB)
Location/Qualifiers

FEATURES source 1. .15
/organism="Mus musculus"
/mol_type="unassigned DNA"

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/db_xref="taxon:10090"
Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 30 GTGCATCCAGAGC 43
|||||
15 GTGCATCCAGTAGC 2

RESULT 481
CS126163/c 15 bp DNA linear PAT 21-JUL-2005
DEFINITION Sequence 22 from Patent WO2005061544.
ACCESSION CS126163
VERSION CS126163.1 GI:71059142
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
AUTHORS Ellis, J.H.
TITLE Nogo-a neutralising immunoglobulins for treatment of neurological
JOURNAL diseases
Patent: WO 2005061544-A 22 07-JUL-2005;
Glaxo Group Limited (GB)
FEATURES
source 1.15
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 30 GTGCATCCAGAGC 43
|||||
15 GTGCATCCAGTAGC 2

RESULT 482
CS249550 15 bp DNA linear PAT 18-JAN-2006
LOCUS CS249550
DEFINITION Sequence 37 from Patent WO2005121359.
ACCESSION CS249550
VERSION CS249550.1 GI:85361754
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Hinmah, S.C.
TITLE A method for detecting analytes in a sample
JOURNAL Patent: WO 2005121359-A 37 22-DEC-2005;
Bovec AG (DE)
FEATURES
source 1.15
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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oligonucleotide for the detection of c-fos mRNA"
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DB 1 GGCTGTGACGCC 14

RESULT 483
E11984/c 15 bp DNA linear PAT 29-SEP-1997
LOCUS E11984
DEFINITION Oligonucleotide.
ACCESSION E11984
VERSION E11984.1 GI:22025605
KEYWORDS JP 1996228798-A/13.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS (bases 1 to 15)
Tanimura, H. and Hosoya, M.
JOURNAL ELUCIDATION OF FUNCTION OF PROTEIN
Patent: JP 1996228798-A 13 10-SEP-1996;
TAKEDA CHEM IND LTD
COMMENT OS None
OC Artificial sequences.
FN JP 1996228798-A/13
PD 10-SEP-1996
PF 01-NOV-1995 JP 1995306423
PR 02-NOV-1994 JP 94P 269417
PI TANIMURA HIROSHI, HOSoya MASARI
PC C1201/68,C07H21/04,C12N15/09//C1201/02;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
FH Key
FT source 1.15
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 910 GACCGTACCACGA 923
|||||
14 GACCGTACCACGA 1

RESULT 484
E31959/c 15 bp DNA linear PAT 18-JUN-2001
LOCUS E31959
DEFINITION Method for assaying biological activity of drug, method for
screening the same and automatic screening device.
ACCESSION E31959
VERSION E31959.1 GI:13021575
KEYWORDS JP 2000041700-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS (bases 1 to 15)
Yukari, I., Satoshi, A. and Yoshiki, Y.
TITLE Method for assaying biological activity of drug, method for
screening the same and automatic screening device
JOURNAL Patent: JP 2000041700-A 2 15-FEB-2000;
BUNSHI BIO HOTONIKUSU KENKUTSHO
COMMENT OS Artificial Sequence
FN JP 2000041700-A/2
PD 15-FEB-2000
PF 31-JUL-1998 JP 1998218025
PR
PI YUKARI IDA, SATOSHI ABE, YOSHIKI YAMADA
PC C1201/68, G01N21/78//C12N15/09, C12N15/00
CC
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FEATURES
source
FH Key Location/Qualifiers
FT source 1.15 /organism='Artificial Sequence'.
1.15 Location/Qualifiers
/organism='synthetic construct'
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/db_xref='taxon:32630'

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1155 CTTCAAGCATGCCT 1168
DB 14 CTTCAAGTATGCCT 1

RESULT 485
LOCUS AR180099/c 15 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 167 from patent US 6333152.
ACCESSION AR180099
VERSION AR180099.1 GI:20222132
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
TITLE Gene expression profiles in normal and cancer cells
JOURNAL Patent: US 6333152-A 167 25-DEC-2001;
FEATURES
source
1.15 Location/Qualifiers
/organism='unknown'
/mol_type='unassigned DNA'

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 367 GTGATGTGATCAT 380
DB 15 GCGATGTGATCAT 2

RESULT 486
LOCUS AR580858 15 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 4 from patent US 6790616.
ACCESSION AR580858
VERSION AR580858.1 GI:56611528
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Moribe,T. and Kaneshige,T.
TITLE Method for typing of HLA class I alleles
JOURNAL Patent: US 6790616-A 4 14-SEP-2004;
Shionogi & Co., Ltd.; Osaka;
MOX;

FEATURES
source
1.15 Location/Qualifiers
/organism='unknown'
/mol_type='genomic DNA'

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1307 AGGAGAGCCGAG 1320
|||||

DB 2 AGGAGAGCCGAG 15

RESULT 487
LOCUS AR774267/c 15 bp DNA linear PAT 08-DEC-2005
DEFINITION Sequence 196 from patent US 6972171.
ACCESSION AR774267
VERSION AR774267.1 GI:83351531
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Schlingensiefen,K.-H. and Brysch,W.
TITLE Antisense oligonucleotide preparation method
JOURNAL Patent: US 6972171-A 196 06-DEC-2005;
Biagnostik Ges. fur biomolekulare Diagnostik mbH; Gottingen;
EPX;

FEATURES
source
1.15 Location/Qualifiers
/organism='unknown'
/mol_type='genomic DNA'

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 936 CAAGCGAAGTGG 949
DB 14 CAAGCGAAGTGG 1

RESULT 488
LOCUS AX419939 15 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 276 from Patent WO0198537.
ACCESSION AX419939
VERSION AX419939.1 GI:21524306
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Iyamichev,V., Allawi,H., Dong,F., Neri,B.P. and Vener,I.T.
TITLE Nucleic acid accessible hybridization sites
JOURNAL Patent: WO 0198537-A 276 27-DEC-2001;
THIRD WAVE TECHNOLOGIES, INC. (US)
FEATURES
source
1.15 Location/Qualifiers
/organism='synthetic construct'
/mol_type='unassigned DNA'
/db_xref='taxon:32630'

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 669 CATCTGGCTCTGG 682
DB 2 CATCTGGCTCTGG 15

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Job time : 12 secs

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OM nucleic - nucleic search, using sw model

Run on: June 12, 2006, 06:13:44 ; Search time 2 Seconds
(without alignments)
2.813 Million cell updates/sec

Title: US-09-930-503A-6

Perfect score: 1766

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 171 seqs, 1593 residues

Total number of hits satisfying chosen parameters: 342

Minimum DB seq length: 8

Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 173 summaries

Database : us-09-930-503a-6.g1.rst4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	12.4	0.7	14	1	ACCESSION:AM075254
C 3	12.4	0.7	15	1	ACCESSION:CF324040
C 4	12.2	0.7	15	1	ACCESSION:CF324040
C 5	11.4	0.6	13	1	ACCESSION:AJ521816
C 6	11.4	0.6	13	1	ACCESSION:AM075481
C 7	11.4	0.6	13	1	ACCESSION:BM396557
C 8	11.4	0.6	13	1	ACCESSION:BM396557
C 9	11.4	0.6	13	1	ACCESSION:BM396557
C 10	11.4	0.6	13	1	ACCESSION:BM396557
C 11	11.4	0.6	13	1	ACCESSION:BM396557
C 12	11.4	0.6	13	1	ACCESSION:BM396557
C 13	11.4	0.6	13	1	ACCESSION:BM396557
C 14	11.4	0.6	13	1	ACCESSION:BM396557
C 15	11.4	0.6	13	1	ACCESSION:BM396557
C 16	11.4	0.6	13	1	ACCESSION:BM396557
C 17	11.4	0.6	13	1	ACCESSION:BM396557
C 18	11.4	0.6	13	1	ACCESSION:BM396557
C 19	11.4	0.6	13	1	ACCESSION:BM396557
C 20	11.4	0.6	13	1	ACCESSION:BM396557
C 21	11.4	0.6	13	1	ACCESSION:BM396557
C 22	11.4	0.6	13	1	ACCESSION:BM396557
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C 24	11.4	0.6	13	1	ACCESSION:BM396557
C 25	11.4	0.6	13	1	ACCESSION:BM396557
C 26	11.4	0.6	13	1	ACCESSION:BM396557
C 27	11.4	0.6	13	1	ACCESSION:BM396557
C 28	11.4	0.6	13	1	ACCESSION:BM396557
C 29	11.4	0.6	13	1	ACCESSION:BM396557
C 30	11.4	0.6	13	1	ACCESSION:BM396557
C 31	11.4	0.6	13	1	ACCESSION:BM396557
C 32	11.4	0.6	13	1	ACCESSION:BM396557
C 33	11.4	0.6	13	1	ACCESSION:BM396557

C 107	7.4	0.4	9	1	CF312817	ACCESSION:CF312817
C 108	7.4	0.4	9	1	CF313414	ACCESSION:CF313414
C 109	7.4	0.4	9	1	CF318771	ACCESSION:CF318771
C 110	7.4	0.4	9	1	CF330649	ACCESSION:CF330649
C 111	7.4	0.4	9	1	CO818814	ACCESSION:CO818814
C 112	7.4	0.4	9	1	CV933314	ACCESSION:CV933314
C 113	7.4	0.4	9	1	CK005921	ACCESSION:CK005921
C 114	7.4	0.4	9	1	DT904968	ACCESSION:DT904968
C 115	7.4	0.4	9	1	DT909435	ACCESSION:DT909435
C 116	7.4	0.4	9	1	DV571332	ACCESSION:DV571332
C 117	7.4	0.4	9	1	CV985814	ACCESSION:CV985814
C 118	7.4	0.4	9	1	CL663701	ACCESSION:CL663701
C 119	7.4	0.4	9	1	CL672804	ACCESSION:CL672804
C 120	7.4	0.4	9	1	CL682372	ACCESSION:CL682372
C 121	7.4	0.4	9	1	DM058225	ACCESSION:DM058225
C 122	7.4	0.4	10	1	BM396011	ACCESSION:BM396011
C 123	7.4	0.4	10	1	BM398849	ACCESSION:BM398849
C 124	7.4	0.4	10	1	CF311011	ACCESSION:CF311011
C 125	7.4	0.4	10	1	CL694909	ACCESSION:CL694909
C 126	7.4	0.4	10	1	AJ592517	ACCESSION:AJ592517
C 127	7.4	0.4	10	1	AJ587026	ACCESSION:AJ587026
C 128	7.4	0.4	11	1	AJ679435	ACCESSION:AJ679435
C 129	7.4	0.4	11	1	AJ681247	ACCESSION:AJ681247
C 130	7.4	0.4	11	1	AJ683713	ACCESSION:AJ683713
C 131	7.4	0.4	11	1	AJ686459	ACCESSION:AJ686459
C 132	7.4	0.4	11	1	BM396384	ACCESSION:BM396384
C 133	7.4	0.4	11	1	BM397892	ACCESSION:BM397892
C 134	7.4	0.4	12	1	BM398341	ACCESSION:BM398341
C 135	7.4	0.4	13	1	AJ666341	ACCESSION:AJ666341
C 136	7.4	0.4	8	1	CF297970	ACCESSION:CF297970
C 137	7.4	0.4	8	1	CF305141	ACCESSION:CF305141
C 138	7.4	0.4	8	1	CF306116	ACCESSION:CF306116
C 139	7.4	0.4	8	1	CF306762	ACCESSION:CF306762
C 140	7.4	0.4	8	1	CF322514	ACCESSION:CF322514
C 141	7.4	0.4	8	1	CF322653	ACCESSION:CF322653
C 142	7.4	0.4	8	1	CF323889	ACCESSION:CF323889
C 143	7.4	0.4	8	1	CF324406	ACCESSION:CF324406
C 144	7.4	0.4	8	1	CF325379	ACCESSION:CF325379
C 145	7.4	0.4	8	1	CF325469	ACCESSION:CF325469
C 146	7.4	0.4	8	1	CF325485	ACCESSION:CF325485
C 147	7.4	0.4	8	1	CF330558	ACCESSION:CF330558
C 148	7.4	0.4	8	1	CF339091	ACCESSION:CF339091
C 149	7.4	0.4	8	1	CV933258	ACCESSION:CV933258
C 150	7.4	0.4	8	1	CV933304	ACCESSION:CV933304
C 151	7.4	0.4	8	1	CK001098	ACCESSION:CK001098
C 152	7.4	0.4	8	1	CK001172	ACCESSION:CK001172
C 153	7.4	0.4	8	1	CK001200	ACCESSION:CK001200
C 154	7.4	0.4	8	1	CK001601	ACCESSION:CK001601
C 155	7.4	0.4	8	1	CK001811	ACCESSION:CK001811
C 156	7.4	0.4	8	1	CK001864	ACCESSION:CK001864
C 157	7.4	0.4	8	1	CK001954	ACCESSION:CK001954
C 158	7.4	0.4	8	1	CK001980	ACCESSION:CK001980
C 159	7.4	0.4	8	1	CK002359	ACCESSION:CK002359
C 160	7.4	0.4	8	1	CK002747	ACCESSION:CK002747
C 161	7.4	0.4	8	1	CK003296	ACCESSION:CK003296
C 162	7.4	0.4	8	1	DR025726	ACCESSION:DR025726
C 163	7.4	0.4	8	1	DT909735	ACCESSION:DT909735
C 164	7.4	0.4	8	1	CL659535	ACCESSION:CL659535
C 165	7.4	0.4	8	1	CL675700	ACCESSION:CL675700
C 166	7.4	0.4	8	1	CL676755	ACCESSION:CL676755
C 167	7.4	0.4	8	1	CL677992	ACCESSION:CL677992
C 168	7.4	0.4	8	1	CL681141	ACCESSION:CL681141
C 169	7.4	0.4	8	1	CL682011	ACCESSION:CL682011
C 170	7.4	0.4	8	1	DU753265	ACCESSION:DU753265
C 171	7.4	0.4	9	1	DX021589	ACCESSION:DX021589
C 172	7.4	0.4	9	1	CNS06E5N	ACCESSION:AJ394689
C 173	7.4	0.4	9	1	CF307008	ACCESSION:CF307008

ALIGNMENTS

RESULT 1

AJ598266/c	15 bp	DNA	linear	GSS 15-JAN-2004
LOCUS	AJ598266	Arabidopsis thaliana T-DNA flanking sequence, left border, clone 465A02, genomic survey sequence.		
DEFINITION	AJ598266	Arabidopsis thaliana		
ACCESSION	AJ598266	1	GI:37947894	
VERSION		GSS; left border; T-DNA flanking sequence.		
KEYWORDS		Arabidopsis thaliana (thale cress)		
SOURCE		Arabidopsis thaliana		
ORGANISM		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.		
REFERENCE		1	Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Crnaud, C., Demare, R., Pelletier, G., Lapiniec, L., Caboche, M., and Leclercq, A.	
AUTHORS		T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites		
TITLE		EMBO Rep. 3 (12), 1152-1157 (2002)		
JOURNAL		12446565		
POBMED		2 (bases 1 to 15)		
REFERENCE		Balzerque, S.		
AUTHORS		Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE		
JOURNAL		PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/ . This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).		
FEATURES		Location/Qualifiers		
SOURCE		1..15		
		/organism="Arabidopsis thaliana"		
		/mol_type="genomic DNA"		
		/db_xref="taxon:3702"		
		/clone="465A02"		
		/clone_lib="Arabidopsis thaliana T-DNA insertion lines"		
		/ecotype="Wassilewskija"		
		1..15		
		/note="T-DNA flanking sequence		
		left border"		
		misc_feature		
		0.8%; Score 13.4; DB 1; Length 15;		
		Best Local Similarity 93.3%; Pred. No. 2.5;		
		Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	1687	GACCAAGCTTTTCCTC	1701	
Db	15	GAGCAGCTTTTCCTC	1	
RESULT 2				
AM075254/c	14 bp	mRNA	linear	EST 14-SEP-2005
LOCUS	AM075254	Chicken immune 1 - CSEORBL08 Gallus gallus CDNA clone C0000222E05_T7, mRNA sequence.		
DEFINITION	AM075254			
ACCESSION	AM075254	1	GI:75475695	
VERSION		EST.		
KEYWORDS		Gallus gallus (chicken)		
SOURCE		Gallus gallus		
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.		
REFERENCE		1 (bases 1 to 14)		
AUTHORS		Smith, J., Speed, D., Hocking, P., Talbot, R. T., Degen, W., Schijne, V., Glass, E. J. and Butt, D.		

TITLE Development of a chicken 5k array
JOURNAL Unpublished (2005)
COMMENT Contact: Smith J
 Genetics and Genomics
 Roslin Institute
 Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
 Vector pBluescript II KS(+), R. Site1: EcoRI R. Site2: NotI 5' Seq
 Primer T7 Strain Lohman Brown layer/Ross 308 broiler cross CDNA
 synthesis was initiated using an oligo(dT) primer, using methylated
 C in the first strand synthesis reaction. Following this first
 strand reaction, double-stranded cDNA was blunted, ligated to NotI
 adapters, digested with EcoRI, size-selected, and cloned into the
 NotI and EcoRI compatible sites of a custom modified MCS of the
 pBluescript (KS+) vector. Clones available from the ARK-Genomics
 Centre for Functional Genomics in Farm Animals, Roslin Institute,
 Midlothian, EH25 9PS, UK see www.ark-genomics.org.
FEATURES
 source
 1..14
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="Lohman Brown layer/Ross 308 broiler cross"
 /db_xref="taxon:9031"
 /clone="C0000222E05.T7"
 /issue_type="Bursa_spleen, Peyer's patch (pooled)"
 /clone_lib="Chicken immune 1 - CSRR08108"
 /note="Vector: pBluescript II KS(+); Site_1: EcoRI;
 Site_2: NotI"

Query Match 0.7%; Score 12.4; DB 1; Length 14;
 Best Local Similarity 92.9%; Pred. No. 4.4;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 GCCACCGCGGCGAG 22
 14 GCCACCGCGGCGAG 1

Db 14 GCCACCGCGGCGAG 1

RESULT 3
LOCUS CFJ24040 15 bp mRNA linear EST 18-AUG-2003
DEFINITION HDN--05-H11.g1 OSHDAC1-overexpressing transgenic rice lambda phage
 cDNA library II (HDN) Oryza sativa (japonica cultivar-group) cDNA
 clone HDN--05-H11, mRNA sequence.
ACCESSION CFJ24040
VERSION CFJ24040.1 GI:33796346
KEYWORDS EST.
ORGANISM Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep
 1 (bases 1 to 15)
REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
AUTHORS Large-scale Sequencing Analysis of Rice ESTs
TITLE Unpublished (2003)
JOURNAL Contact: Nahm B.H.
COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnaah@gbio.com, bhnaah@bio.myongji.ac.kr.
 Location/Qualifiers
 1..15
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="HDN--05-H11"
 /issue_type="callus"
 /dev_stages="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli SOLR"

Qy 1223 CGGCCCAAGGCCA 1336
 1 CGGCCCAAGGCCA 14

Db 1 CGGCCCAAGGCCA 14

RESULT 4
LOCUS ATH521816 15 bp DNA linear GSS 08-FEB-2006
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone
 279D04, genomic survey sequence.
ACCESSION AJ521816
VERSION AJ521816.1 GI:26790052
KEYWORDS GSS; left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsie.
REFERENCE 1
AUTHORS Brunaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samsen,F.,
 Chauvin,S., Bechtold,N., Chenu,C., DeRose,R., Pelletier,G.,
 Lepoint,L., Caboche,M. and Lecharny,A.
 T-DNA integration into the Arabidopsis genome depends on sequences
 of pre-insertion sites
 EMBO Rep. 3 (12), 1152-1157 (2002)
TITLE Arabidopsis thaliana T-DNA flanking sequence, left border, clone
 279D04, genomic survey sequence.
JOURNAL Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue
 Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana
 plants from INRA (Versailles). The DNA fragment(s) resulting from
 the PCR were directly sequenced from the left or the right border
 to determine the genomic sequence flanking the insertion. T-DNA
 derived sequences were removed. Information to order the
 corresponding mutant line and a link to a database providing a
 graphical display of the insertion site are available at
<http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has
 been generated in the framework of the French plant genomics
 program 'Genoplante' (<http://www.genoplante.com> and
<http://genoplante-info.inbio.gen.fr>).
 Location/Qualifiers
 1..15
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /cultivar="MassillaewskiJa"
 /db_xref="taxon:3702"
 /clone="279D04"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="MassillaewskiJa"
 1..15
 /note="T-DNA flanking sequence
 left border"

Qy 1045 CTGAAGAAGTTT 1056
 1045 CTGAAGAAGTTT 1056

Db 1045 CTGAAGAAGTTT 1056

Query Match 0.7%; Score 12; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3 CTGAAGAAGTTT 14

RESULT 5
AM075481/c

LOCUS
DEFINITION AM075481 Chicken immune 5 - CSEQRBN30 Gallus gallus CDNA clone

ACCESSION
VERSION AM075481

KEYWORDS
SOURCE AM075481.1 GI:75476052

ORGANISM
Gallus gallus (chicken)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

REFERENCE
AUTHORS 1 (bases 1 to 13)
Smith, J., Speed, D., Hocking, P., Talbot, R.T., Degen, W., Schjns, V., Glass, E.J. and Burt, D.

TITLE
JOURNAL Development of a chicken 5k array

COMMENT
Unpublished (2005)
Contact: Smith J
Genetics and Genomics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Vector: pBluescript II KS(+) R. Site1: EcoRI R. Site2: NotI 5' Seq
Primer T7 Strain Lohman Brown Layer/Ross 308 Prolifer cross This
normalized library was constructed from 1 million independent
clones. cDNA synthesis was initiated using an oligo(dT) primer,
using methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA was
blunted, ligated to NotI adapters, digested with EcoRI,
size-selected, and cloned into the NotI and EcoRI compatible sites
of a custom modified MCS of the pBluescript (KS+) vector. The
library was normalized in 2 rounds using conditions adapted from
Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldi et al., Genome
Research 6 (1996): 791, except that a significantly longer
reannealing hybridization was used. Clones available from the
ARK-Genomics Centre for Functional Genomics in Farm Animals, Roslin
Institute, Midlothian, EH25 9PS, UK see www.ark-genomics.org.

FEATURES
source
1..13
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="C0000798E15_77"
/tissue="thymus"
/clone_id="Chicken immune 5 - CSEQRBN30"

Query Match 0.6%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 7.3;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 9 GCCACCGCGGCA 21
13 GCCACCGCGGGA 1

RESULT 6
BM396557/c

LOCUS
DEFINITION BM396557 13 bp mRNA linear EST 17-JAN-2002

ACCESSION
VERSION BM396557

KEYWORDS
SOURCE BM396557.1 GI:18196625

ORGANISM
Tetrahymena thermophila

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenida; Tetrahymenidae; Tetrahymena.

REFERENCE
AUTHORS 1 (bases 1 to 13)
Turkewitz, A.P., Karer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel, J. and Klobutcher, L.

TITLE
JOURNAL EST from Tetrahymena thermophila, strain CU428.1, growing cells

COMMENT
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
source
1..13
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_id="Chilcoat/Turkewitz SK-; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 0.6%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 7.3;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 8 AGCCACCGCGGC 20
13 AGCCACCGCGGTC 1

RESULT 7
AJ587382/c

LOCUS
DEFINITION AJ587382 13 bp DNA linear GSS 15-JAN-2004

ACCESSION
VERSION AJ587382

KEYWORDS
SOURCE GSS: left border; T-DNA flanking sequence.

ORGANISM
Arabidopsis thaliana (thale cress)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
AUTHORS 1
Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., Denose, R., Pelletier, G., Lepoint, L., Caboche, M. and Leclercq, A.

TITLE
JOURNAL T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites

COMMENT
EMBO Rep. 3 (12), 1152-1157 (2002)
12446565
2 (bases 1 to 13)
Balzerque, S.
Direct Submision
Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
<http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (<http://www.genoplante.com> and
<http://genoplante-info.infobiogen.fr>).

FEATURES
source
1..13
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="270B03"


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misc_feature
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Maslleskija"
/nc="T-DNA flanking sequence
left border"

Query Match      0.6%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 7.3;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 716 CAACACAGAGAC 728
    |||||
Db 13 CAACACAGAGTC 1

RESULT 8
AJ679435/c
LOCUS
DEFINITION AJ679435 CSEORAN04 Sus scrofa cDNA clone C0001779_B18, mRNA
ACCESSION AJ679435
VERSION AJ679435.1 GI:49412022
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
1 (bases 1 to 11)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross_match with the -minscore 20
and -mismatch 12 options. Vector:pb1uescriptII(KS+) R. Site1: EcORI
R. Site2: NotI 5' Seg Primer M13F Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.
Location/Qualifiers
1..11
/organism="Sus scrofa"
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/db_xref="taxon:9823"
/clone="C0001779_B18"
/issue_type="uterus"
/clone_lib="CSEORAN04"
/nc="Vector: pb1uescriptII(KS+); Site 1: EcORI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pig uterus."

FEATURES
source

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Query Match      0.6%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 9 GCCACCGCGGG 19
    |||||
Db 11 GCCACCGCGGG 1

RESULT 9
AJ681247/c
LOCUS
DEFINITION AJ681247 CSEORAN04 Sus scrofa cDNA clone C0001795_I24, mRNA
ACCESSION AJ681247
VERSION AJ681247.1 GI:49413837
KEYWORDS EST.
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```
SOURCE
ORGANISM
Sus scrofa (pig)
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
1 (bases 1 to 11)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross_match with the -minscore 20
and -mismatch 12 options. Vector:pb1uescriptII(KS+) R. Site1: EcORI
R. Site2: NotI 5' Seg Primer M13F Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.
Location/Qualifiers
1..11

FEATURES
source

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Query Match      0.6%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 9 GCCACCGCGGG 19
    |||||
Db 11 GCCACCGCGGG 1

RESULT 10
AJ683713/c
LOCUS
DEFINITION AJ683713 CSEORAN04 Sus scrofa cDNA clone C0001802_O06, mRNA
ACCESSION AJ683713
VERSION AJ683713.1 GI:49416303
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
1 (bases 1 to 11)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross_match with the -minscore 20
and -mismatch 12 options. Vector:pb1uescriptII(KS+) R. Site1: EcORI
R. Site2: NotI 5' Seg Primer M13F Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.
Location/Qualifiers
1..11

FEATURES
source
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/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001802_006"
/tissue_type="uterus"
/clone_id="CSEQRAN04"
/note="Vector: pBluescriptII (KS+); Site_1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pig uterus."

Query Match      0.6%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      9 GCCACCGCGGG 19
        |||||
        11 GCCACCGCGGG 1

RESULT 11
AJ686459      11 bp mRNA linear EST 29-JUN-2004
LOCUS      AJ686459 CSEQRAN04 Sus scrofa cDNA clone C0001811_K23, mRNA
DEFINITION      sequence.
ACCESSION      AJ686459.1 GI:49419049
VERSION      AJ686459.1
KEYWORDS      EST.
SOURCE      Sus scrofa (pig)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;
Sus.
REFERENCE      1 (bases 1 to 11)
AUTHORS      Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLES      Development of cDNA and EST resources for studying reproduction and
JOURNAL      embryo development in pigs and cattle
COMMENT      unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -mismatch 12 options. Vector:pBluescriptII (KS+). R. Site1: EcoRI
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.

FEATURES
source
1..11
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001811_K23"
/tissue_type="uterus"
/clone_id="CSEQRAN04"
/note="Vector: pBluescriptII (KS+); Site_1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pig uterus."

Query Match      0.6%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      9 GCCACCGCGGG 19
        |||||
        11 GCCACCGCGGG 1

RESULT 12
CF337407      12 bp mRNA linear EST 18-AUG-2003
LOCUS      CF337407 JMT--07-N08.D1 AtUMT-overexpressing transgenic rice plasmid cDNA
DEFINITION
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library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--07-N08, mRNA sequence.
CF337407
CF337407.1 GI:33823214
EST.
ACCESSION      Oryza sativa (japonica cultivar-group)
VERSION      Oryza sativa (japonica cultivar-group)
KEYWORDS      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
SOURCE      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
ORGANISM      clade; Ehrhartoidae; Oryzaceae; Oryza.
REFERENCE      1 (bases 1 to 12)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Sung,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLES      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
location/Qualifiers
1..12
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--07-N08"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/leaf_host="E.coli DH10B"
/clone_id="AtUMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
pared from Arabidopsis jasmonate Carboxyl
methyltransferase overexpression line."

Query Match      0.6%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 12;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1393 ATGCAGAGAGC 1404
        |||||
        12 ATGCAGAGAGC 1

RESULT 13
AJ666341      13 bp mRNA linear EST 28-JUN-2004
LOCUS      AJ666341 CSEQRAN09 Sus scrofa cDNA clone C0000033_C09, mRNA
DEFINITION      sequence.
ACCESSION      AJ666341
VERSION      AJ666341.1 GI:49350792
KEYWORDS      EST.
SOURCE      Sus scrofa (pig)
ORGANISM      Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;
Sus.
REFERENCE      1 (bases 1 to 13)
AUTHORS      Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLES      Development of cDNA and EST resources for studying reproduction and
JOURNAL      embryo development in pigs and cattle
COMMENT      unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -mismatch 12 options. Vector:pBluescriptII (KS+) R. Site 1:
```

ECORI R. Site 2: NotI Description: Normalised library constructed from pooled tissue from day 30 placentas. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES

source

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1. .13
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0000033_C09"
/tissue_type="Placenta"
/clone_lib="GSEORAN09"
/notes="Vector: pBluescriptII (KS+); Site 1: EcorI; Site 2: NotI; Single pass sequencing. Normalised library constructed from pooled tissue from day 30 placentas."
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Query Match
Best Local Similarity 91.7%; Pred. No. 19;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1495 GGAATTCCTT 1506
Db 2 GGAATTCCTT 13

RESULT 14
AJ590935/c 13 bp DNA linear GSS 15-JAN-2004
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence, left border, clone 577B08, genomic survey sequence.

ACCESSION
AJ590935.1 GI:37940559
VERSION
GSS; left border; T-DNA flanking sequence.
KEYWORDS
Arabidopsis thaliana (chale cress)
SOURCE
Arabidopsis thaliana
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosid II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

AUTHORS

1
Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechthold, N., Cruaud, C., Derose, R., Pelletier, G., Lepoint, L., Caboche, M. and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites

JOURNAL
EMBO Rep. 3 (12), 1152-1157 (2002)
PUBMED
12446565

2 (bases 1 to 13)
Balzergue, S.

Direct Submission
Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue

Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr/>).

COMMENT

JOURNAL

Location/Qualifiers
1. .13
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="577B08"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Wassilewskija"
1. .13
/note="T-DNA flanking sequence
left border"

FEATURES

source

misc_feature
left border"

Query Match
Best Local Similarity 91.7%; Pred. No. 19;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 952 AAATGATGATT 963
Db 13 AAAAGATGATT 2

RESULT 15
CF324040 15 bp mRNA linear EST 18-AUG-2003
LOCUS
DEFINITION
HDN-05-H11.g1 OSHDAC1-overexpressing transgenic rice lambda phage cDNA library II (HDN) Oryza sativa (japonica cultivar-group) cDNA clone HDN-05-H11, mRNA sequence.

ACCESSION
CF324040
VERSION
CF324040.1 GI:33796346
KEYWORDS
EST.

SOURCE
Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
1 (bases 1 to 15)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

```
1. .15
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HDN--05-H11"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OSHDAC1-overexpressing transgenic rice lambda phage cDNA library II (HDN)"
/notes="Vector: pBluescript SK(+); Site 1: EcorI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcorI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."
```

Query Match
Best Local Similarity 80.0%; Pred. No. 49;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 305 TTGTCTTTGGCGAG 319
Db 15 TTGGCTTTGGGCGG 1

RESULT 16
BM396011 10 bp mRNA linear EST 17-JAN-2002
LOCUS
DEFINITION
5009-0-15-B12.t.2 Chilcoac/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION
BM396011 GI:18196064
VERSION
BM396011.1
KEYWORDS
EST.
SOURCE
Tetrahymena thermophila
ORGANISM
Tetrahymena thermophila

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hyenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena. 1 (bases 1 to 10)
 Turkewitz,A.P., Karrer,K.M., Jahn,C., Orías,E., Kirk,K.E., Frankel,J. and Klobutcher,L.
 EST from Tetrahymena thermophila, strain CU428.1, growing cells
 Unpublished (2002)
 CONTACT: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3.
 Location/Qualifiers
 1..10
 /organism="Tetrahymena thermophila"
 /mol_type="mRNA"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."
 Query Match 0.6%; Score 10; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.2;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 9 GCCACCGCGG 18
 Db 10 GCCACCGCGG 1
 RESULT 17 10 bp mRNA linear EST 17-JAN-2002
 BM398849/c
 LOCUS 5009-0-5-G06.t.1 Chilcoat/Turkewitz cDNA (large fraction)
 DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.
 ACCESSION BM398849
 VERSION BM398849.1 GI:18198902
 KEYWORDS EST.
 SOURCE Tetrahymena thermophila
 ORGANISM Tetrahymena thermophila
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hyenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena. 1 (bases 1 to 10)
 Turkewitz,A.P., Karrer,K.M., Jahn,C., Orías,E., Kirk,K.E., Frankel,J. and Klobutcher,L.
 EST from Tetrahymena thermophila, strain CU428.1, growing cells
 Unpublished (2002)
 CONTACT: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3.
 Location/Qualifiers
 1..10
 /organism="Tetrahymena thermophila"
 /mol_type="mRNA"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."
 Query Match 0.6%; Score 10; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.2;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 9 GCCACCGCGG 18
 Db 10 GCCACCGCGG 1
 RESULT 19 10 bp DNA linear GSS 09-JUL-2004
 CL659790/c
 LOCUS PRI0135b.B11 - PRI0135b.B21 (10) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic survey sequence.
 ACCESSION CL659790
 VERSION CL659790.1 GI:50144248
 KEYWORDS GSS.
 SOURCE Pristionchus pacificus
 ORGANISM Pristionchus pacificus
 Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 9 GCCACCGCGG 18
 Db 10 GCCACCGCGG 1
 RESULT 18 10 bp DNA linear GSS 28-DEC-2004
 CW979862
 LOCUS KBxH003N20F KBxH, Brassica rapa HindIII BAC library Brassica rapa subsp. pekinensis genomic clone KBxH003N20, genomic survey sequence.
 DEFINITION subsp. pekinensis genomic clone KBxH003N20, genomic survey sequence.
 ACCESSION CW979862
 VERSION CW979862.1 GI:56811149
 KEYWORDS GSS.
 SOURCE Brassica rapa subsp. pekinensis
 ORGANISM Brassica rapa subsp. pekinensis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica. 1 (bases 1 to 10)
 Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M., Park,J.Y., Lim,M.H., Kim,H.I., Lim,Y.P. and Park,B.S.
 End sequence of Brassica rapa HindIII BAC library (KBxH) Unpublished (2004)
 CONTACT: Beom-Seok Park
 Brassica Genomics Team
 National Institute of Agricultural Biotechnology
 225 Seodun-Dong, Suwon, 441-707, Korea
 Tel: +82-31-299-1672
 Fax: +82-31-299-1670
 Email: pbeom@rda.go.kr
 BAC end sequence of Brassica rapa ssp. pekinensis HindIII BAC clone KBxH003N20
 Seq primer: T7
 Class: BAC ends.
 Location/Qualifiers
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 /organism="Brassica rapa subsp. pekinensis"
 /mol_type="genomic DNA"
 /cultivar="Chilfu"
 /sub_species="pekinensis"
 /db_xref="taxon:51351"
 /clone="KBxH003N20"
 /issue_type="young leaves"
 /lab_host="E.coli DH10B"
 /clone_lib="KBxH, Brassica rapa HindIII BAC library"
 /note="Vector: pCUGBac1; Site 1: HindIII; Brassica rapa ssp. pekinensis indred line Chilfu BAC library (KBxH BAC) is provided by Yong-Pyo Lim."
 Query Match 0.6%; Score 10; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.2;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 531 CCACAATTC 540
 Db 1 CCACAATTC 10
 RESULT 19 10 bp DNA linear GSS 09-JUL-2004
 CL659790/c
 LOCUS PRI0135b.B11 - PRI0135b.B21 (10) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic survey sequence.
 ACCESSION CL659790
 VERSION CL659790.1 GI:50144248
 KEYWORDS GSS.
 SOURCE Pristionchus pacificus
 ORGANISM Pristionchus pacificus
 Eukaryota; Metazoa; Nematoda; Diplogasterida;

REFERENCE 1 (bases 1 to 10)
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE Appadi: an Acedb database for the nematode satellite organism
JOURNAL Pristionchus pacificus
PUBMED Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT 14681447
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
1..10
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pGpifos-5 Fosmid vector"

Query Match 0.6%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 891 GATCCCCGGG 900
|||||
10 GATCCCCGGG 1

RESULT 20
AJ686546/c 11 bp mRNA linear EST 29-JUN-2004
LOCUS AJ686546 CSEORAN04 Sus scrofa cDNA clone C0001812_C13, mRNA
DEFINITION
ACCESSION AJ686546
VERSION AJ686546.1 GI:49419136
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
1 (bases 1 to 11)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -mismatch 12 options. Vector:pBluescriptII(KS+). R. Site1: EcoRI
R. Site2: NotI 5' Seq Primer M13P Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.
Location/Qualifiers
1..11
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001812_C13"
/issue_type="uterns"
/clone_lib="CSEORAN04"
/note="Vector: pBluescriptII(KS+); Site_1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pig uterus."

REFERENCE 1 (bases 1 to 11)
AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
JOURNAL Unpublished (2004)
COMMENT Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -mismatch 12 options. Vector:pBluescriptII(KS+) R. Site1: EcoRI
R. Site2: NotI 5' Seq Primer M13P Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.
Location/Qualifiers
1..11
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001812_E11"
/issue_type="uterns"
/clone_lib="CSEORAN04"
/note="Vector: pBluescriptII(KS+); Site_1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pig uterus."

FEATURES
source

/clone_lib="CSEORAN04"
/note="Vector: pBluescriptII(KS+); Site_1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pig uterus."

Query Match 0.6%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCCACCGCGG 18
|||||
11 GCCACCGCGG 2

RESULT 21
AJ686590/c 11 bp mRNA linear EST 29-JUN-2004
LOCUS AJ686590 CSEORAN04 Sus scrofa cDNA clone C0001812_E11, mRNA
DEFINITION
ACCESSION AJ686590
VERSION AJ686590.1 GI:49419180
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
1 (bases 1 to 11)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -mismatch 12 options. Vector:pBluescriptII(KS+) R. Site1: EcoRI
R. Site2: NotI 5' Seq Primer M13P Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.
Location/Qualifiers
1..11
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001812_E11"
/issue_type="uterns"
/clone_lib="CSEORAN04"
/note="Vector: pBluescriptII(KS+); Site_1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pig uterus."

FEATURES
source

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 12)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross_match with the minscore 20 and -mismatch 12 options. Vector:PB1uescriptII(SK+) R. Site1: EcorI R. Site2: NotI 5' Seg Primer M13F Normalised library constructed from pooled early embryos, from 8-cell stage to blastocysts. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org

FEATURES
source
1..12
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0005190.G13"
/cissue_type="embryo"
/clone_lib="KN277"
/note="Vector: pBluescriptII(SK+); Site_1: EcorI; Site_2: NotI; Single pass sequencing. Normalised library constructed from pooled early embryos, from 8-cell stage to blastocysts."

Query Match
Best Local Similarity 100.0%; Pred. No. 17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1283 TCTCCACAGT 1292
|||
10 TCTCCACAGT 1

RESULT 23
BM395918/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BM395918 12 bp mRNA linear EST 17-JAN-2002
5009-0-14-B05.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
BM395918
BM395918.1 GI:18195971
EST.
Tetrahymena thermophila
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
1 (bases 1 to 12)
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers

FEATURES
source
1..12
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 11)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross_match with the minscore 20 and -mismatch 12 options. Vector:PB1uescriptII(SK+) R. Site1: EcorI R. Site2: NotI 5' Seg Primer M13F Normalised library constructed from pooled early embryos, from 8-cell stage to blastocysts. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org

FEATURES
source
1..12
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0005190.G13"
/cissue_type="embryo"
/clone_lib="KN277"
/note="Vector: pBluescriptII(SK+); Site_1: EcorI; Site_2: NotI; Single pass sequencing. Normalised library constructed from pooled early embryos, from 8-cell stage to blastocysts."

Query Match
Best Local Similarity 100.0%; Pred. No. 17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1283 TCTCCACAGT 1292
|||
10 TCTCCACAGT 1

RESULT 24
BM398341/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BM398341 12 bp mRNA linear EST 17-JAN-2002
5009-0-44-D05.t.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
BM398341
BM398341.1 GI:18198394
EST.
Tetrahymena thermophila
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
1 (bases 1 to 12)
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers

FEATURES
source
1..12
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
JOURNAL Unpublished (2004)
COMMENT Contact: Anderson SI
 Genomics and Bioinformatics
 Roslin Institute

Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
 Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -minscore 20 and -mismatch 12 options. Vector: pBluescriptII(SK+) R. Site1: EcoRI R. Site2: NotI 5' Seg Primer M13 Normalised library constructed from pooled early embryos, from 8-cell stage to blastocysts. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES
SOURCE Location/Qualifiers

1..11
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /clone="C0005190_K23"
 /tissue_type="embryo"
 /clone_lib="KN277"
 /note="Vector: pBluescriptII(SK+); Site 1: EcoRI; Site 2: NotI; Single pass sequencing. Normalised library constructed from pooled early embryos, from 8-cell stage to blastocysts."

Query Match 0.5%; Score 9.4; DB 1; Length 11;
 Best Local Similarity 90.9%; Pred. No. 17;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 821 TCTACTCTCTC 831
 ||| |||||
 Db 11 TCTCTCTCTC 1

RESULT 26
LOCUS AJ657108 11 bp mRNA linear EST 28-JUN-2004
DEFINITION AJ657108 KN277 Sus scrofa cDNA clone C0005196_K06, mRNA sequence.
ACCESSION AJ657108
VERSION AJ657108.1 GI:49341140
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 11)
AUTHORS Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
JOURNAL Unpublished (2004)
COMMENT Contact: Anderson SI
 Genomics and Bioinformatics
 Roslin Institute

Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
 Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -minscore 20 and -mismatch 12 options. Vector: pBluescriptII(SK+) R. Site1: EcoRI R. Site2: NotI 5' Seg Primer M13 Normalised library constructed from pooled early embryos, from 8-cell stage to blastocysts. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES
SOURCE Location/Qualifiers

1..11
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /clone="C0005196_K06"
 /tissue_type="embryo"

/clone_lib="KN277"
 /note="Vector: pBluescriptII(SK+); Site 1: EcoRI; Site 2: NotI; Single pass sequencing. Normalised library constructed from pooled early embryos, from 8-cell stage to blastocysts."

Query Match 0.5%; Score 9.4; DB 1; Length 11;
 Best Local Similarity 90.9%; Pred. No. 17;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 825 CTTCTCTCCCC 835
 ||| |||||
 Db 11 CTTCTCTCCCC 1

RESULT 27
LOCUS CF323154 11 bp mRNA linear EST 18-AUG-2003
DEFINITION HDN--03-B04.g1 OSHDAC1-overexpressing transgenic rice lambda phage cDNA library II (HDN) Oryza sativa [japonica cultivar-group] cDNA clone HDN--03-B04, mRNA sequence.
ACCESSION CF323154
VERSION CF323154.1 GI:33794534
KEYWORDS EST.
ORGANISM Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep clade; Ehrhartodeae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 11)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Gyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
SOURCE Location/Qualifiers

1..11
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="HDN--03-B04"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli SOLR"
 /clone_lib="OSHDAC1-overexpressing transgenic rice lambda phage cDNA library II (HDN)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.5%; Score 9.4; DB 1; Length 11;
 Best Local Similarity 90.9%; Pred. No. 17;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1337 CACCCTGTGCC 1347
 ||| |||||
 Db 11 CACCCTGTGCC 1

RESULT 28
LOCUS CX000541 11 bp mRNA linear EST 03-DEC-2004
DEFINITION i58406.g1 Right Cardiac Ventricle (DOEST6) Canis familiaris cDNA, mRNA sequence.

```

ACCESSION      CX000541
VERSION        CX000541.1  GI:56271958
KEYWORDS       EST.
SOURCE         Canis familiaris (dog)
ORGANISM       Canis familiaris
               Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
               Canis.
REFERENCE      1 (bases 1 to 11)
AUTHORS       Ballja,V.S., Nasclimento,L.U. and McCombie,W.R.
TITLE         ESTs from Canis familiaris right cardiac ventricle (dog)
JOURNAL       Unpublished (2004)
COMMENT       Contact: W. Richard McCombie
               Lita Amentberg Hazen Genome Sequencing Center
               Cold Spring Harbor Laboratory
               PO Box 100, Cold Spring Harbor, NY 11724, USA
               Tel: 516 367 8884
               Fax: 516 367 8874
               Email: mccombie@cshl.org.

FEATURES
source
1..11
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
/tissue_type="Cardiac muscle"
/dev_stage="3 month old normal canine"
/lab_host="XL10 Gold"
/clone_idb="Right Cardiac Ventricle (DOEST6)"
/note="Organ: Heart; Vector: pBluescript II SK; Site: 1;
ECORI; Site 2: XhoI; Library constructed using pBluescript
XR kit from Stratagene. Cloned cDNA was size selected
between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD,
Pathology and Medical Genetics, School of Veterinary
Medicine, University of Pennsylvania, 3800 Spruce Street,
Philadelphia, PA 19104-6051"

Query Match      0.5%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.3%; Pred. No. 17;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1337 CACCCTCGTCC 1347
        |||||
        11 CACCTCGTGC 1

Db
11 CACCTCGTGC 1

RESULT 29
AJ592230/c
LOCUS        AJ592230
DEFINITION   Arabidopsis thaliana T-DNA flanking sequence, right border, clone
609B09, genomic survey sequence.
ACCESSION    AJ592230
VERSION      AJ592230.1  GI:37941854
KEYWORDS     GSS; right border; T-DNA flanking sequence.
SOURCE       Arabidopsis thaliana (thale cress)
ORGANISM     Arabidopsis thaliana
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
               rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE    1
AUTHORS      Brunaud,V., Balergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
               Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
               Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE        T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
JOURNAL      EMBO Rep. 3 (12), 1152-1157 (2002)
PUBMED      12446565
REFERENCE    2 (bases 1 to 11)
AUTHORS      Balzergue,S.
TITLE        Direct Submision
JOURNAL      Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT      PCR was performed on DNA from transformants of Arabidopsis thaliana

```

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plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program "Genoplante" (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
location/Qualifiers
1..11
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone_idb="609B09"
/clone_idb="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Wassilewskija"
1..11
/note="T-DNA flanking sequence
right border"

misc_feature
1..11
/note="T-DNA flanking sequence
right border"

Query Match      0.5%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.3%; Pred. No. 17;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1594 AAAATCTCAAT 1604
        |||||
        11 AAAATCTCAAT 1

Db
11 AAAATCTCAAT 1

RESULT 30
AJ587382
LOCUS        AJ587382
DEFINITION   Arabidopsis thaliana T-DNA flanking sequence, left border, clone
270B03, genomic survey sequence.
ACCESSION    AJ587382
VERSION      AJ587382.1  GI:37937006
KEYWORDS     GSS; left border; T-DNA flanking sequence.
SOURCE       Arabidopsis thaliana (thale cress)
ORGANISM     Arabidopsis thaliana
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
               rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE    1
AUTHORS      Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
               Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
               Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE        T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
JOURNAL      EMBO Rep. 3 (12), 1152-1157 (2002)
PUBMED      12446565
REFERENCE    2 (bases 1 to 13)
AUTHORS      Balzergue,S.
TITLE        Direct Submision
JOURNAL      Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT      PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program "Genoplante" (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
location/Qualifiers
1..13
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"

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misc_feature
    /clone="270B03"
    /ecotype="Arabidopsis thaliana T-DNA insertion lines"
    /ecotype="massilewski"
    1..13
    /note="T-DNA flanking sequence
    left border"

Query Match      0.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 45;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      345 CTCGTGTGTGG 355
Db      3 CTCGTGTGTG 13

RESULT 31
CA850899/c
LOCUS      CA850899
DEFINITION CA850899 9 bp mRNA linear EST 01-AUG-2003
            D07H02.O14.15.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
VERSION     CA850899
KEYWORDS    CA850899.1 GI:33387692
SOURCE      EST.
ORGANISM    Glycine max (soybean)
            Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseolae;
            Glycine.
            1 (bases 1 to 9)
REFERENCE   1
AUTHORS    Alkharouf,N., Khan,R. and Matthews,B.
TITLE      Analysis of expressed sequence tags from roots of resistant soybean
JOURNAL    Genome 47 (2), 380-388 (2004)
PUBMED     15060591
COMMENT     Contact: Alkharouf, N.W.
            Soybean Genomics and Improvement Laboratory (SGIL)
            US Department of Agriculture (USDA), ARS, PSI
            Bldg 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
            USA
            Tel: 301 504 5750
            Fax: 301 504 5728
            Email: alkharouf@ars.usda.gov.
            Location/Qualifiers
            source
            1..9
            /organism="Glycine max"
            /mol_type="mRNA"
            /cultivar="Peking"
            /db_xref="taxon:3847"
            /clone="D07H02"
            /cissue_type="Roots"
            /dev_stage="Seedling8"
            /clone.lib="CA850899 Peking library 2, 4 day SCN3"
            /note="Vector: pJuescript SK-; cDNA clones from mRNA
            extracted from Peking roots 2 and 4 days post invasion."

Query Match      0.5%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1114 CCCATCATC 1122
Db      9 CCCATCATC 1

RESULT 32
CF311011/c
LOCUS      CF311011
DEFINITION ABR--06-B02.b1 ABR3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABR--06-B02, mRNA sequence.
ACCESSION   CF311011

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```

VERSION     CF311011.1 GI:33682772
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzaceae; Oryza.
            1 (bases 1 to 10)
REFERENCE   1
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, Greengene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
            Location/Qualifiers
            source
            1..10
            /organism="Oryza sativa (japonica cultivar-group)"
            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:39947"
            /clone="ABF--06-B02"
            /cissue_type="leaf"
            /dev_stage="14 days after germination"
            /lab_host="E.coli DH10B"
            /clone.lib="ABF3-overexpressing transgenic rice plasmid
            cDNA library (ABF)"
            /note="Vector: PCR4-TOP0, Site 1: EcoRI, leaf was dried
            for 2hrs. Oligo-capped mRNA was reverse transcribed and
            then used for PCR. mRNA was prepared from ABA-responsive
            element binding transcription factor 3 overexpression
            line."

Query Match      0.5%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1306 GAGGAGGAG 1314
Db      10 GAGGAGGAG 2

RESULT 33
AJ591555/c
LOCUS      AJ591555
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone
            587C11, genomic survey sequence.
ACCESSION   AJ591555
VERSION     AJ591555.1 GI:37941179
KEYWORDS    GSS; left border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsie.
            1
REFERENCE   1
AUTHORS    Brunaud,V., Balergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Gruaud,C., Denose,R., Pelleier,G.,
            Lepoint,L., Caboche,M. and Lecharny,A.
TITLE      T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
JOURNAL     EMBO Rep. 3 (12), 1152-1157 (2002)
PUBMED     12446565
REFERENCE   2
AUTHORS    Balergue,S.
TITLE      Direct Submersion
JOURNAL     Submitted (23-OCT-2003) Balergue S., UMRGV, INRA/CNRs, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana

```

plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr/>).

```

FEATURES
  source
    location/Qualifiers
    1..10
    /organism="Arabidopsis thaliana"
    /mol_type="Genomic DNA"
    /db_xref="taxon:3702"
    /clone="587C11"
    /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
    /ecotype="wassilewskij"
    1..10
  misc_feature
    /note="T-DNA flanking sequence
    left border"

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Query Match	0.5%	Score 9	DB 1	Length 10
Best Local Similarity	100.0%	Pred. No. 14		
Matches	9	Conservative	0	Mismatches 0; Indels 0; Gaps 0;
QY	944	AGGTGGCTCA	952	
db	9	AGGTGGCTCA	1	

RESULT	34
LOCUS	AJ599033/c
DEFINITION	AJ599033 10 bp DNA linear GS5_15-JAN-2004 <i>Arbidopsis thaliana</i> T-DNA flanking sequence, right border, clone 479B09, genomic survey sequence.

ACCESSION	AJ559033	GI:37948661
VERSION	AJ559033.1	
KEYWORDS	GSS: right border; T-DNA flanking sequence	
SOURCE	Arabidopsis thaliana (Thale cress)	
ORGANISM	Arabidopsis thaliana	

REFERENCE

1. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

AUTHORS
Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepintec, L., Caboche, M. and Lecharny, A.

TITLE	JOURNAL	PUBMED	REFERENCE
T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites	EMBO Rep. 3 (12), 1152-1157 (2002)	12445565	2 (bases 1 to 10)

AUTHORS Balzergue, S.
 TITLE Direct Submission
 JOURNAL Submitted (23-OCT-2003) Balzergue S., IMRGV, INRA/CNRS, 2 rue
 Gaston Cremieux, 91057 Evry cedex, FRANCE
 COMMENT PCR was performed on DNA from transformants of *Arabidopsis thaliana*

plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbseqg.versailles.inra.fr/publications/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobioingen.fr>).

```

FEATURES
source      Location/Qualifiers
1. .10
            /organism="Arabidopsis thaliana"
            /mol_type="genomic DNA"
            /db_xref="taxon:3702"

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misc_feature
    /clone="479B09"
    /clone_lb="Arabidopsis thaliana T-DNA insertion lines"
    /ecotype="Maslilewskija"
    1..10
    /note="T-DNA flanking sequence
    right border"
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Query Match	0.5%;	Score 9;	DB 1;	Length 10;
Best Local Similarity	100.0%;	Pred. No. 14;		
Matches	9;	Conservative	0;	Mismatches
			0;	Indels
				Gaps
				0;

QY	1547	AAAAAGCGT	1555
Db	10	AAAAAGCGT	2

RESULT 35	LOCUS	DEFINITION
AJ681839	11 bp	EST 29-JUN-2004
AJ681839	CSEGRAN04	Sus scrofa cDNA clone C0001797_F06, mRNA

ACCESSION	AJ681839
VERSION	AJ681839.1
KEYWORDS	EST.
SOURCE	Sus scrofa (pig)

Eukaryota; Metazoa: Chordata; Vertebrata: Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae; Sus.

REFERENCE
1 (Bases 1 to 11)
AUTHORS
Anderson, S.T., Finlayson, H.A. and Archibald, A.L.
TITLE
Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle

JOURNAL
COMMENT

Genomics and Bioinformatics
Roslin Institute
EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020423.c. Vector identified by cross match with the -mncore 20
and -minmatch 12 options. Vector:phagescript1(KS+). R. Sites: Rcor1
R. Sites: Not1 5' Seg Primer M13P Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK.
EH25 9PS, www.arkgenomics.org.

FEATURES

```

/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="caxon:3823"
/clone="C0001797_F06"
/tissue_type="uterus"
/clone_id="CSEGRAND4"
/note="Vector: pBlueScriptII (KS+), Site_1: EcoRI, Site_2
NotI, Single pass sequencing. Normalised library
constructed from pig uterus."

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Query Match	0.5%;	Score 9;	DB 1;	Length 11;
Best Local Similarity	100.0%;	Pred. No. 25;		
Matches 9;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 10 CCACCGCGG 1
|||
Db 1 CCACCGCGG 9

RESULT 36
AJ682947

LOCUS	AJ682947	11 bp	mRNA	linear	EST 29-JUN-2004
DEFINITION	AJ682947	CSEQRAN04 Sus scrofa cDNA clone C0001800_K12, mRNA			

ACCESSION	AJ682947
VERSION	AJ682947.1
	GI:49415537

KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae; Suidae;

REFERENCE 1 (bases 1 to 11)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
Unpublished (2004)

JOURNAL Contact: Anderson SI
Genomics and Bioinformatics

COMMENT Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -m1nscore 20 and -m1match 12 options. Vector:BluescriptII(KS+) R. Site1: EcoRI R. Site2: NotI 5' Seg Primer M13F Normalised library constructed from pig uterus. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
Location/Qualifiers

FEATURES source

1..11
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001800_K12"
/tissue_type="uterus"
/clone_id="CSEORAN04"
/note="Vector: pBluescriptII(KS+); Site_1: EcoRI; Site_2: NotI; Single pass sequencing. Normalised library constructed from pig uterus."

Query Match 0.5%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CCACCGCG 18
|||||
1 CCACCGCG 9

Db 1 CCACCGCG 9

RESULT 37 AJ685455 11 bp mRNA linear EST 29-JUN-2004
AJ685455 CSEORAN04 Sus scrofa cDNA clone C0001808_P05, mRNA sequence.

ACCESSION AJ685455

VERSION AJ685455.1 GI:49418045

KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae; Suidae;

REFERENCE 1 (bases 1 to 11)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
Unpublished (2004)

JOURNAL Contact: Anderson SI
Genomics and Bioinformatics

COMMENT Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -m1nscore 20 and -m1match 12 options. Vector:BluescriptII(KS+) R. Site1: EcoRI R. Site2: NotI 5' Seg Primer M13F Normalised library constructed from pig uterus. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
Location/Qualifiers

FEATURES source

1..11
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001800_K12"
/tissue_type="uterus"
/clone_id="CSEORAN04"
/note="Vector: pBluescriptII(KS+); Site_1: EcoRI; Site_2: NotI; Single pass sequencing. Normalised library constructed from pig uterus."

source

1..11
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001808_P05"
/tissue_type="uterus"
/clone_id="CSEORAN04"
/note="Vector: pBluescriptII(KS+); Site_1: EcoRI; Site_2: NotI; Single pass sequencing. Normalised library constructed from pig uterus."

Query Match 0.5%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CCACCGCG 18
|||||
1 CCACCGCG 9

Db 1 CCACCGCG 9

RESULT 38 BM396384 11 bp mRNA linear EST 17-JAN-2002
BM396384 5009-0-2-H08.t.2 Chilcoat/Turkewitz cDNA (large fraction)

ACCESSION BM396384

VERSION BM396384.1 GI:18196422

KEYWORDS EST.

SOURCE Tetrahymena thermophila

ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomida; Tetrahymenina; Tetrahymenidae; Tetrahymena.

REFERENCE 1 (bases 1 to 11)
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orías,E., Kirk,K.E., Frankel,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)

JOURNAL Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seg primer: T3.

COMMENT Location/Qualifiers

1..11
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_id="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

FEATURES source

1..11
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001808_P05"
/tissue_type="uterus"
/clone_id="CSEORAN04"
/note="Vector: pBluescriptII(KS+); Site_1: EcoRI; Site_2: NotI; Single pass sequencing. Normalised library constructed from pig uterus."

Query Match 0.5%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCCACCGCG 17
|||||
11 GCCACCGCG 3

Db 11 GCCACCGCG 3

RESULT 39 BM397892 11 bp mRNA linear EST 17-JAN-2002
BM397892 5009-0-38-F04.t.1 Chilcoat/Turkewitz cDNA (large fraction)

ACCESSION BM397892

VERSION BM397892.1 GI:18197945

KEYWORDS EST.

SOURCE
ORGANISM Tetrahymena thermophila
REFERENCE Tetrahymena thermophila
AUTHORS Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenotomastix; Tetrahymenina; Tetrahymenidae; Tetrahymena. 1 (bases 1 to 11)
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel, J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells Unpublished (2002)
JOURNAL
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers

FEATURES
source 1..11
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."
Query Match 0.5%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GCCACCGCG 17
Db 11 GCCACCGCG 3

RESULT 40
CF300559 11 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--05-B09.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--05-B09, mRNA
sequence.
ACCESSION CF300559
VERSION CF300559.1 GI:33672320
KEYWORDS EST
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 11)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, U.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Yonsei University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source 1..11
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--05-B09"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
Query Match 0.5%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1673 AAATAAAA 1681
Db 3 AAATAAAA 11

RESULT 41
CF543159 11 bp mRNA linear EST 22-SEP-2003
LOCUS S014678-024-030-006-SP6 MP12-ADIS-024-leaf Beta vulgaris cDNA clone
DEFINITION 024-030-006 5-PRIME, mRNA sequence.
ACCESSION CF543159
VERSION CF543159.1 GI:34891599
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 11)
Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfach, M., Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
12472698
Contact: Weishaar B
ADIS DNA core facility at MP12
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert length: 11 Std Error: 0.00
Plate: 30 row: 0 column: 06
Seq primer: SP6.
Location/Qualifiers

FEATURES
source 1..11
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:936619"
/db_xref="taxon:161934"
/tissue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MP12-ADIS-024-leaf"
/note="Vector: PCWSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleimanzelebener Saatnucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-SalI-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-BEET project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Qy 788 AGAAAGTGT 796
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 10 AGAAGTCT 2

RESULT 42
LOCUS DUT73106/c

DEFINITION DUT73106 11 bp DNA linear GSS 27-JAN-2006
ABR12073.g3 HF70_10-07-02 uncultured marine microorganism
HF70_10-07-02 genomic clone HF0070_029A08, genomic survey sequence.

ACCESSION DUT73106
VERSION DUT73106
KEYWORDS GSS.
SOURCE unclashed marine microorganism HF70_10-07-02
unclashed sequences; environmental samples.

ORANISM 1 (bases 1 to 11)
AUTHORS Delong,E.F., Preston,C.M., Mincer,T., Rich,V., Hallam,S.J.,
Frigaard,N.U., Martinez,A., Sullivan,M., Edwards,R., Chisholm,S.W.
and Karl,D.M.

REFERENCE Comparative genomics reveals ecological trends in stratified
microbial communities in the ocean's interior
Science (2006) in press
Contact: Susan Lucas, Alex Copeland, Sam Pitluck, Alla Lapidus,
Kerrie Barry, Tijana Glavinadelirio, David Bruce, Paul Richardson
and Edward Delong

JOURNAL US DOE Joint Genome Institute
US DOE Joint Genome Institute
2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA
Tel: 617-253-5271
Fax: 617-253-2679

COMMENT Email: pmlrichardson@lbl.gov; delong@mit.edu
Sample Date: 10/7/2002 Coordinates: 22.45 N, 158 W Depth 70 m
Temperature: 24.93 C Salinity: 35.21 psu Oxygen: 217.4 umol/Kg
Class: foamid ends.

FEATURES
source
1..11
/organism="uncultured marine microorganism HF70_10-07-02"
/mol_type="genomic DNA"
/db_xref="taxon:36114"
/clone="HF0070_029A08"
/cell_type="marine picoplankton, less than 1.8 um, greater
than 0.22 um fraction"
/clone_lib="HF70_10-07-02"
/note="Vector: pCC1FOS; North Pacific Subtropical Gyre
(Hawaii) picoplankton genomic formid DNA library prepared
from marine picoplankton in the less than 1.6 um, greater
than 0.22 um fraction. Picoplankton collected at 70 m
depth on 10/7/2002, Coordinates: 22.45 N, 158 W Sample
Date: 10/7/2002 Coordinates: 22.45 N, 158 W Depth 70 m
Temperature: 24.93 C Salinity: 35.21 psu Oxygen: 217.4
umol/Kg"

Query Match 0.5%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 947 TGTGCAAA 955
|||||
10 TGTGCAAAA 2

RESULT 43
LOCUS CF337407
DEFINITION JMT--07-N08.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--07-N08, mRNA sequence.

ACCESSION CF337407
VERSION CF337407.1 GI:33823214
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

REFERENCE clade; Ehrhartoideae; Oryzaceae; Oryza.
AUTHORS 1 (bases 1 to 12)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..12
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/culivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--07-N08"
/issue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis jasmonic acid Carboxyl
methyltransferase overexpression line."

Query Match 0.5%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 929 TCTCTGCCA 937
|||||
3 TCTCTGCCA 11

RESULT 44
LOCUS AM075481
DEFINITION AM075481 Chicken immune 5 - CSEGRBN30 Gallus gallus cDNA clone
C0000798B15.T7, mRNA sequence.

ACCESSION AM075481
VERSION AM075481.1 GI:75476052
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 13)
Smith,J., Speed,D., Hocking,P., Talbot,R.T., Degen,W., Schijns,V.,
Glase,E.J. and Burt,D.
TITLE Development of a chicken 5k array
JOURNAL Unpublished (2005)
COMMENT Contact: Smith J
Genetics and Genomics
Roelin Institute
Roelin, Midlothian, EH25 9PS, UNITED KINGDOM
Vector pBluescript II KS(+). R. Site1: EcoRI. R. Site2: NotI 5' Seq
Primer T7 Strain Lohman Brown layer/Ross 308 broiler cross This
normalized library was constructed from 1 million independent
clones. cDNA synthesis was initiated using an oligo(dT) primer,
using methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA was
blunted, ligated to NotI adapters, digested with EcoRI,
size-selected, and cloned into the NotI and EcoRI compatible sites
of a custom modified MCS of the pBluescript (KS+) vector. The
library was normalized in 2 rounds using conditions adapted from
Scores et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome
Research 6 (1996): 791, except that a significantly longer

reannealing hybridization was used. Clones available from the ARK-Genomics Centre for Functional Genomics in Farm Animals, Roslin Institute, Midlothian, EH25 9PS, UK see www.ark-genomics.org.

FEATURES

Source

```
1..13
/organism="Gallus gallus"
/mol_type="mrna"
/db_xref="taxon:9031"
/cclone="C0000798E15.T7"
/tissue_type="thymus"
clone_lib="Chicken immune 5 - CSE0REN30"0"
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Query Match	0.5%	Score 8.8;	DB 1,	Length 13;
Best Local Similarity	83.3%	Pred. No. 70;		
Matches 10;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

QY	221	TCCTCCCGGTGG	232
Db	1	TCCCCGCGGTGG	12

RESULT 45
BM396557

DEFINITION 5009-0-22-F07.t.c.1 Chilcoat/Turkewitz CDNA (1) Tetrahymena thermophila cDNA, mRNA sequence

ACCESSION	BM39655 /	GI:18196625
VERSION	BM39655.1	
KEYWORDS	EST.	
SOURCE	Tetrahymena	thermophila
ORGANISM	Tetrahymena	thermophila

REFERENCE	TITLE	JOURNAL	COMMENT
1 (bases 1 to 13) Turkewitz, A. P., Karrer, R. M., Jahn, C., Orias, E., Kirk, K. E., Frankel, J., and Klobuchner, L. EST from <i>Tetrahymena thermophila</i> , strain CU428.1, growing cells Unpublished (2002) Contact: Turkewitz AP			

COMMENT

FEATURES

Source

```

/organism="Tetranychus thermophilus"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_id="Chilcoat/Turkewitz cDNA (large fraction)"
/notes="Vector: Bluescript/P2 SK+; details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98 : 8709-8713."

```

Query Match	0.5%;	Score 8.8;	DB 1;	Length 13;
Best Local Similarity	83.3%;	Pred. No. 70;		
Matches 10;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

QY 579 GACGGCTGTGC 590
||| ||| |||
Db 1 GACCGCGGTGC 12

RESULT 4
AM075254

LOCUS	AM075254	14 bp	RNA	linear	EST 14-SEP-2005
DEFINITION	AM075254	Chicken immune 1 - CSEORBL08	Gallus gallus	CDNA clone	
	C0000222E05.T7, mRNA sequence.				

ACCESSION	AM075254	-
VERSION	AM075254.1	GI:75475695

KEYWORDS
SOURCE

ORGANISM

EST.
Gallus gallus (chicken)
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
Archosauavis; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
19141

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (Pages 1 to 14)	Smith, J., Speed, B., Hocking, P., Talbot, R. T., Degen, W., Schijns, V., Glass, E. J., and Burt, D.	Development of a chicken 5k array	Unpublished (2005)	Contact: Smith J

FEATURES

Source

```

1..14
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Lohman Brown layer/Ross 308 broiler cross"
/db_xref="Taxon:9031"
/clone="C0000222E05_T7"
/tissue_type="Bursa_spleen, Peyer's patch (pooled)"
/clone_lib="Chicken immune 1 - CGRRL08"
/note="Vector: pBluescript II KS(+), Site_1: EcoRI,
Site_2: NotI"

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Query Match 0.5%; Score 8.8; DB 1; Length 14;
Best Local Similarity .83.3%; Pred. No. 87;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY	221	TCCTCCCGGTGG	232
Db	2	TCCCCGCGGTGG	13

RESULT 47
ATH521816/

LOCUS ATH521816 15 bp DNA linear GSS-08-FEB-2000
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone
 279D04, genomic survey sequence.

Accession number: AJ521816.1
GI: 26790052
Version: GSS; left border; T-DNA flanking sequence
Keywords: Arabidopsis thaliana (thale cress)
Source: Arabidopsis thaliana
Organism: Arabidopsis thaliana

REFERENCE	AUTHORS	TITLE
1	Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechthold, N., Crnaud, C., Derose, R., Pelletier, G., Lepoint, L., Caboche, M. and Lecharny, A.	T-DNA integration into the Arabidopsis genome depends on sequence

JOURNAL	Or ple-association sites
EMBO Rep. 3 (12), 1152-1157 (2002)	
PUBMED	12446565
REFERENCE	2 (bases 1 to 15)
AUTHORS	Balzerque, S.
TITLE	Direct Submission
JOURNAL	Submitted (21-NOV-2002)
COMMENT	Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE PCR was performed on DNA from transformants of Arabidopsis thaliana

plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program "Genoplante" (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

FEATURES

source

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1..15
  /organism="Arabidopsis thaliana"
  /mol_type="genomic DNA"
  /cultivar="Wassilewskija"
  /db_xref="taxon:3702"
  /clone="279D04"
  /clone_1lb="Arabidopsis thaliana T-DNA insertion lines"
  /ecotype="Wassilewskija"
misc_feature
  1..15 "T-DNA flanking sequence
  left border"
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Query Match 0.5%; Score 8.6; DB 1; Length 15;
Best Local Similarity 73.3%; Pred. No. 98;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1004 ACATCTTCTCTCTC 1018
Db 15 AAACCTCTCAGCC 1

RESULT 48

BM396082 10 bp mRNA linear EST 17-JAN-2002
LOCUS 5009-0-16-H04.t.1 Chilcoat/Turkewitz cDNA (large fraction)
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM396082
VERSION BM396082.1 GI:18196135
KEYWORDS EST.
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
1 (bases 1 to 10)
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)

REFERENCE
AUTHORS Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

COMMENT

FEATURES
source Location/Qualifiers

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1..10
  /organism="Tetrahymena thermophila"
  /mol_type="mRNA"
  /strain="CU428.1"
  /db_xref="taxon:5911"
  /clone_1lb="Chilcoat/Turkewitz cDNA (large fraction)"
  /note="Vector: Bluescript SK+; Details on library
  preparation can be found in Chilcoat and Turkewitz (2001)
  Proc. Natl. Acad. Sci USA, 98: 8709-8713."
```

Query Match 0.5%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CCACCGCGG 19

Db 10 CCACCGCGG 1

RESULT 49 10 bp mRNA linear EST 15-AUG-2003
CF304081
LOCUS ABF1--04-A07.g1 ABF3-overexpressing transgenic rice lambda phage
DEFINITION cDNA library (ABF1) Oryza sativa (japonica cultivar-group) cDNA
clone ABF1--04-A07, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CF304081.1 GI:33675842
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 10)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
JOURNAL
COMMENT Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

```
1..10
  /organism="Oryza sativa (japonica cultivar-group)"
  /mol_type="mRNA"
  /cultivar="Nackdong"
  /db_xref="taxon:39947"
  /clone="ABF1--04-A07"
  /issue_type="leaf"
  /tissue_type="leaf"
  /dev_stage="14 days after germination"
  /lab_host="E.coli SOLR"
  /clone_1lb="ABF3-overexpressing transgenic rice lambda
  phage cDNA library (ABF1)"
  /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
  XhoI; Leaf was dried for 2hrs. cDNA was inserted into
  lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end
  with XhoI site. mRNA was prepared from ABA-responseive
  element binding transcription factor 3 overexpression
  line."
```

Query Match 0.5%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1012 TTCTCTCTGC 1021
Db 10 TTCTCTCTGC 1

RESULT 50 10 bp mRNA linear EST 18-AUG-2003
CF333615
LOCUS JMT--02-J09.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
DEFINITION library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--02-J09, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CF333615.1 GI:33815525
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 10)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 TITLE Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 JOURNAL Large-scale Sequencing Analysis of Rice ESTs
 COMMENT Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source Location/Qualifiers
 1..10
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="JMT-02-C04"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="AtUMT-overexpressing transgenic rice plasmid
 cDNA library (JMT)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis thaliana Carboxyl
 methyltransferase overexpression line."

Query Match 0.5%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 25;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 401 GGACGATGAC 410
 Db 1 GGACGATGAC 10

RESULT 51
 CF336905 10 bp mRNA linear EST 18-AUG-2003
 LOCUS JMT--07-C04.g1 AtUMT-overexpressing transgenic rice plasmid cDNA
 DEFINITION library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
 JMT--07-C04, mRNA sequence.
 ACCESSION CF336905
 VERSION CF336905.1 GI:33822181
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 BUKARYOTA; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep
 clade; Eriophytidae; Oryzae; Oryza.
 1 (bases 1 to 10)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source Location/Qualifiers
 1..10
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="JMT-07-C04"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"

1..10
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="JMT-07-C04"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"

/clone_lib="AtUMT-overexpressing transgenic rice plasmid
 cDNA library (JMT)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis thaliana Carboxyl
 methyltransferase overexpression line."

Query Match 0.5%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 25;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 75 AAAAGAGTGC 84
 Db 1 AAAAGAGTGC 10

RESULT 52
 CF336905/c 10 bp mRNA linear EST 18-AUG-2003
 LOCUS JMT--07-C04.g1 AtUMT-overexpressing transgenic rice plasmid cDNA
 DEFINITION library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
 JMT--07-C04, mRNA sequence.
 ACCESSION CF336905
 VERSION CF336905.1 GI:33822181
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 BUKARYOTA; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep
 clade; Eriophytidae; Oryzae; Oryza.
 1 (bases 1 to 10)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source Location/Qualifiers
 1..10
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="JMT-07-C04"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="AtUMT-overexpressing transgenic rice plasmid
 cDNA library (JMT)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis thaliana Carboxyl
 methyltransferase overexpression line."

Query Match 0.5%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 25;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 411 GAACATTTT 420
 Db 10 GAACATTTT 1

RESULT 53
 CV933324/c 10 bp mRNA linear EST 25-JAN-2005
 LOCUS P4pccm 0785 mating of 88069 (A1) and 618 (A2) Phycophthora infestans
 DEFINITION cDNA, mRNA sequence.

ACCESSION	CV933324
VERSION	CV933324.1
KEYWORDS	GI:58122939
SOURCE	EST.
ORGANISM	Phytophthora infestans (potato late blight agent)
REFERENCE	Phytophthora infestans Eukaryota; stramenopiles; Oomycetes; Peronosporales; Phytophthora. 1 (bases 1 to 10)
AUTHORS	Randall,T., Dwyer,R.A., Huitema,E., Beyer,K., Cvitanich,C., Kelkar,H., Fong,A.M., Gates,K., Roberts,S., Yatzkan,E., Gaffney,T., Law,M., Testa,A., Torto-Alalibo,A., Zhang,M., Zheng,L., Mueller,E., Windsap,J., Binder,A., Birch,P.R.J., Gisi,U., Govers,F., Gow,N.A., Mauch,F., van West,P., Maugh,M.E., Yu,J., Bolter,T., Kamoun,S., Lam,S.T. and Judelson,H.S.
TITLE	Large-scale gene discovery in the oomycete Phytophthora infestans reveals likely components of phytopathogenicity shared with true fungi
JOURNAL	Mol. Plant-Microbe Interact. 18 (3), 229-243 (2005)
PUBMED	15782637
COMMENT	Contact: Judelson HS Department of Plant Pathology University of California Webster Hall, Riverside, CA 92521, USA Tel: 909 787 4199 Fax: 909 787 4294
FEATURES	source
Query Match	0.5%; Score 8.4; DB 1; Length 10;
Best Local Similarity	90.0%; Pred.No.25;
Matches	9; Conservative 0; Mismatches 1; Indels 0; Gaps 0.
Dq	196 ACGCCTAGCT 205 10 ACGCCAGCT 1
RESULT 54	CV933903 10 bp mRNA linear EST 25-JAN-2005
LOCUS	PMPCm_5366 mating of 88069 (A1) and 618 (A2) Phytophthora
DEFINITION	infestans cDNA, mRNA sequence.
ACCESSION	CV933903
VERSION	CV933903.1
KEYWORDS	GI:58123518
ORGANISM	EST.
REFERENCE	Phytophthora infestans (potato late blight agent) Phytophthora infestans Eukaryota; stramenopiles; Oomycetes; Peronosporales; Phytophthora. 1 (bases 1 to 10)
AUTHORS	Randall,T., Dwyer,R.A., Huitema,E., Beyer,K., Cvitanich,C., Kelkar,H., Fong,A.M., Gates,K., Roberts,S., Yatzkan,E., Gaffney,T., Law,M., Testa,A., Torto-Alalibo,A., Zhang,M., Zheng,L., Mueller,E., Windsap,J., Binder,A., Birch,P.R.J., Gisi,U., Govers,F., Gow,N.A., Mauch,F., van West,P., Maugh,M.E., Yu,J., Bolter,T., Kamoun,S., Lam,S.T. and Judelson,H.S.
TITLE	Large-scale gene discovery in the oomycete Phytophthora infestans reveals likely components of phytopathogenicity shared with true fungi
JOURNAL	Mol. Plant-Microbe Interact. 18 (3), 229-243 (2005)
PUBMED	15782637
COMMENT	Contact: Judelson HS Department of Plant Pathology University of California Webster Hall, Riverside, CA 92521, USA Tel: 909 787 4199 Fax: 909 787 4294

FEATURES		Email: howard.judelson@ucr.edu.	
source		Location/Qualifiers	
1..10		/organism="Phytophthora infestans"	
		/mol_type="mRNA"	
		/strain="88069 and 618"	
		/db_xref="taxon:4787"	
		/seq="A1 and A2"	
		/clone_lib="mating of 88069 (A1) and 618 (A2)"	
		/note="Vector: pSPORT1"	
Query Match	0.5%;	Score 8.4;	DB 1; Length 10;
Best Local Similarity	90.0%;	Pred. No. 25;	
Matches	9;	Conservative	0; Mismatches 1; Indels 0; Gaps 0;
QY	1279	ACCATCTCCA	1288
Db	10	ACGAGCTCCA	1
RESULT 55			
CV998934/c		10 bp	mRNA linear EST 03-DEC-2004
LOCUS			
DEFINITION	CV998934		iv47e09.b1 Right Cardiac Ventricle (DOGEST6) Canis familiaris cDNA.
ACCESSION	CV998934		mRNA sequence.
VERSION	CV998934.1		GI:56269265
KEYWORDS	EST.		
SOURCE	Canis familiaris		
ORGANISM	Canis familiaris		
	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;		
	Canis.		
REFERENCE	1 (bases 1 to 10)		
AUTHORS	Balla, V.S., Nascimento, L.U. and McCombie, W.R.		
TITLE	ESTs from Canis familiaris right cardiac ventricle (dog)		
JOURNAL	Unpublished (2004)		
COMMENT	Contact: W. Richard McCombie Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory PO Box 100, Cold Spring Harbor, NY 11724, USA Tel: 516 367 8884 Fax: 516 367 8874 Email: mcombie@cshl.org.		
FEATURES			
source			
	Location/Qualifiers		
	1..10		
	/organism="Canis familiaris"		
	/mol_type="mRNA"		
	/db_xref="taxon:9615"		
	/seq="unknown"		
	/tissue_type="Cardiac muscle"		
	/dev_stage="3 month old normal canine"		
	/lab_host="XL10 Gold"		
	/clone_lib="Right Cardiac Ventricle (DOGEST6)"		
	/note="Organ: Heart; Vector: pBluescript II SK; Site 1: EcoRI; Site 2: XhoI; Library constructed using pBluescript XR kit from Stratagene. Cloned cDNA was size selected between 1-3 kb. Tissue supplied by Mark Haekins VMD, PhD, Pathology and Medical Genetics, School of Veterinary Medicine, University of Pennsylvania, 3800 Spruce Street, Philadelphia, PA 19104-6051"		
Query Match	0.5%;	Score 8.4;	DB 1; Length 10;
Best Local Similarity	90.0%;	Pred. No. 25;	
Matches	9;	Conservative	0; Mismatches 1; Indels 0; Gaps 0;
QY	1294	GTGGGGGCC	1303
Db	10	GGGGGGGCC	1
RESULT 56			
DN953871/c			

LOCUS DN953871 10 bp mRNA linear EST 04-MAY-2005
 DEFINITION it65e04.g1 Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA
 sequence.
 ACCESSION DN953871
 VERSION DN953871.1 GI:63026009
 KEYWORDS EST.
 SOURCE Gnetum gnemon
 ORGANISM Gnetum gnemon
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales.
 1 (bases 1 to 10)
 Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,
 O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W.,
 Bentley, P., Coruzzi, G., and Stevenson, D.
 Expressed tag sequences from Gnetum female cone (NYBG)
 Unpublished (2003)
 TITLE Lita Annenberg Hazen Genome Sequencing Center
 JOURNAL Cold Spring Harbor Laboratory
 COMMENT PO Box 100, Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mcombie@cshl.org
 Seq primer: -21M3UnivRev.
 FEATURES
 source
 1..10
 Location/Qualifiers
 /organism="Gnetum gnemon"
 /mol_type="mRNA"
 /db_xref="taxon:3382"
 /sex="female"
 /clone_1id="Gnetum female cone (NYBG)"
 /note="Organ: mature, unfertilized reproductive strobili;
 Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Date:
 Completed 02/11/02, submitted for sequencing 02/12/02.
 Library: Stratagene ZAP Express cDNA Synthesis Kit. The
 library was size-fractionated to enrich for large inserts.
 Sample: NYBG accession number #436/84"
 Query Match 0.5%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 25;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1339 CCTCGTCC 1348
 Db 10 CCTCGTCC 1
 RESULT 57
 DR063352 10 bp mRNA linear EST 06-JUN-2005
 LOCUS ip64b02.g2 Ginkgo megasporophyll (NYBG) Ginkgo biloba cDNA 3', mRNA
 DEFINITION sequence.
 ACCESSION DR063352
 VERSION DR063352.1 GI:66986920
 KEYWORDS EST.
 SOURCE Ginkgo biloba (maidenhair tree)
 ORGANISM Ginkgo biloba
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
 1 (bases 1 to 10)
 Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,
 O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W.,
 Bentley, P., Coruzzi, G., and Stevenson, D.
 Expressed tag sequences from Ginkgo megasporophyll (NYBG)
 Unpublished (2005)
 TITLE Lita Annenberg Hazen Genome Sequencing Center
 JOURNAL Cold Spring Harbor Laboratory
 COMMENT PO Box 100, Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mcombie@cshl.org
 Seq primer: -21M3UnivRev.

FEATURES
 source
 Location/Qualifiers
 1..10
 /organism="Ginkgo biloba"
 /mol_type="mRNA"
 /db_xref="taxon:3311"
 /sex="female"
 /clone_1id="Ginkgo megasporophyll (NYBG)"
 /note="Organ: megasporophyll; Vector: pBK-CMV; Site 1:
 XhoI; Site 2: Eco RI; Stratagene ZAP Express cDNA
 Synthesis Kit. The library was size-fractionated to enrich
 for large inserts."
 Query Match 0.5%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 25;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1339 CCTCGTCC 1348
 Db 10 CCTCGTCC 1
 RESULT 58
 DW386439 10 bp mRNA linear EST 14-JAN-2006
 LOCUS LRAGB02322 Liver regeneration after partial hepatectomy Rattus
 DEFINITION norvegicus cDNA, mRNA sequence.
 ACCESSION DW386439
 VERSION DW386439.1 GI:84890561
 KEYWORDS EST.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Muridae; Murinae; Rattus.
 1 (bases 1 to 10)
 Xu, C.S.
 Liver regeneration after PH
 Unpublished (2003)
 TITLE Contact: Cun-Shuan Xu
 JOURNAL Henan Bioengineering Key Lab
 COMMENT No. 148 Jianshe Road, Xinxiang City, P.R.China
 Tel: 00863733328084
 Fax: 00863733326524
 Email: xucse@x263.net.
 FEATURES
 source
 Location/Qualifiers
 1..10
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /db_xref="taxon:10116"
 /tissue_type="liver"
 /clone_1id="Liver regeneration after partial hepatectomy"
 Query Match 0.5%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 25;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 813 TGTGCTGTC 822
 Db 1 TGTGCTGTC 1
 RESULT 59
 CL652677 10 bp DNA linear GSS 09-JUL-2004
 LOCUS PRI0115C.A09 - PRI0115C.B21 (10) Mixed stage foetid library of P.
 DEFINITION pacificus var. California Pristionchus pacificus genomic, genomic
 survey sequence.
 ACCESSION CL652677
 VERSION CL652677.1 GI:50131455
 KEYWORDS GSS.
 SOURCE Pristionchus pacificus
 ORGANISM Pristionchus pacificus

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT

Eukaryota; Metazoa; Nematoda; Chromodorea; Diplogasterida;
Noodiologasteridae; Pristionchus.
1 (bases 1 to 10)
Srinivasan,U., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
Appads: an Acce database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
14681447
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.

FEATURES
source
1. 10
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pBf105-5 Fosmid vector"

Query Match 0.5%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 887 GTGAGATCCC 896
||| |||||
10 GTGGGATCCC 1

RESULT 60
CL694909
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT

CL694909 10 bp DNA linear GSS 10-JUN-2004
PI10165C.BR (10) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
CL694909
CL694909.1 GI:50216817
GSS.
Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromodorea; Diplogasterida;
Noodiologasteridae; Pristionchus.
1 (bases 1 to 10)
Srinivasan,U., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
Appads: an Acce database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
14681447
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.

FEATURES
source
1. 10
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT

/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pBf105-5 Fosmid vector"

Query Match 0.5%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1561 TGGGTTAGCG 1570
|||||
1 TGGGTTAGCG 10

RESULT 61
DX040234/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT

DX040234 10 bp DNA linear GSS 10-JAN-2006
KBRB039023R KBRB, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBRB039023, genomic survey
sequence.
DX040234
DX040234.1 GI:84734531
GSS.
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 10)
Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
End sequence of Brassica rapa BamHI (KBRB) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa esp. pekinensis BamHI BAC clone
KBRB039023
Seq primer: M13 Reverse
Class: BAC ends.

FEATURES
source
1. 10
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chilfu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBRB039023"
/lab_host="E.coli DH10B"
/clone_lib="KBRB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp
pekinensis var. Chilfu BAC library (KBRB BAC) is provided
by Yong-Pyo Lim (CNU)."

Query Match 0.5%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 214 GATACGCTCC 223
|||||
10 GATACGCTCC 1

RESULT 62
AJ592517/c
LOCUS
DEFINITION

AJ592517 10 bp DNA linear GSS 15-JAN-2004
Arabidopsis thaliana T-DNA flanking sequence, right border, clone
621G09, genomic survey sequence.

ACCESSION AJ592517
 VERSION AJ592517.1 GI:37942141
 KEYWORDS GSS; right border; T-DNA flanking sequence.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
 AUTHORS Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepointec, L., Caboche, M. and Lecharny, A.
 T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
 EMBO Rep. 3 (12), 1152-1157 (2002)

JOURNAL
 PUBLISHED 12446565
 REFERENCE 2 (bases 1 to 10)
 AUTHORS Balzerque, S.
 TITLE Direct Submission
 JOURNAL Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
 PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

FEATURES
 source
 1..10
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /db_xref="taxon:3702"
 /clone="621G09"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="Wassilewskija"
 /note="T-DNA flanking sequence
 left border"

misc_feature
 1..10
 /note="T-DNA flanking sequence
 right border"

Query Match 0.5%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 25;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 990 CTGGCTGCC 999
 |||||
 |||||
 10 CTGGCGGCC 1

Db 10 CTGGCGGCC 1

RESULT 63
 AJ593578 10 bp DNA linear GSS 15-JAN-2004
 LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone 383D03, genomic survey sequence.
 ACCESSION AJ593578
 VERSION AJ593578.1 GI:37943202
 KEYWORDS GSS; left border; T-DNA flanking sequence.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
 AUTHORS Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepointec, L., Caboche, M. and Lecharny, A.
 T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
 EMBO Rep. 3 (12), 1152-1157 (2002)

JOURNAL
 PUBLISHED 12446565
 REFERENCE 2 (bases 1 to 10)
 AUTHORS Balzerque, S.
 TITLE Direct Submission
 JOURNAL Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
 PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics

PUBLISHED 12446565
 REFERENCE 2 (bases 1 to 10)
 AUTHORS Balzerque, S.
 TITLE Direct Submission
 JOURNAL Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
 PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

FEATURES
 source
 1..10
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /db_xref="taxon:3702"
 /clone="383D03"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="Wassilewskija"
 /note="T-DNA flanking sequence
 left border"

misc_feature
 1..10
 /note="T-DNA flanking sequence
 left border"

Query Match 0.5%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 25;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 496 AACGATGCT 505
 |||||
 |||||
 1 AACGATGAT 10

Db 1 AACGATGAT 10

RESULT 64
 AJ594650/c 10 bp DNA linear GSS 15-JAN-2004
 LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone 403C10, genomic survey sequence.
 ACCESSION AJ594650
 VERSION AJ594650.1 GI:37944274
 KEYWORDS GSS; left border; T-DNA flanking sequence.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
 AUTHORS Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepointec, L., Caboche, M. and Lecharny, A.
 T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
 EMBO Rep. 3 (12), 1152-1157 (2002)

JOURNAL
 PUBLISHED 12446565
 REFERENCE 2 (bases 1 to 10)
 AUTHORS Balzerque, S.
 TITLE Direct Submission
 JOURNAL Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
 PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics

program 'Genoplatne' (<http://www.genoplatne.com> and
<http://genoplatne-info.infobiogen.fr>).

FEATURES

source

1..10
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /db_xref="taxon:3702"
 /clone="403C10"
 /clone_1lb="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="Wassilewskija"
 1..10
 /note="T-DNA flanking sequence
 left border"

Query Match 0.5%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 25;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1572 AAACATCCA 1581
 Db 10 AAACATCGA 1

RESULT 65
 AJ600523 10 bp DNA linear GSS 15-JAN-2004
 LOCUS Arabidopsis thaliana T-DNA flanking sequence, right border, clone
 DEFINITION 508B03, genomic survey sequence.
 ACCESSION AJ600523
 VERSION AJ600523.1 GI:37950151
 KEYWORDS GSS; right border; T-DNA flanking sequence.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1
 Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F.,
 Chauvin, S., Bechtold, N., Cruaud, C., Dehose, R., Pelletier, G.,
 Lepoint, L., Caboche, M., and Lecharny, A.
 T-DNA integration into the Arabidopsis genome depends on sequences
 of pre-insertion sites
 EMBO Rep. 3 (12), 1152-1157 (2002)

JOURNAL PUBMED 12446565
 REFERENCE 2 (bases 1 to 10)
 Balzerque, S.
 Direct Submission
 Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
 Gaston Creteil, 91057 Evry cedex, FRANCE

COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana
 plants from INRA (Versailles). The DNA fragment(s) resulting from
 the PCR were directly sequenced from the left or the right border
 to determine the genomic sequence flanking the insertion. T-DNA
 derived sequences were removed. Information to order the
 corresponding mutant line and a link to a database providing a
 graphical display of the insertion site are available at
<http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has
 been generated in the framework of the French plant genomics
 program 'Genoplatne' (<http://www.genoplatne.com> and
<http://genoplatne-info.infobiogen.fr>).

FEATURES

source

1..10
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /db_xref="taxon:3702"
 /clone="508B03"
 /clone_1lb="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="Wassilewskija"
 1..10
 /note="T-DNA flanking sequence
 right border"

Query Match 0.5%; Score 8.4; DB 1; Length 10;

Best Local Similarity 90.0%; Pred. No. 25;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1591 CAAAATCT 1600
 Db 1 CAAAATTT 10

RESULT 66
 ATH521087 10 bp DNA linear GSS 08-FEB-2006
 LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone
 DEFINITION 052D09, genomic survey sequence.
 ACCESSION AJ521087
 VERSION AJ521087.1 GI:26789323
 KEYWORDS GSS; left border; T-DNA flanking sequence.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

AUTHORS

1
 Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F.,
 Chauvin, S., Bechtold, N., Cruaud, C., Dehose, R., Pelletier, G.,
 Lepoint, L., Caboche, M., and Lecharny, A.
 T-DNA integration into the Arabidopsis genome depends on sequences
 of pre-insertion sites
 EMBO Rep. 3 (12), 1152-1157 (2002)

REFERENCE

AUTHORS

2 (bases 1 to 10)
 Balzerque, S.
 Direct Submission
 Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue
 Gaston Creteil, 91057 Evry cedex, FRANCE

COMMENT

PCR was performed on DNA from transformants of Arabidopsis thaliana
 plants from INRA (Versailles). The DNA fragment(s) resulting from
 the PCR were directly sequenced from the left or the right border
 to determine the genomic sequence flanking the insertion. T-DNA
 derived sequences were removed. Information to order the
 corresponding mutant line and a link to a database providing a
 graphical display of the insertion site are available at
<http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has
 been generated in the framework of the French plant genomics
 program 'Genoplatne' (<http://www.genoplatne.com> and
<http://genoplatne-info.infobiogen.fr>).

FEATURES

source

1..10
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /cultivar="Wassilewskija"
 /db_xref="taxon:3702"
 /clone="052D09"
 /clone_1lb="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="Wassilewskija"
 1..10
 /note="T-DNA flanking sequence
 left border"

Query Match 0.5%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 25;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1595 AATTCAT 1604
 Db 10 AAACCTCAT 1

RESULT 67
 ATH521360 10 bp DNA linear GSS 08-FEB-2006
 LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone
 DEFINITION 053G10, genomic survey sequence.
 ACCESSION AJ521360

VERSION AJ521360.1 GI:26789596
 KEYWORDS GSS; left border; T-DNA flanking sequence.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; eudicotyledons; core eudicotyledons; rosids; eurosid II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
 AUTHORS Brunaud,V., Balergue,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., Derose,R., Pelletier,G., Lepintec,L., Caboche,M. and Lecharny,A.
 TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
 JOURNAL EMO Rep. 3 (12), 1152-1157 (2002)
 PUBMED 12446565
 REFERENCE 2 (bases 1 to 10)
 AUTHORS Balergue,S.
 TITLE Direct Submission
 JOURNAL Submitted (21-NOV-2002) Balergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
 COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplatane' (<http://www.genoplatane.com> and <http://genoplatane-info.infobiogen.fr>).
 FEATURES
 source location/Qualifiers
 1..10
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /cultivar="Wassilewskija"
 /db_xref="taxon:3702"
 /clone="053G10"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="Wassilewskija"
 /note="T-DNA flanking sequence
 left border"

misc_feature
 1..10
 /note="T-DNA flanking sequence
 left border"

Query Match 0.5%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 25;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 775 AACAAATTT 784
 |||||
 1 AACAAATTT 10

Db

RESULT 68
 AJ590935 13 bp DNA linear GSS 15-JAN-2004
 LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone 577B08, genomic survey sequence.
 ACCESSION AJ590935
 VERSION AJ590935.1 GI:37940559
 KEYWORDS GSS; left border; T-DNA flanking sequence.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; eudicotyledons; core eudicotyledons; rosids; eurosid II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
 AUTHORS Brunaud,V., Balergue,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., Derose,R., Pelletier,G., Lepintec,L., Caboche,M. and Lecharny,A.
 TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
 JOURNAL EMO Rep. 3 (12), 1152-1157 (2002)

PUBMED 12446565
 REFERENCE 2 (bases 1 to 13)
 AUTHORS Balergue,S.
 TITLE Direct Submission
 JOURNAL Submitted (23-OCT-2003) Balergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
 COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplatane' (<http://www.genoplatane.com> and <http://genoplatane-info.infobiogen.fr>).
 FEATURES
 source location/Qualifiers
 1..13
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /db_xref="taxon:3702"
 /clone="577B08"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="Wassilewskija"
 /note="T-DNA flanking sequence
 left border"

misc_feature
 1..13
 /note="T-DNA flanking sequence
 left border"

Query Match 0.5%; Score 8.4; DB 1; Length 13;
 Best Local Similarity 90.0%; Pred. No. 87;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 374 GAATCATCTT 383
 |||||
 1 GAATCATCTT 10

Db

RESULT 69
 AL037095 8 bp mRNA linear EST 06-JUL-2004
 LOCUS DKFZP564I2064.r1.564 (synonym: hfbp2) Homo sapiens cDNA clone DKFZP564I2064, mRNA sequence.
 ACCESSION AL037095
 VERSION AL037095.1 GI:49681937
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 8)
 Duesterhoeft,A., lauber,J., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
 EST (Duesterhoeft, et al.)
 JOURNAL Unpublished (1999)
 COMMENT Contact: MIPS
 MIPS

REFERENCE
 AUTHORS Duesterhoeft,A., lauber,J., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
 TITLE EST (Duesterhoeft, et al.)
 JOURNAL Unpublished (1999)
 COMMENT Contact: MIPS
 MIPS

Ingolstaedter Landstr.1, D-85764 Neuberg, Germany.
 FEATURES
 source location/Qualifiers
 1..8
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFZP564I2064"
 /tissue_type="brain"
 /dev_stage="fetal"
 /lab_host="X1-2blue"
 /clone_lib="564 (synonym: hfbp2)"
 /note="Vector: pAMP1, Site_1: NotI, Site_2: SalI"

Query Match 0.5%; Score 8; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 708 CTACTACT 715
 |||||
 Db 1 CTACTACT 8

RESULT 70
 CF338362/c 8 bp mRNA linear EST 18-AUG-2003
 LOCUS RCL1--01-H06.g1 Regenerated callus lambda phage cDNA library (RCL1)
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone RCL1--01-H06,
 mRNA sequence.

ACCESSION CF338362
 VERSION CF338362.1 GI:33825117
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 8)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)

TITLE JOURNAL
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 321 6355
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers

FEATURES
 source
 1..8
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="RCL1--01-H06"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli SOLR"
 /clone_lib="Regenerated callus lambda phage cDNA library (RCL1)"
 /note="Vector: pBluescript SK(+); Site_1: SctI; Site_2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SctI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

Query Match 0.5%; Score 8; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1689 CCAGCTTT 1696
 |||||
 Db 8 CCAGCTTT 1

RESULT 71
 CF339016/c 8 bp mRNA linear EST 18-AUG-2003
 LOCUS RCL1--03-111.g1 Regenerated callus lambda phage cDNA library (RCL1)
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone RCL1--03-111,
 mRNA sequence.

ACCESSION CF339016
 VERSION CF339016.1 GI:33826415
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

REFERENCE 1 (bases 1 to 8)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)

TITLE JOURNAL
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 321 6355
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers

FEATURES
 source
 1..8
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="RCL1--05-K22"

Query Match 0.5%; Score 8; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1689 CCAGCTTT 1696
 |||||
 Db 8 CCAGCTTT 1

RESULT 72
 CF339699/c 8 bp mRNA linear EST 18-AUG-2003
 LOCUS RCL1--05-K22.g1 Regenerated callus lambda phage cDNA library (RCL1)
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone RCL1--05-K22,
 mRNA sequence.

ACCESSION CF339699
 VERSION CF339699.1 GI:33827769
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 8)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)

TITLE JOURNAL
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 321 6355
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers

FEATURES
 source
 1..8
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="RCL1--05-K22"

/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library (RCL1)"
/note="Vector: pBluescript SK(+); Site 1: SctI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SctI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

Query Match 0.5%; Score 8; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1689 CCAGCTTT 1696
|||||
8 CCAGCTTT 1

RESULT 73
LOCUS CF340204/c 8 bp mRNA linear EST 18-AUG-2003
DEFINITION RCL1--07-E15.g1 Regenerated callus lambda phage cDNA library (RCL1)
Oryza sativa (japonica cultivar-group) cDNA clone RCL1--07-E15,
mRNA sequence.

ACCESSION CF340204 GI:33828768
VERSION CF340204.1
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep
clade; Elnatroidae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 8)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,D.K., Kim,Y.-K. and Nam,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
COMMENT Contact: Nam B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnamh@gbio.com, bnamh@bio.myongji.ac.kr.

FEATURES
SOURCE Location/Qualifiers
1..8
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultiyar="Nackdong"
/db_xref="taxon:39947"
/clone="RCL1--07-E15"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library (RCL1)"
/note="Vector: pBluescript SK(+); Site 1: SctI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SctI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

Query Match 0.5%; Score 8; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1689 CCAGCTTT 1696
|||||
8 CCAGCTTT 1

RESULT 74
LOCUS CO790866/c 8 bp mRNA linear EST 05-AUG-2004
DEFINITION NT010D D03 St18-22 Neural tube (NT) Ambystoma mexicanum cDNA 5'
similar to hypothetical protein, mRNA sequence.

ACCESSION CO790866 GI:51006837
VERSION CO790866.1
KEYWORDS EST.
SOURCE Ambystoma mexicanum (axolotl)
ORGANISM Ambystoma mexicanum
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroides; Ambystomatidae;
Ambystoma.

REFERENCE 1 (bases 1 to 8)
Habermann,B., Bebin,A.G., Herklitz,S., Volkmmer,M., Eckel,K.,
Pehlike,K., Eppelstein,H.H., Schackert,H.K., Wiebe,G. and Tanaka,E.M.
An Ambystoma mexicanum EST sequencing project: Analysis of 17,352
expressed sequence tags from embryonic and regenerating blastema
cDNA libraries
Genome Biol. (2004) In press
COMMENT Contact: Eily M. Tanaka
Tanaka Lab
Max Planck Institute of Molecular Cell Biology and Genetics,
Dresden
Pfeifenhauserstrasse 108, 01307 Dresden, Germany
Tel: 0049 351 210 2620
Fax: 0049 351 210 1489
Email: tanaka@mpi-cbg.de
Plate: NT010D row: 03 column: D
Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.
Location/Qualifiers
1..8
/organism="Ambystoma mexicanum"
/mol_type="mRNA"
/db_xref="taxon:8296"
/tissue_type="Neural Tube, Notochord, Somites"
/cell_type="Includes Neural tube, notochord, somites"
/dev_stage="Stage 18-22"
/clone_lib="St18-22 Neural tube (NT)"
/note="Vector: pCMVSPORT6, Site 1: NotI; Site 2: SalI;
Unnormalized cDNA plasmid library prepared by Invitrogen.
Size fractionated mRNA was plasmid primed and cloned into
NotI-SalI site of pCMVSPORT6. Bacterial host is
EMDH10B-TONA. Average insert size is 1.5 KB.
TAG_LIB=NT"

FEATURES
SOURCE Location/Qualifiers
1..8
/organism="Ambystoma mexicanum"
/mol_type="mRNA"
/db_xref="taxon:8296"
/tissue_type="Neural Tube, Notochord, Somites"
/cell_type="Includes Neural tube, notochord, somites"
/dev_stage="Stage 18-22"
/clone_lib="St18-22 Neural tube (NT)"
/note="Vector: pCMVSPORT6, Site 1: NotI; Site 2: SalI;
Unnormalized cDNA plasmid library prepared by Invitrogen.
Size fractionated mRNA was plasmid primed and cloned into
NotI-SalI site of pCMVSPORT6. Bacterial host is
EMDH10B-TONA. Average insert size is 1.5 KB.
TAG_LIB=NT"

Query Match 0.5%; Score 8; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 GGTGTGT 179
|||||
8 GGTGTGT 1

RESULT 75
LOCUS CL887698 8 bp DNA linear GSS 30-AUG-2004
DEFINITION abf86c02.x1 Soybean random, unfiltered genomic library Glycine max
genomic, genomic survey sequence.
ACCESSION CL887698
VERSION CL887698.1 GI:51629775
KEYWORDS GSS.
SOURCE Glycine max (soybean)
ORGANISM Glycine max (soybean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 8)
Numbering: A., Bedell,J.A., Citek,R.W., Robbins,D., McMenamy,J.,
Peterson,S., Jones,J., Fries,J., Budiman,M.A., Nguyen,H. and
Stacey,G.

REFERENCE
AUTHORS Peterson,S., Jones,J., Fries,J., Budiman,M.A., Nguyen,H. and
Stacey,G.

TITLE Methylation filtered genomic sequences from Glycine max
JOURNAL Unpublished (2004)
COMMENT Contact: Gary Stacey
University of Missouri
108 Waters Hall, Columbia, MO 65211, USA
Tel: 573-884-1267
Fax: 573-882-0588
Email: gstacey@missouri.edu
Lidid: 230
Class: shotgun.

FEATURES
source Location/Qualifiers
1..8

/organism="Glycine max"
/mol_type="genomic DNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
/tissue_type="Young leaves"
/clone_lib="Soybean random, unfiltered genomic library"
/note="Vector: pOT2, Site_1: BstXI; Randomly sheared genomic DNA ranging from 0.7-1.5 kb were end repaired and ligated to BstXI linkers prior to cloning in BstXI-cut pOT2. Libid: 230"

Query Match 0.5%; Score 8; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1420 ATTGTGCT 1427
1 ATTGTGCT 8

RESULT 76 9 bp mRNA linear EST 01-AUG-2003
CA853358/c LOCUS B07D03.5eq CDNA Peking library 12hr SCN3 Glycine max cDNA clone
DEFINITION B07D03.5, mRNA sequence.
ACCESSION CA853358
VERSION CA853358.1 GI:33390151
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max

Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

1 (bases 1 to 9)
Alkharouf, N., Khan, R. and Matthews, B.
Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode
Genome 47 (2), 380-388 (2004)
15060591

COMMENT Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350, USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.usda.gov.

FEATURES
source Location/Qualifiers
1..9

/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="B07D03"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="CDNA Peking library 12hr SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA extracted from roots of soybean cv. Peking 12 hrs after infection by SCN race 3. These are cloned in pBluescript

SK-phagemid. "

Query Match 0.5%; Score 8; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1688 ACCAGCTTT 1696
9 ACNAGCTTT 1

RESULT 77 9 bp mRNA linear EST 15-AUG-2003
CF309109 LOCUS ABF-03-C20.b1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) CDNA clone
ABF-03-C20, mRNA sequence.
ACCESSION CF309109
VERSION CF309109.1 GI:33680870
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 9)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source Location/Qualifiers
1..9

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF-03-C20"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E. coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: pCR4-TOPO, Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.5%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1603 ATTCTTC 1610
1 ATTCTTC 8

RESULT 78 9 bp mRNA linear EST 17-MAY-2005
DN988509/c LOCUS ZBBRA_2F_2-11_04_ZBBRA_2F_2-11_04 G05.ab1 Bermuda grass line Zebra
DEFINITION subcloned cold acclimated cDNA library Cynodon dactylon cDNA clone
ZBBRA_2F_2-11_04_ZBBRA_2F_2-11_04 G05.ab1, mRNA sequence.
ACCESSION DN988509
VERSION DN988509.1 GI:66248336
KEYWORDS EST.

SOURCE Cynodon dactylon (Bermuda grass)
ORGANISM Cynodon dactylon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Chloridoideae; Cynodonteae; Cynodon.
REFERENCE 1 (bases 1 to 9)
AUTHORS Meimaitee,K.; Elavarthi,S. and Guenzi,A.C.
TITLE Identification of differentially expressed genes associated with cold acclimation using suppression subtraction hybridization (SSH) and cDNA microarrays
JOURNAL unpublished (2005)
COMMENT Contact: Guenzi AC
Dep. of Plant and Soil Sciences
Oklahoma State University
368 Agriculture Hall, Stillwater, OK 74078-6028, USA
Tel: 405-744-6028
Fax: 405 744 6039
Email: acg@mail.pss.okstate.edu
PCR primers
FORWARD: M13 forward
BACKWARD: M13 Reverse
Seq primer: M13 Forward.
Location/Qualifiers
1..9
/organism="Cynodon dactylon"
/mol_type="mRNA"
/cultivar="Zebra"
/db_xref="taxon:28909"
/clone="ZEBRA_2F_2-11_04_ZEBRA_2F_2-11_04_G05.ab1"
/issue_type="Crown"
/lab_host="E. coli"
/clone_lib="Bermudagrass line Zebra subtracted cold acclimated cDNA library"
/note="Vector: Qiagen's pDrive; Messenger RNA was extracted from control and cold acclimated bermudagrass crown tissue at 2 and 28 days after acclimation and cDNA library was constructed following Clontech PCR-select cDNA subtraction procedure."

Query Match 0.5%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 TTCACCC 107
Db 9 TTCACCC 2

RESULT 79
CL659917/c
LOCUS PRI0135c.F08 - PRI0135c.B21 (9) Mixed stage fosmid library of P.
DEFINITION pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.
ACCESSION CL659917
VERSION CL659917
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromodorea; Diplogasterida; Neodiplogasterida; Pristionchus.
REFERENCE 1 (bases 1 to 9)
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppaDB: an Acedb database for the nematode satellite organism Pristionchus pacificus
JOURNAL Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498

Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
1..9
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus var. California"
/note="Vector: pBifos-5 Fosmid vector"

Query Match 0.5%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 305 TTGTCTT 312
Db 1 TTGTCTT 8

RESULT 80
CL681447
LOCUS PRI0131a.G08_2 - PRI0131a.BR (9) Mixed stage fosmid library of P.
DEFINITION pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.
ACCESSION CL681447
VERSION CL681447
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromodorea; Diplogasterida; Neodiplogasterida; Pristionchus.
REFERENCE 1 (bases 1 to 9)
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppaDB: an Acedb database for the nematode satellite organism Pristionchus pacificus
JOURNAL Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
1..9
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus var. California"
/note="Vector: pBifos-5 Fosmid vector"

RESULT 81
CL659790 10 bp DNA linear GSS 09-JUN-2004
LOCUS PRI0135b.B11 - PRI0135b.B21 (10) Mixed stage fosmid library of P.
DEFINITION pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
ACCESSION CL659790
VERSION CL659790.1 GI:50144248
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Necodiplogasterida; Pristionchus.
REFERENCE 1 (bases 1 to 10)
Srinivasan,V., Otto,G.W., Kahlow,U., Gelsler,R. and Sommer,R.J.
ArapAD: an Acedb database base for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
14681447
JOURNAL PUBMED
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@uebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
FEATURES
Location/Qualifiers
1..10
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pGpfos-5 Fosmid vector"

Query Match 0.5%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 895 CCGCGGGA 902
|||||
1 CCGCGGGA 8

RESULT 82
CF304081 10 bp mRNA linear EST 15-AUG-2003
LOCUS ABF1--04-A07.g1 ABF3-overexpressing transgenic rice lambda phage
DEFINITION cDNA library (ABF1) Oryza sativa (japonica cultivar-group) cDNA
clone ABF1--04-A07, mRNA sequence.
ACCESSION CF304081
VERSION CF304081.1 GI:33675842
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BBP
Clade; Erihartoideae; Oryzaceae; Oryza.
1 (bases 1 to 10)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193

Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..10
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF1--04-A07"
/issue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E. coli SOLR"
/clone_lib="ABF3-overexpressing transgenic rice lambda
phage cDNA library (ABF1)"
/note="Vector: Bluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was dried for 2hrs. cDNA was inserted into
lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end
with XhoI site. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.5%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1303 CACGAGGA 1310
|||||
2 CACGAGGA 9

RESULT 83
BM393918 10 bp mRNA linear EST 17-JAN-2002
LOCUS 50072-2-11-H06.r.1 Chilcoat/Turkewitz cDNA (large fraction)
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM393918
VERSION BM393918.1 GI:18193971
KEYWORDS EST.
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomata; Tetrahymenida; Tetrahymenidae; Tetrahymena.
1 (bases 1 to 10)
Turkewitz,A.P., Karrer,K.M., Jahn,C., Oriss,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
FEATURES
Location/Qualifiers
1..10
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 0.5%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1296 GGGGGCCC 1303
|||||
10 GGGGGCCC 3

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RESULT 84
BM395575/c      10 bp  mRNA  linear  EST 17-JAN-2002
LOCUS
DEFINITION      5009-0-1-A03.c.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
BM395575
BM395575.1  GI:18195628
EST.
SOURCE
Tetrahymena thermophila
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
1 (bases 1 to 10)
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J., and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1..10
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/notes="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match      0.5%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 CCACCGCG 17
        |||||
Db      10 CCACCGCG 3

FEATURES
source
1..10
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/notes="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

RESULT 85
BM396023/c      10 bp  mRNA  linear  EST 17-JAN-2002
LOCUS
DEFINITION      5009-0-15-F12.c.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
BM396023
BM396023.1  GI:18196076
EST.
SOURCE
Tetrahymena thermophila
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
1 (bases 1 to 10)
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J., and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers

TITLE
JOURNAL
AUTHORS
COMMENT
FEATURES

```

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source
1..10
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/notes="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match      0.5%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 CCACCGCG 17
        |||||
Db      10 CCACCGCG 3

RESULT 86
BM397885/c      10 bp  mRNA  linear  EST 17-JAN-2002
LOCUS
DEFINITION      5009-0-38-E03.c.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
BM397885
BM397885.1  GI:18197938
EST.
SOURCE
Tetrahymena thermophila
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
1 (bases 1 to 10)
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J., and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers

TITLE
JOURNAL
AUTHORS
COMMENT
FEATURES
source
1..10
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/notes="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match      0.5%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 CCACCGCG 17
        |||||
Db      10 CCACCGCG 3

RESULT 87
CF921234/c      10 bp  mRNA  linear  EST 05-NOV-2003
LOCUS
DEFINITION      gmirhw3-07 B06_1.046 Soybean root hair subtracted cDNA library
gmirhw3 Glycine max cDNA, mRNA sequence.
ACCESSION
CF921234
CF921234.1  GI:38192028
EST.
SOURCE
Glycine max (soybean)

```

ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE 1 (bases 1 to 10)
AUTHORS Scheffler, B.E., Huang, S., Liu, X., Nguyen, H., Duke, M. and Stacey, G.
TITLE Expressed sequence tags from soybean root hair subtractive cDNA library
JOURNAL Unpublished (2003)
COMMENT Contact: Gary Stacey
University of Missouri
108 Waters Hall, Columbia, MO 65211, USA
Tel: 573-884-4752
Fax: 573-882-0588
Email: staceyg@missouri.edu
Single pass sequence
Seq primer: T7.

FEATURES
source location/Qualifiers
1..10
/organism="Glycine max"
/mol_type="mRNA"
/culivar="Williams 82"
/db_xref="taxon:3847"
/tissue_type="root hairs"
/clone_id="Soybean root hair subtracted cDNA library gmHRW3"
/note="Organ: root hairs; Vector: PCR2-1 Topo; cDNA clones generated from soybean root hair tissue treated with Bradyrhizobium japonicum for 3 hours."

Query Match 0.5%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 891 GATCCCGC 898
Db 9 GATCCCGC 2

RESULT 88
LOCUS CL681384
DEFINITION Cl681384 10 bp DNA linear GSS 09-JUN-2004
PRIO1313a.B05_2 - PRIO1313a.BR (10) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.
ACCESSION CL681384
VERSION CL681384.1 GI:50188392
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromodorea; Diplogasterida; Neodiplogasteridae; Pristionchus.
1 (bases 1 to 10)
Stintvaan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
Apbapdb: an Acceid database for the nematode satellite organism Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
14681447
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@uebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
location/Qualifiers
1..10
/organism="Pristionchus pacificus"

/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_id="Mixed stage fosmid library of P. pacificus var. California"
/note="Vector: pBifos-5 Fosmid vector"

Query Match 0.5%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 200 CTAGCTTC 207
Db 1 CTAGCTTC 8

RESULT 89
LOCUS AJ587026/c
DEFINITION AJ587026 10 bp DNA linear GSS 15-JAN-2004
Arabidopsis thaliana T-DNA flanking sequence, left border, clone 062F10, genomic survey sequence.
ACCESSION AJ587026
VERSION AJ587026.1 GI:37936615
KEYWORDS GSS; left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsia.

REFERENCE 1
AUTHORS Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Crund, C., Denoese, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
PUBMED 1246565
COMMENT 2 (bases 1 to 10)
Balzerque, S.
Direct Submission
Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).
location/Qualifiers
1..10
/organism="Arabidopsis thaliana"
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/db_xref="taxon:3702"
/clone="062F10"
/clone_id="Arabidopsis thaliana T-DNA insertion lines"
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/note="T-DNA flanking sequence
left border"

misc_feature
left border

Query Match 0.5%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 209 AAATGAT 216
Db 9 AAATGAT 2

RESULT 90
AJ598138/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE

AJ598138
10 bp DNA linear GSS 15-JAN-2004
Arabidopsis thaliana T-DNA flanking sequence, left border, clone 462E04, genomic survey sequence.

AJ598138
GSS; left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1
Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., Derose, R., Pelletier, G., Lepoint, L., Caboche, M. and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)

JOURNAL
PUBMED
12446565
2 (bases 1 to 10)
Balzerque, S.
Direct Submission
Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

FEATURES
source
1..10
/organism="Arabidopsis thaliana"
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/db_xref="taxon:3702"
/clone="462E04"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Maslilewskija"
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/note="T-DNA flanking sequence
left border"

misc_feature
1..10
/note="T-DNA flanking sequence
left border"

Query Match 0.5%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1514 AACCATCA 1521
|||||
Db 9 AACCATCA 2

RESULT 91
ATH523869
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE

ATH523869
10 bp DNA linear GSS 08-FEB-2006
Arabidopsis thaliana T-DNA flanking sequence, left border, clone 063E02, genomic survey sequence.

AJ523869
GSS; left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1

AUTHORS
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., Derose, R., Pelletier, G., Lepoint, L., Caboche, M. and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)

2 (bases 1 to 10)
Balzerque, S.
Direct Submission
Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

FEATURES
source
1..10
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Maslilewskija"
/db_xref="taxon:3702"
/clone="063E02"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Maslilewskija"
1..10
/note="T-DNA flanking sequence
left border"

misc_feature
1..10
/note="T-DNA flanking sequence
left border"

Query Match 0.5%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1755 CATTTCAG 1762
|||||
Db 1 CATTTCAG 8

RESULT 92
ATH526713/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

ATH526713
10 bp DNA linear GSS 08-FEB-2006
Arabidopsis thaliana T-DNA flanking sequence, left border, clone 125C02, genomic survey sequence.

AJ526713
GSS; left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1
Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., Derose, R., Pelletier, G., Lepoint, L., Caboche, M. and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)

2 (bases 1 to 10)
Balzerque, S.
Direct Submission
Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from

the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

FEATURES

source

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1. 10
    /organism="Arabidopsis thaliana"
    /mol_type="genomic DNA"
    /cultivar="Wassilewskija"
    /db_xref="taxon:3702"
    /clone="125C02"
    /ecotype="Arabidopsis thaliana T-DNA insertion lines"
    /note="T-DNA flanking sequence
    left border"
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Query Match 0.5%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1214 AAATGAAA 1221

Db 9 AAATGAAA 2

RESULT 93
ATH527413 10 bp DNA linear GSS 08-FEB-2006
LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone
DEFINITION AJ527413 genomic survey sequence.

ACCESSION AJ527413.1 GI:26795673
VERSION GSS; left border; T-DNA flanking sequence.
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1
AUTHORS Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F.,
Chaudin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
Lepointec, L., Caboche, M. and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites

JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
PUBMED 12446565
2 (bases 1 to 10)
REFERENCE Balzerque, S.
AUTHORS Direct Submission
JOURNAL Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
<http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (<http://www.genoplante.com> and
<http://genoplante-info.infobiogen.fr>).

COMMENT

JOURNAL

PUBMED

AUTHORS

TITLE

JOURNAL

1. 10
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /cultivar="Wassilewskija"
 /db_xref="taxon:3702"
 /clone="125C02"
 /ecotype="Arabidopsis thaliana T-DNA insertion lines"
 /note="T-DNA flanking sequence
 left border"

FEATURES

source

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1. 10
    /organism="Arabidopsis thaliana"
    /mol_type="genomic DNA"
    /cultivar="Wassilewskija"
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/db_xref="taxon:3702"
/clone="139F01"
/clone_1b="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Wassilewskija"
1. 10
 /note="T-DNA flanking sequence
 left border"

Query Match 0.5%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 412 AACTATT 419

Db 3 AACTATT 10

RESULT 94
ATH553779 10 bp DNA linear GSS 08-FEB-2006
LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone
DEFINITION AJ553779 genomic survey sequence.

ACCESSION AJ553779.1 GI:29370246
VERSION GSS; left border; T-DNA flanking sequence.
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1
AUTHORS Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F.,
Chaudin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
Lepointec, L., Caboche, M. and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites

JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
PUBMED 12446565
2 (bases 1 to 10)
REFERENCE Balzerque, S.
AUTHORS Direct Submission
JOURNAL Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
<http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (<http://www.genoplante.com> and
<http://genoplante-info.infobiogen.fr>).

COMMENT
JOURNAL
PUBMED
AUTHORS
TITLE
JOURNAL

FEATURES

source

```
1. 10
    /organism="Arabidopsis thaliana"
    /mol_type="genomic DNA"
    /cultivar="Wassilewskija"
    /db_xref="taxon:3702"
    /clone="382B01"
    /ecotype="Arabidopsis thaliana T-DNA insertion lines"
    /note="T-DNA flanking sequence
    left border"
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Query Match 0.5%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 TGTACAGA 184

|||||||

Db 2 TGACAGA 9

RESULT 95
AJ681839/c 11 bp mRNA linear EST 29-JUN-2004
LOCUS AJ681839 CSEQRAN04 Sus scrofa cDNA C0001797_P06, mRNA
DEFINITION AJ681839 CSEQRAN04 Sus scrofa cDNA C0001797_P06, mRNA
SEQUENCE.
AJ681839
VERSION AJ681839.1 GI:49414429
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa (pig)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae; Suidae;
Sus.

REFERENCE
AUTHORS 1 (bases 1 to 11)
TITLE Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
JOURNAL Development of cDNA and EST resources for studying reproduction and
COMMENT embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -mismatch 12 options. Vector:pbluescriptII(KS+) R. Site1: EcoRI
R. Site2: NotI 5' Seg Primer M13F Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arxgenomics.org.
Location/Qualifiers
1..11
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001797_P06"
/issue_type="uterus"
/clone_lib="CSEQRAN04"
/note="Vector: pbluescriptII(KS+); Site_1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pig uterus."

FEATURES
source

Query Match 0.5%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CACCGCG 18
Db 11 CACCGCG 4

RESULT 96
AJ682947/c 11 bp mRNA linear EST 29-JUN-2004
LOCUS AJ682947 CSEQRAN04 Sus scrofa cDNA clone C0001800_K12, mRNA
DEFINITION AJ682947 CSEQRAN04 Sus scrofa cDNA clone C0001800_K12, mRNA
SEQUENCE.
AJ682947
VERSION AJ682947.1 GI:49415537
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa (pig)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae; Suidae;
Sus.

REFERENCE
AUTHORS 1 (bases 1 to 11)
TITLE Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
JOURNAL Development of cDNA and EST resources for studying reproduction and
COMMENT embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics

Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -mismatch 12 options. Vector:pbluescriptII(KS+) R. Site1: EcoRI
R. Site2: NotI 5' Seg Primer M13F Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arxgenomics.org.
Location/Qualifiers
1..11
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001800_K12"
/issue_type="uterus"
/clone_lib="CSEQRAN04"
/note="Vector: pbluescriptII(KS+); Site_1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pig uterus."

Query Match 0.5%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CACCGCG 18
Db 11 CACCGCG 4

RESULT 97
AJ685455/c 11 bp mRNA linear EST 29-JUN-2004
LOCUS AJ685455 CSEQRAN04 Sus scrofa cDNA clone C0001808_P05, mRNA
DEFINITION AJ685455 CSEQRAN04 Sus scrofa cDNA clone C0001808_P05, mRNA
SEQUENCE.
AJ685455
VERSION AJ685455.1 GI:49418045
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa (pig)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae; Suidae;
Sus.

REFERENCE
AUTHORS 1 (bases 1 to 11)
TITLE Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
JOURNAL Development of cDNA and EST resources for studying reproduction and
COMMENT embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -mismatch 12 options. Vector:pbluescriptII(KS+) R. Site1: EcoRI
R. Site2: NotI 5' Seg Primer M13F Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arxgenomics.org.
Location/Qualifiers
1..11
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001808_P05"
/issue_type="uterus"
/clone_lib="CSEQRAN04"
/note="Vector: pbluescriptII(KS+); Site_1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pig uterus."

FEATURES
source

Query Match 0.5%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 59;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 CACCGCGG 18
|||
Db 11 CACCGCGG 4

RESULT 98
AJ686546 11 bp mRNA linear EST 29-JUN-2004
LOCUS AJ686546 CSEQRAN04 Sus scrofa cDNA clone C0001812_C13, mRNA
DEFINITION sequence.
AJ686546
ACCESSION AJ686546.1 GI:49419136
VERSION
KEYWORDS
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.

REFERENCE
1 (bases 1 to 11)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
AUTHORS Development of cDNA and EST resources for studying reproduction and
TITLE embryo development in pigs and cattle
JOURNAL unpublished (2004)
COMMENT Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross_match with the -mincore 20
and -mismatch 12 options. Vector:PBHescriptII(KS+). R. Site1: EcorI
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.
Location/Qualifiers
1..11
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001812_C13"
/tissue_type="uterus"
/clone_lib="CSEQRAN04"
/note="Vector: PBHescriptII(KS+); Site_1: EcorI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pig uterus."

FEATURES
source

Query Match 0.4%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 69;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 580 ACGCGTGGC 590
|||
Db 1 ACCGCGTGGC 11

RESULT 99
AJ686590 11 bp mRNA linear EST 29-JUN-2004
LOCUS AJ686590 CSEQRAN04 Sus scrofa cDNA clone C0001812_E11, mRNA
DEFINITION sequence.
AJ686590
ACCESSION AJ686590.1 GI:49419180
VERSION
KEYWORDS
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.

REFERENCE
1 (bases 1 to 11)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
AUTHORS Development of cDNA and EST resources for studying reproduction and
TITLE embryo development in pigs and cattle

JOURNAL
COMMENT unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross_match with the -mincore 20
and -mismatch 12 options. Vector:PBHescriptII(KS+). R. Site1: EcorI
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.
Location/Qualifiers
1..11
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001812_E11"
/tissue_type="uterus"
/clone_lib="CSEQRAN04"
/note="Vector: PBHescriptII(KS+); Site_1: EcorI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pig uterus."

FEATURES
source

Query Match 0.4%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 69;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 580 ACGCGTGGC 590
|||
Db 1 ACCGCGTGGC 11

RESULT 100
DUT33106 11 bp DNA linear GSS 27-JAN-2006
LOCUS DUT33106
DEFINITION APK12073_g3 HF70_10-07-02 uncultured marine microorganism
HF70_10-07-02 genomic clone HF0070_029A08, genomic survey sequence.
DUT33106
ACCESSION DUT33106.1 GI:85742940
VERSION
KEYWORDS
SOURCE GSS.
ORGANISM uncultured marine microorganism HF70_10-07-02
unclassified sequences; environmental samples.
REFERENCE
1 (bases 1 to 11)
DeLong,E.F., Preston,C.M., Mincer,T., Rich,V., Hallam,S.J.,
Frigaard,N.U., Martinez,A., Sullivan,M., Edwards,R., Chisholm,S.W.
and Karl,D.M.
TITLE Comparative genomics reveals ecological trends in stratified
microbial communities in the ocean's interior
JOURNAL Science (2006) in press
COMMENT Contact: Susan Lucas, Alex Copeland, Sam Pitluck, Alla Lapidus,
Kerrie Barry, Tijana Glavanadelirio, David Bruce, Paul Richardson
and Edward Delong
US DOE Joint Genome Institute
US DOE Joint Genome Institute
2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA
Tel: 617-253-5271
Fax: 617-253-2679
Email: PRichardson@lbl.gov; delong@mit.edu
Sample Date: 10/7/2002 Coordinates: 22.45 N, 158 W Depth 70 m
Temperature: 24.93 C Salinity: 35.21 psu Oxygen: 217.4 umol/Kg
Class: formid ends.
Location/Qualifiers
1..11
/organism="uncultured marine microorganism HF70_10-07-02"
/mol_type="genomic DNA"
/db_xref="taxon:361144"
/clone="HF0070_029A08"
/cell_type="marine picoplankton, less than 1.8 um, greater
than 0.22 um fraction"
/clone_lib="HF70_10-07-02"

/note="Vector: pCC1F0S; North Pacific Subtropical Gyre (Hawaii) picoplankton genomic fosmid DNA library prepared from marine picoplankton in the less than 1.6 um, greater than 0.22 um fraction. Picoplankton collected at 70 m depth on 10/7/2002, Coordinates: 22.45 N, 158 W Sample Date: 10/7/2002 Coordinates: 22.45 N, 158 W Depth 70 m Temperature: 24.93 C Salinity: 35.21 psu Oxygen: 217.4 umol/kg"

Query Match 0.4%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 69;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1469 CCTTGACCTG 1479
Db 1 CTTTGACCAG 11

RESULT 101
AJ655540 12 bp mRNA linear EST 28-JUN-2004
LOCUS AJ655540 KN277 Sus scrofa cDNA clone C0005190_G13, mRNA sequence.
ACCESSION AJ655540
VERSION AJ655540.1 GI:49339572
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa (pig)

REFERENCE
AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
JOURNAL Unpublished (2004)
COMMENT Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM

Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross_match with the -minscore 20 and -mismatch 12 options. Vector:PBuescriptII(SK+) R. Site1: EcoRI R. Site2: NotI 5' Seq Primer M13f Normalised library constructed from pooled early embryos, from 8-cell stage to blastocysts. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.atkenomics.org.

FEATURES
SOURCE Location/Qualifiers
1..12

/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0005190_G13"
/tissue_type="embryo"
/clone_id="KN277"
/note="Vector: PBuescriptII(SK+); Site 1: EcoRI; Site 2: NotI; Single pass sequencing. Normalised library constructed from pooled early embryos, from 8-cell stage to blastocysts."

Query Match 0.4%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 94;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 466 ACAGTGTGAA 476
Db 1 ACTGTGAGAA 11

RESULT 102
BM395918 12 bp mRNA linear EST 17-JAN-2002
LOCUS BM395918
DEFINITION 5009-0-14-B05.t.1 Chilcoat/Turkewitz cDNA (large fraction)

ACCESSION Tetrahymena thermophila cDNA, mRNA sequence.
BM395918

VERSION BM395918.1 GI:18195971

KEYWORDS EST.

SOURCE Tetrahymena thermophila

ORGANISM Tetrahymena thermophila

REFERENCE
AUTHORS Eukaryotes; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena. 1 (bases 1 to 12)

Turkewitz,A.P., Karer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel,J., and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)

COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
SOURCE Location/Qualifiers
1..12

/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_id="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript 2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 0.4%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 94;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 438 CGCGAGGCGCT 448
Db 2 CGCGGTGGCTT 12

RESULT 103
CNS06E5N 9 bp DNA linear GSS 17-JUN-2001
LOCUS T3 end of clone A00A018H04 of library A00A from strain CBS 732 of
DEFINITION Zygosaccharomyces rouxii, genomic survey sequence.
ACCESSION AL394689
VERSION AL394689.1 GI:12145788
KEYWORDS GSS.

SOURCE Zygosaccharomyces rouxii
ORGANISM Zygosaccharomyces rouxii
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Zygosaccharomyces.

REFERENCE
AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G., Bolestin-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durrens,P., Leplingle,A., Llorente,B., Malpertuy,A., Neuvéglise,C., Ozeri-Kalogeropoulos,O., Potier,S., Saurin,W., Tekala,F., Toffano-Nicche,C., Webolowski-Louvel,M., Wincker,P. and Weissenbach,J.

Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
PUBMED 11152876

TITLE 2 (bases 1 to 9)
JOURNAL de Montigny,J., Straub,M., Potier,S., Tekala,F., Dujon,B., Wincker,P., Artiguenave,F. and Souciet,J.
Genomic exploration of the hemiascomycetous yeasts: 8.

JOURNAL FEBS Lett. 487 (1), 52-55 (2000)
PUBMED 11152883
REFERENCE 3 (bases 1 to 9)
AUTHORS GenomeScope.

TITLE Direct Submission
JOURNAL Submitted (06-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
segreg@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT This GSS is part of a random genomic sequencing program of thirteen
yeast species: *Saccharomyces bayanus* var. *uvarum*, *Saccharomyces*
exiguus, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*,
Saccharomyces kluyveri, *Kluyveromyces thermotolerans*, *Kluyveromyces*
lactis var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia*
angusta, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*,
Candida tropicalis and *Yarrowia lipolytica*. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
Location/Qualifiers
1..9
/organism="Zygosaccharomyces rouxii"
/mol_type="genomic DNA"
/strain="CBS 732"
/db_xref="taxon:4956"
/clone="AR0A018H04"
/clone_lib="AR0AA"
/note="end : T3"
Query Match 0.4%; Score 7.6; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Oy 951 CAAATGA 958
Db 1 CAAATGA 8
RESULT 104 9 bp mRNA linear EST 17-MAY-2005
LOCUS ZEBRA_2F_2-II_04_ZEBRA_2F_2-II_04_G05.ab1 Bermuda grass line Zebra
DEFINITION ZEBRA_2F_2-II_04_ZEBRA_2F_2-II_04_G05.ab1 Bermuda grass line Zebra
subtracted cold acclimated cDNA library Cynodon dactylon cDNA clone
DN988509
ZEBRA_2F_2-II_04_ZEBRA_2F_2-II_04_G05.ab1, mRNA sequence.
DN988509
DN988509.1 GI:66248336
EST.
Cynodon dactylon (Bermuda grass)
Cynodon dactylon
Cynodon dactylon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Chloridoideae; Cynodonteae; Cynodon.
1 (bases 1 to 9)
REFERENCE Melmaee,K., Elavarthi,S. and Guenzi,A.C.
AUTHORS Identification of differentially expressed genes associated with
TITLE cold acclimation using suppression subtraction hybridization (SSH)
and cDNA microarrays
JOURNAL Unpublished (2005)
COMMENT Contact: Guenzi AC
Dep. of Plant and Soil Sciences
Oklahoma State University
368 Agriculture Hall, Stillwater, OK 74078-6028, USA
Tel: 405-744-6028
Fax: 405 744 6039
Email: acg@mail.pss.okstate.edu
PCR Primers
FORWARD: M13 forward
BACKWARD: M13 Reverse
Seq primer: M13 Forward.
Location/Qualifiers
1..9
/organism="Cynodon dactylon"
/mol_type="mRNA"
/cultivar="Zebra"
/db_xref="taxon:28909"
/clone="ZEBRA_2F_2-II_04_ZEBRA_2F_2-II_04_G05.ab1"
/issue_type="crown"
/lab_host="B. coli"

/clone_lib="Bermuda grass line Zebra subtracted cold
acclimated cDNA library"
/note="Vector: Qiagen's pDrive; Messenger RNA was
extracted from control and cold acclimated bermudagrass
crown tissue at 2 and 28 days after acclimation and cDNA
library was constructed following Clontech PCR- select
cDNA subtraction procedure."
Query Match 0.4%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1207 GGGCTGGA 1215
Db 1 GGGCTGGA 9
RESULT 105 9 bp mRNA linear EST 25-MAR-2004
LOCUS BU101621
DEFINITION PRODIGID193F1 Compugen_targeted_mRNA_sequencing Homo sapiens cDNA,
mRNA sequence.
BU101621
BU101621
ACCESSION BU101621.1 GI:45737021
VERSION BU101621
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 9)
REFERENCE Xie,H., Diber,A., Pollack,S., Nemzer,S., Safer,H., Meloon,B.,
AUTHORS Olson,A., Hwang,J.-J., Endress,G.A., Savitsky,K. and Gill-More,R.
TITLE Bridging expressed sequence alignments through targeted cDNA
sequencing
JOURNAL Genomics 83 (4), 572-576 (2004)
COMMENT PUBLISHED 15028280
Contact: Xie H
Compugen
7 Center Drive, Suite 9, Jamesburg, NJ 08831, USA
Tel: 609-655-5105 X 26
Fax: 609-655-5114
Email: han@compugen.com.
Location/Qualifiers
1..9
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="Compugen_targeted_mRNA_sequencing"
/note="These sequences resulted from single pass
sequencing of PCR products from Compugen targeted mRNA
sequencing project. PCR primers and nested primers were
designed to join two neighboring expressed sequence
contigs based on Compugen LEADS expressed sequence
cluster and assembly platform. Reverse transcriptase PCR and
nested PCR reactions were performed by Prodyne Inc.
(Windor, CT 06095, USA) on normal human heart, brain,
lung, liver, placenta, and testis poly mRNA preparations
from Origin (Rockville, MD 20850, USA) with reagents from
Invitrogen (Carlsbad, California 92008). PCR products were
sequenced by Qiagen (Valencia, CA 91355)."
Query Match 0.4%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 501 ATGCTACTA 509
Db 1 ATGCTACTA 9
RESULT 106
CF307008/c

LOCUS CF307008 9 bp mRNA linear EST 15-AUG-2003
 DEFINITION HDAl--05-H11.g1 OSHDAC1-overexpressing transgenic rice lambda phage
 CDNA library 1 (HDAl) Oryza sativa (japonica cultivar-group) cDNA
 clone HDAl--05-H11, mRNA sequence.
 ACCESSION CF307008
 VERSION CF307008.1 GI:33678769
 SOURCE EST.
 ORGANISM Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 9)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT: Nahm B.H.
 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC.; DIVISION
 OF BIOSCIENCE AND BIOINFORMATICS, MYONGJI UNIVERSITY
 YONGJIN, KYEONGGI, KOREA
 TEL: 82 31 330 6193
 FAX: 82 31 321 6355
 EMAIL: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 LOCATION/Qualifiers
 1..9
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="HDAl--05-H11"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli SOUR"
 /clone_lib="OSHDA1-overexpressing transgenic rice lambda
 phage CDNA library 1 (HDAl)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
 XhoI; Callus was treated with ABA(20um) for 1hour. cDNA
 was inserted into lambda uni-ZAP XR vector at 5' end with
 EcoRI and 3' end with XhoI site. mRNA was derived from
 rice Histone Deacetylase overexpression line."

Query Match 0.4%; Score 7.4; DB 1; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1339 CCCTGTCG 1347
 Db 9 CCCTGTCG 1

RESULT 107
 CF312817 9 bp mRNA linear EST 15-AUG-2003
 DEFINITION ABR--08-L15.b1 ABR3-overexpressing transgenic rice plasmid cDNA
 library (ABR) Oryza sativa (japonica cultivar-group) cDNA clone
 ABR--08-L15, mRNA sequence.
 ACCESSION CF312817
 VERSION CF312817.1 GI:33684578
 SOURCE EST.
 ORGANISM Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 9)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT: Nahm B.H.
 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC.; DIVISION
 OF BIOSCIENCE AND BIOINFORMATICS, MYONGJI UNIVERSITY

Yongjin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 LOCATION/Qualifiers
 1..9
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="ABR--08-L15"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ABR3-overexpressing transgenic rice plasmid
 cDNA library (ABR)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; leaf was dried
 for 2hrs. Oligo-capped mRNA was reverse transcribed and
 then used for PCR. mRNA was prepared from ABA-responsive
 element binding transcription factor 3 overexpression
 line."

Query Match 0.4%; Score 7.4; DB 1; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1673 AAAATATA 1681
 Db 9 AAAAAAAAA 1

RESULT 108
 CF313414 9 bp mRNA linear EST 15-AUG-2003
 DEFINITION HD--01-115.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
 library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
 HD--01-115, mRNA sequence.
 ACCESSION CF313414
 VERSION CF313414.1 GI:33685175
 SOURCE EST.
 ORGANISM Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 9)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT: Nahm B.H.
 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC.; DIVISION
 OF BIOSCIENCE AND BIOINFORMATICS, MYONGJI UNIVERSITY
 YONGJIN, KYEONGGI, KOREA
 TEL: 82 31 330 6193
 FAX: 82 31 321 6355
 EMAIL: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 LOCATION/Qualifiers
 1..9
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="HD--01-115"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OSHDA1-overexpressing transgenic rice plasmid
 cDNA library (HD)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was
 reverse transcribed and then used for PCR. mRNA was
 derived from rice Histone Deacetylase overexpression

line."

Query Match 0.4%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 107 CTCGCTCT 115
Db 9 CTCGCTCT 1

RESULT 109
LOCUS CF318771/c 9 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--09-A13.g1 OshDACT1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--09-A13, mRNA sequence.
CF318771
ACCESSION CF318771.1 GI:33690532
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 9)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source 1..9
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--09-A13"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_id="OshDACT1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: PCR4-TOPO, Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.4%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1673 AAAATPAAA 1681
Db 9 AAAATPAAA 1

RESULT 110
LOCUS CF330649/c 9 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--06-H06.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--06-H06, mRNA sequence.
CF330649
ACCESSION CF330649.1 GI:33809535
KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 9)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source 1..9
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--06-H06"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_id="E.coli DH10B"
/note="Vector: PCR4-TOPO, Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.4%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1673 AAAATPAAA 1681
Db 9 AAAATPAAA 1

RESULT 111
LOCUS CO818814 9 bp mRNA linear EST 09-AUG-2004
DEFINITION CSECS120A07.PREN0028 CabSau Normalised Berry Fruit Set Stage 28 (PREN0028) Vitis vinifera cDNA clone CSECS120A07 3', mRNA sequence.
CO818814
ACCESSION CO818814.1 GI:51050957
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitis.
1 (bases 1 to 9)
Iocco,P., Davies,C. and Thomas,M.R.
Expressed sequence tags from the grapevine cultivar Cabernet Sauvignon (2004)
Unpublished (2004)
Contact: Mark R. Thomas
CSIRO Plant Industry
CSIRO
PO Box 350, Glen Osmond, SA, 5064, Australia
Tel: 61 8 83038600
Fax: 61 8 83038601
Email: Mark.R.Thomas@csiro.au
Seq primer: CCCAGTCACGACGTTGTAACAAG (M13 Forward)
POLY-A=yes
Location/Qualifiers

FEATURES
source 1..9
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"

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/db_xref="taxon:29760"
/clone="CSECS120A07"
/sex="Hermaphrodite"
/dev_stage="28 - modified E-L system"
/clone_1ib="CabSau Normalised Berry Fruit Set Stage 28
(PRE0028)"
/note="Organ: Fruit; Vector: pBL; A cDNA library from
prevaraison fruit, 1-2 weeks post anthesis, at stage 28 of
the modified E-L system. Tissue collected from field grown
plants. A description of the modified E-L system can be
found in the paper by B. G. Coombe 'Adoption of a system
for identifying grapevine growth stages' (1995) Aust. J.
Grape and Wine Res. 1: 104-110."

Query Match      0.4%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1508 ATCTGGAAC 1516
Db      1 ATCTGGAAC 9

RESULT 112
LOCUS      CV933314      9 bp      mRNA      linear      EST 25-JAN-2005
DEFINITION      PMOcm_0671 mating of 88069 (A1) and 618 (A2) Phytophthora infestans
ACCESSION      CV933314
VERSION      CV933314.1 GI:58122929
KEYWORDS      EST.
SOURCE      Phytophthora infestans (potato late blight agent)
ORGANISM      Eukaryota; stramenopiles; Oomycetes; Peronosporales; Phytophthora.
REFERENCE      1 (bases 1 to 9)
AUTHORS      Randall,T., Dwyer,R.A., Huitema,E., Beyer,K., Cvitanich,C.,
Kelkar,H., Fong,A.M., Gates,K., Roberts,S., Yatzen,B., Gaffney,T.,
Law,M., Testa,A., Torto-Alalibo,A., Gisi,U., Govers,F., Gow,N.A.,
Windass,J., Binder,A., Birch,P.R.U., Ghislin,U., Govers,F., Gow,N.A.,
Mauch,F., van West,P., Maugh,M.E., Yu,D., Boller,T., Kamoun,S.,
Lam,S.T. and Judelson,H.S.
Title      Large-scale gene discovery in the oomycete Phytophthora infestans
reveals likely components of phytopathogenicity shared with true
fungi
JOURNAL      Mol. Plant-Microbe Interact. 18 (3), 229-243 (2005)
PUBMED      15782637
COMMENT      Contact: Judelson HS
Department of Plant Pathology
University of California
Weber Hall, Riverside, CA 92521, USA
Tel: 909 787 4199
Fax: 909 787 4294
Email: howard.judelson@ucr.edu.
Location/Qualifiers
1..9
/organism="Phytophthora infestans"
/mol_type="mRNA"
/strain="88069 and 618"
/db_xref="taxon:4787"
/sex="A1 and A2"
/clone_1ib="mating of 88069 (A1) and 618 (A2)"
/note="Vector: pSPORT1"

Query Match      0.4%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1651 CACTGAACT 1659
Db      1 CACCGAACT 9

RESULT 113

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CX005921
LOCUS      CX005921      9 bp      mRNA      linear      EST 03-DEC-2004
DEFINITION      iv22h10.g1 Brain - Cerebellum Library (DOGEST8) Canis familiaris
CNA, mRNA sequence.
ACCESSION      CX005921
VERSION      CX005921.1 GI:56277337
KEYWORDS      EST.
SOURCE      Canis familiaris (dog)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
1 (bases 1 to 9)
Baliya,V., Nascimento,L.U. and McCombie,W.R.
ESTs from Canis familiaris cerebellum (dog)
Unpublished (2004)
Contact: W. Richard McCombie
Iltis Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org.
Location/Qualifiers
1..9
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
/tissue_type="Cerebellum"
/dev_stage="3 month old normal canine"
/lab_host="XL10 Gold"
/clone_1ib="Brain - Cerebellum Library (DOGEST8)"
/note="Organ: Brain; Vector: pBluescript II SK; Site 1:
ECORI; Site 2: XhoI; Library constructed using plunscript
XR kit from Stratagene. Cloned cDNA was size selected
between 1-3 kb. Mark Haskins VMD, PhD, Pathology and
Medical Genetics, School of Veterinary Medicine,
University of Pennsylvania, 3800 Spruce Street,
Philadelphia, PA 19104-6051"

Query Match      0.4%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      293 CACCTGGC 301
Db      1 CACCTGAC 9

RESULT 114
LOCUS      DT904968/c      9 bp      mRNA      linear      EST 19-SEP-2005
DEFINITION      BMSB16761 Hematopoietic stem cells Mus musculus cDNA, mRNA
sequence.
ACCESSION      DT904968
VERSION      DT904968.1 GI:75865454
KEYWORDS      EST.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 9)
Pritsker,M., Doniger,T.T., Kramer,L.C., Westcott,S.E. and
Lemischka,I.R.
Diversification of Stem Cell Molecular Repertoire by Alternative
Splicing
Proc. Natl. Acad. Sci. U.S.A. (2005) In press
Contact: Pritsker M
Lab of Ihor Lemischka, Department of Molecular Biology
Princeton University
Princeton, NJ 08544, USA

```

Tel: 609 258 5657
Fax: 609 258 1704
Email: pritsker@molbio.princeton.edu.
Location/Qualifiers

FEATURES

source

1..9
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/tissue_type="Hematopoietic stem cells"
/cell_type="Hematopoietic stem cells"
/clone_lib="Hematopoietic stem cells"
/note="CDNA library was made from FACS-purified hematopoietic stem cells"

Query Match 0.4%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1042 TACCTGAAG 1050
|||||
Db 9 TACCTGCAG 1

RESULT 115
LOCUS DT909435 9 bp mRNA linear EST 19-SEP-2005
DEFINITION BMSB17098 Hematopoietic stem cells Mus musculus CDNA, mRNA
Sequence.

ACCESSION DT909435
VERSION DT909435.1 GI:75889921
KEYWORDS EST.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 9)

AUTHORS Pritsker, M., Doniger, T. T., Kramer, L. C., Westcott, S. E. and Lemischka, I. R.

TITLE Diversification of Stem Cell Molecular Repertoire by Alternative Splicing

JOURNAL Proc. Natl. Acad. Sci. U.S.A. (2005) In press

COMMENT Contact: Pritsker M
Lab of Ihor Lemischka, Department of Molecular Biology
Princeton University
Princeton, NJ 08544, USA
Tel: 609 258 5657
Fax: 609 258 1704
Email: pritsker@molbio.princeton.edu.

FEATURES Location/Qualifiers

1..9
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/tissue_type="Hematopoietic stem cells"
/cell_type="Hematopoietic stem cells"
/clone_lib="Hematopoietic stem cells"
/note="CDNA library was made from FACS-purified hematopoietic stem cells"

Query Match 0.4%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 428 ACCTGGCCT 436
|||||
Db 1 ACCGGGCCT 9

RESULT 116
LOCUS DV571332 9 bp mRNA linear EST 04-NOV-2005
DEFINITION 0058P0010A01_3' library 58 - normalized (50 mix pooled juveniles +

adults) - female Taeniopygia guttata CDNA clone 0058P0010A01 3'
similar to unknown 0058P0010A01, mRNA sequence.

ACCESSION DV571332
VERSION DV571332.1 GI:78432685
KEYWORDS EST.

SOURCE Taeniopygia guttata

ORGANISM Taeniopygia guttata
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Passeriformes; Estrildidae; Estrildidae; Taeniopygia.

REFERENCE 1 (bases 1 to 9)

AUTHORS Wada, K., Howard, J. T., McConnell, P., Lints, T., Rivas, M. V., Whitney, O., Horita, H., Patterson, M. A., White, S., Zhao, S., Sakaguchi, H., Hagihara, M., Shiraki, T., Hirozane-Kishikawa, T., Skene, P., Hayashizaki, Y., Carninci, P. and Jarvis, E. D.

A molecular neuroethological approach for identifying and characterizing a melody of behaviorally regulated genes unpublished (2005)

Other ESTs: 0058P00102.x0 A01

COMMENT Contact: Kazuhiro Wada and Erich Jarvis

Duke University Medical Center - Department of Neurobiology
Box 3209 Bryan Research Building, Durham, NC 27710, USA
Tel: 919 681-1681

Email: wada@neuro.duke.edu and jarvis@neuro.duke.edu
Plate: 0058P0010 row: A column: 01
POLYA=NO.

FEATURES Location/Qualifiers

1..9
/organism="Taeniopygia guttata"
/mol_type="mRNA"
/db_xref="taxon:59729"
/clone="0058P0010A01"
/sex="female"
/tissue_type="brain"
/dev_stage="adult and juvenile"
/clone_lib="library 58 - normalized (50 mix pooled juveniles + adults) - female"
/note="Organ: brain; Vector: pFLC-1; Site 1: EcoRI; Site 2: BamHI; The library was constructed as described by Carninci, P. (2003) in DNA Microarrays: A Molecular Cloning Manual, eds. Bowtell, D. & Sambrook, J. (Cold Spring Harbor, NY), pp. 647-670.
TAG_TISSUE=whole brain
TAG_SEQ=gatccaacatagctnnnnnnnn"

Query Match 0.4%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 826 TTCTCTCCC 834
|||||
Db 1 TTGCTCCCC 9

RESULT 117
LOCUS CW985814 9 bp DNA linear GSS 29-DEC-2004
DEFINITION KBH011P15R KBHr, Brassica rapa HindIII BAC library Brassica rapa subsp. pekinensis genomic clone KBH011P15, genomic survey sequence.

ACCESSION CW985814
VERSION CW985814.1 GI:56851838
KEYWORDS GSS.

SOURCE Brassica rapa subsp. pekinensis

ORGANISM Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 9)

REFERENCE Yang, T. J., Kwon, S. J., Kim, J. A., Kim, J. S., Lim, K. B., Jin, M., Park, J. Y., Lim, M. H., Kim, H. I., Lim, Y. P. and Park, B. S.
End sequence of Brassica rapa HindIII BAC library (KBHr)

JOURNAL Unpublished (2004)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis HindIII BAC clone
KBH011P15
Seq primer: M13 Reverse
Class: BAC ends.

FEATURES
source Location/Qualifiers
1..9
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBH011P15"
/isue_type="Young leaves"
/lab_host="E.coli DH10B"
/clone_lib="KBH, Brassica rapa HindIII BAC library"
/note="Vector: pCUGIac1; Site 1: HindIII; Brassica rapa
ssp. pekinensis inbred line Chifu BAC library (KBH BAC)
is provided by Yong-Pyo Lim."

Query Match 0.4%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1035 AGATCTCTA 1043
|||||
1 AGATCTATA 9

RESULT 118
LOCUS CL663701 9 bp DNA linear GSS 09-JUL-2004
DEFINITION PRI0145a_F06 - PRI0145a.B21.1 (9) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
ACCESSION CL663701
VERSION CL663701.1 GI:50153095
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Nedoplogasteridae; Pristionchus.
1 (bases 1 to 9)
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
AppADB: an Acedb database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
14681447
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
1..9
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus"

FEATURES
source Location/Qualifiers
1..9
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus"

var. California"
/note="Vector: pBpfos-5 Fosmid vector"

Query Match 0.4%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1422 TGTGCTCTC 1430
|||||
1 TGTGCTTTC 9

RESULT 119
LOCUS CL672804 9 bp DNA linear GSS 09-JUL-2004
DEFINITION PRI017d_E02 - PRI017d.B21 (9) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
ACCESSION CL672804
VERSION CL672804.1 GI:50173549
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Nedoplogasteridae; Pristionchus.
1 (bases 1 to 9)
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
AppADB: an Acedb database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
14681447
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
1..9
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pBpfos-5 Fosmid vector"

Query Match 0.4%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 264 CACCTCGGA 272
|||||
1 CACCTCCGA 9

RESULT 120
LOCUS CL682372 9 bp DNA linear GSS 09-JUL-2004
DEFINITION PRI0133d_D05_2 - PRI0133d.BR (9) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
ACCESSION CL682372
VERSION CL682372.1 GI:50189761
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;

REFERENCE 1 Neodiplogasteridae; Pristionchus.
1 (bases 1 to 9)
AUTHORS Sriinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE Apadabi: an Acedb database for the nematode satellite organism
JOURNAL Pristionchus pacificus
PUBMED Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT 14681447
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@uebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.

FEATURES
source
1..9
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pGP105-5 Fosmid vector"

Query Match 0.4%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1681 AGGTGGAC 1689
|||
1 AGATGGAC 9

Db

RESULT 121 9 bp DNA linear GSS 10-JAN-2006
DX058225 KBRB063119 KBRB, Brassica rapa BamHI BAC library Brassica rapa
LOCUS subsp. pekinensis genomic clone KBRB063119, genomic survey
DEFINITION
sequence.
ACCESSION DX058225.1 GI:84752521
VERSION
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 9)
AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
End sequence of Brassica rapa BamHI (KBRB) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel.: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBRB063119
Seq primer: M13 Reverse
Class: BAC ends.

FEATURES
source
1..9
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/culturivar="Chilfu"

REFERENCE 1 /sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBRB063119"
/lab_host="E.coli DH10B"
/clone_lib="KBRB, Brassica rapa BamHI BAC library"
/note="Vector: pCUG1BAC1; Site 1: BamHI; Brassica rapa ssp
pekinensis var. Chilfu BAC library (KBRB BAC) is provided
by Yong-Pyo Lim (CNU)."

Query Match 0.4%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 CCGCAGCA 741
|||||
9 CCGCAGCA 1

Db

RESULT 122 10 bp mRNA linear EST 17-JAN-2002
BM396011
LOCUS 5009-0-15-E12.t.2 Chilcoat/Turkewitz cDNA (large fraction)
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM396011 GI:18196064
VERSION
KEYWORDS EST.
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomata; Tetrahymenida; Tetrahymenidae; Tetrahymena.
1 (bases 1 to 10)
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
source
1..10
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 0.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 438 CGCGAGGC 446
|||||
2 CGCGAGGC 10

Db

RESULT 123 10 bp mRNA linear EST 17-JAN-2002
BM398849
LOCUS 5009-0-5-G06.t.1 Chilcoat/Turkewitz cDNA (large fraction)
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM398849 GI:18198902
VERSION
KEYWORDS EST.
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
 Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
 1 (bases 1 to 10)
 Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,
 Frankel, J., and Klobutcher, L.
 EST from Tetrahymena thermophila, strain CU428.1, growing cells
 Unpublished (2002)
 Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3.
 Location/Qualifiers
 1..10
 /organism="Tetrahymena thermophila"
 /mol_type="mRNA"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript SK+; Details on library
 preparation can be found in Chilcoat and Turkewitz (2001)
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 0.4%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 59;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 438 CGCGGAGGC 446
 |||||
 2 CGCGGTGCG 10

RESULT 124
 CF311011 10 bp mRNA linear EST 15-AUG-2003
 LOCUS ABF-06-B02.B1 ABF3-overexpressing transgenic rice plasmid cDNA
 DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
 ABF-06-B02, mRNA sequence.
 CF311011
 CF311011.1 GI:33682772
 EST.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep
 1 (bases 1 to 10)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers
 1..10
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="ABF-06-B02"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E. coli DH10B"
 /clone_lib="ABF3-overexpressing transgenic rice plasmid
 cDNA library (ABF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
 for 2hrs. Oligo-capped mRNA was reverse transcribed and
 then used for PCR. mRNA was prepared from ABA-responsive
 element binding transcription factor 3 overexpression
 line."

Query Match 0.4%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 59;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1410 CTCTCTCTC 1418
 |||||
 2 CTCTCTCTC 10

RESULT 125
 CL694909/c 10 bp DNA linear GSS 10-JUL-2004
 LOCUS PRI0165C_A04.2 - PRI0165C.BR (10) Mixed stage fosmid library of P.
 DEFINITION pacificus var. California Pristionchus pacificus genomic, genomic
 survey sequence.
 CL694909
 CL694909.1 GI:50216817
 GSS.
 Pristionchus pacificus
 Pristionchus pacificus
 Pristionchus pacificus
 Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
 Neodiplogasteridae; Pristionchus.
 1 (bases 1 to 10)
 Sriwatsan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
 AppadB: an AcedB database for the nematode satellite organism
 Pristionchus pacificus
 Nucleic Acids Res. 32 (1), D421-D422 (2004)
 14681447
 Contact: Sommer RJ
 Evolutionary Biology
 Max-Planck-Institute for Developmental Biology
 Spemannstr. 37-39, Tuebingen D-72076, Germany
 Tel: 00497071601371
 Fax: 00497071601498
 Email: ralf.sommer@tuebingen.mpg.de
 This library was generated at Caltech, Pasadena, USA and end
 sequenced at Vancouver, Canada.
 Seq primer: T7
 Class: fosmid ends.
 Location/Qualifiers
 1..10
 /organism="Pristionchus pacificus"
 /mol_type="genomic DNA"
 /strain="California"
 /db_xref="taxon:54126"
 /clone_lib="Mixed stage fosmid library of P. pacificus
 var. California"
 /note="Vector: pBplfos-5 Fosmid vector"

Query Match 0.4%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 59;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 269 CGGACCCA 277
 |||||
 9 CGTACCCA 1

RESULT 126
 AJ592517 10 bp DNA linear GSS 15-JAN-2004
 LOCUS Arabidopsis thaliana T-DNA flanking sequence, right border, clone
 DEFINITION 621G09, genomic survey sequence.
 AJ592517
 AJ592517.1 GI:37942141
 GSS.
 Pristionchus pacificus
 Pristionchus pacificus
 Pristionchus pacificus
 Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
 Neodiplogasteridae; Pristionchus.
 1 (bases 1 to 10)
 Sriwatsan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
 AppadB: an AcedB database for the nematode satellite organism
 Pristionchus pacificus
 Nucleic Acids Res. 32 (1), D421-D422 (2004)
 14681447
 Contact: Sommer RJ
 Evolutionary Biology
 Max-Planck-Institute for Developmental Biology
 Spemannstr. 37-39, Tuebingen D-72076, Germany
 Tel: 00497071601371
 Fax: 00497071601498
 Email: ralf.sommer@tuebingen.mpg.de
 This library was generated at Caltech, Pasadena, USA and end
 sequenced at Vancouver, Canada.
 Seq primer: T7
 Class: fosmid ends.
 Location/Qualifiers
 1..10
 /organism="Pristionchus pacificus"
 /mol_type="genomic DNA"
 /strain="California"
 /db_xref="taxon:54126"
 /clone_lib="Mixed stage fosmid library of P. pacificus
 var. California"
 /note="Vector: pBplfos-5 Fosmid vector"

ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1
AUTHORS Brunaud V., Balergue S., Dubreucq B., Aubourg S., Samson F., Chauvin S., Bechtold N., Cruaud C., Derose R., Pelletier G., Lepoint J., Caboche M. and Lecharny A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
PUBMED 12446565
REFERENCE 2 (bases 1 to 10)
AUTHORS Balergue S.
TITLE Direct Submission
COMMENT Submitted (23-OCT-2003) Balergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomes program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>). Location/Qualifiers

FEATURES
source
1..10
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="621G09"
/clone_1lb="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Wassilewskija"
1..10
/note="T-DNA flanking sequence
right border"

Query Match 0.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 22 GCGCGGCAG 30
|||||
2 GCGCGGCAG 10

RESULT 127
AJ587026 10 bp DNA linear GSS 15-JAN-2004
LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone 062F10, genomic survey sequence.
ACCESSION AJ587026
VERSION AJ587026.1 GI:37936615
KEYWORDS GSS; left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1
AUTHORS Brunaud V., Balergue S., Dubreucq B., Aubourg S., Samson F., Chauvin S., Bechtold N., Cruaud C., Derose R., Pelletier G., Lepoint J., Caboche M. and Lecharny A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
PUBMED 12446565
REFERENCE 2 (bases 1 to 10)
AUTHORS Balergue S.
TITLE Direct Submission

JOURNAL Submitted (23-OCT-2003) Balergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomes program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>). Location/Qualifiers

FEATURES
source
1..10
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="062F10"
/clone_1lb="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Wassilewskija"
1..10
/note="T-DNA flanking sequence
left border"

Query Match 0.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 1715 ATTGCATTT 1723
|||||
1 AATTCATTT 9

RESULT 128
AJ679435 11 bp mRNA linear EST 29-JUN-2004
LOCUS AJ679435 CSEORAN04 Sus scrofa cDNA clone C0001779_B18, mRNA sequence.
ACCESSION AJ679435
VERSION AJ679435.1 GI:49412022
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 11)
AUTHORS Anderson S.I., Finlayson H.A. and Archibald A.L.
TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
JOURNAL Unpublished (2004)
COMMENT Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -minscore 20 and -mismatch 12 options. Vector: pBluescriptII (KS+) R. Site1: EcoRI R. Site2: NotI 5' Seq Primer M13F Normalised library constructed from pig uterus. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.ukgenomiceb.org. Location/Qualifiers

FEATURES
source
1..11
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001779_B18"
/issue_type="uterus"
/clone_1lb="CSEORAN04"
/note="Vector: pBluescriptII (KS+); Site 1: EcoRI; Site 2: NotI; Single pass sequencing. Normalised library

constructed from pig uterus."

Query Match 0.4%; Score 7.4; DB 1; Length 11;
AUTHORS
Best Local Similarity 88.9%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 438 CGCGAGGC 446
|||||
Db 3 CGCGGTGSC 11

RESULT 129
AJ681247 11 bp mRNA linear EST 29-JUN-2004
LOCUS
DEFINITION AJ681247 CSEQRAN04 Sus scrofa cDNA clone C001795_I24, mRNA
SEQUENCE
ACCESSION AJ681247
VERSION AJ681247.1 GI:49413837
KEYWORDS
SOURCE EST.
ORGANISM Sus scrofa (pig)
Sus scrofa (pig)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.

REFERENCE
AUTHORS 1 (bases 1 to 11)
TITLE Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
JOURNAL Development of cDNA and EST resources for studying reproduction and
COMMENT embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -mismatch 12 options. Vector:PB1uescriptII(KS+) R. Site1: EcoRI
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.
Location/Qualifiers
1. 11
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001795_I24"
/issue_type="uterus"
/clone_lib="CSEQRAN04"
/note="Vector: PB1uescriptII(KS+); Site_1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pig uterus."

FEATURES
source
1. 11
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001795_I24"
/issue_type="uterus"
/clone_lib="CSEQRAN04"
/note="Vector: PB1uescriptII(KS+); Site_1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pig uterus."

Query Match 0.4%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 438 CGCGAGGC 446
|||||
Db 3 CGCGGTGSC 11

RESULT 130
AJ683713 11 bp mRNA linear EST 29-JUN-2004
LOCUS
DEFINITION AJ683713 CSEQRAN04 Sus scrofa cDNA clone C001802_O06, mRNA
SEQUENCE
ACCESSION AJ683713
VERSION AJ683713.1 GI:49416303
KEYWORDS
SOURCE EST.
ORGANISM Sus scrofa (pig)
Sus scrofa (pig)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.

FEATURES
source
1. 11
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001802_O06"
/issue_type="uterus"
/clone_lib="CSEQRAN04"
/note="Vector: PB1uescriptII(KS+); Site_1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pig uterus."

REFERENCE
AUTHORS 1 (bases 1 to 11)
TITLE Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
JOURNAL Development of cDNA and EST resources for studying reproduction and
COMMENT embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -mismatch 12 options. Vector:PB1uescriptII(KS+) R. Site1: EcoRI
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.
Location/Qualifiers
1. 11
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001802_O06"
/issue_type="uterus"
/clone_lib="CSEQRAN04"
/note="Vector: PB1uescriptII(KS+); Site_1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pig uterus."

FEATURES
source
1. 11
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001802_O06"
/issue_type="uterus"
/clone_lib="CSEQRAN04"
/note="Vector: PB1uescriptII(KS+); Site_1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pig uterus."

Query Match 0.4%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 438 CGCGAGGC 446
|||||
Db 3 CGCGGTGSC 11

RESULT 131
AJ686459 11 bp mRNA linear EST 29-JUN-2004
LOCUS
DEFINITION AJ686459 CSEQRAN04 Sus scrofa cDNA clone C0001811_K23, mRNA
SEQUENCE
ACCESSION AJ686459
VERSION AJ686459.1 GI:49419049
KEYWORDS
SOURCE EST.
ORGANISM Sus scrofa (pig)
Sus scrofa (pig)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.

REFERENCE
AUTHORS 1 (bases 1 to 11)
TITLE Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
JOURNAL Development of cDNA and EST resources for studying reproduction and
COMMENT embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -mismatch 12 options. Vector:PB1uescriptII(KS+) R. Site1: EcoRI
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.
Location/Qualifiers
1. 11
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001811_K23"

FEATURES
source
1. 11
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001811_K23"

FEATURES
source
1. 11
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001811_K23"

/tissue_type="uterus"
/clone_id="CSEORAN04"
/note="Vector: pBluescriptII (KS+); Site 1: EcoRI; Site 2:
NotI; Single pass sequencing. Normalised library
constructed from pig uterus."

Query Match 0.4%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 438 CGCGAGGC 446
|||||
Db 3 CGCGGTGCG 11

RESULT 132
BM396384 11 bp mRNA linear EST 17-JAN-2002
LOCUS
DEFINITION 5009-0-2-H08.c.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION BM396384
VERSION BM396384.1 GI:18196422
KEYWORDS EST.
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila

REFERENCE Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.

AUTHORS Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,
Frankel, J., and Klobutcher, L.

TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP

Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
source location/Qualifiers

1..11
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_id="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 0.4%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 438 CGCGAGGC 446
|||||
Db 3 CGCGGTGCG 11

RESULT 133
BM397892 11 bp mRNA linear EST 17-JAN-2002
LOCUS
DEFINITION 5009-0-38-F04.c.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION BM397892
VERSION BM397892.1 GI:18197945
KEYWORDS EST.

SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila

REFERENCE Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
1 (bases 1 to 11)

AUTHORS Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,
Frankel, J., and Klobutcher, L.

TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)

COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
source location/Qualifiers

1..11
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_id="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 0.4%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 438 CGCGAGGC 446
|||||
Db 3 CGCGGTGCG 11

RESULT 134
BM398341 12 bp mRNA linear EST 17-JAN-2002
LOCUS
DEFINITION 5009-0-44-D05.c.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION BM398341
VERSION BM398341.1 GI:18198394
KEYWORDS EST.

SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila

REFERENCE Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.

AUTHORS Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,
Frankel, J., and Klobutcher, L.

TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP

Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
source location/Qualifiers

1..12
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_id="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 0.4%; Score 7.4; DB 1; Length 12;
Best Local Similarity 88.9%; Pred. No. 11e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 438 CGCGAGGC 446

Db 2 GCCTGTGC 10

RESULT 135
AJ666341/c
LOCUS

DEFINITION AJ666341 CSEORAN09 Sus scrofa cDNA clone C0000033_C09, mRNA

ACCESSION AJ666341
VERSION AJ666341.1 GI:49350792
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sub.

REFERENCE 1 (bases 1 to 13)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
Unpublished (2004)
COMMENT Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross_match with the -mismscore 20 and -mismatch 12 options. Vector:pbLuescriptII(KS+). R. Site 1: EcoRI R. Site 2: NotI Description: Normalised library constructed from pooled tissue from day 30 placentas. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.atkgenomics.org.

FEATURES
source location/Qualifiers
1..13
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0000033_C09"
/tissue_type="placenta"
/clone_lib="CSEORAN09"
/note="Vector: pbLuescriptII(KS+); Site_1: EcoRI; Site_2: NotI; Single pass sequencing. Normalised library constructed from pooled tissue from day 30 placentas."

Query Match 0.4%; Score 7.4; DB 1; Length 13;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1496 GAAATTCCTC 1504
||| |||||
9 GAATTTCCC 1

Db

RESULT 136
CF297970/c
LOCUS

DEFINITION CF297970 8 bp mRNA linear EST 15-AUG-2003
7LEAF--01-C16.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--01-C16, mRNA sequence.

ACCESSION CF297970
VERSION CF297970.1 GI:33669731
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 8)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source location/Qualifiers
1..8
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF1-06-009"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="ABF3-overexpressing transgenic rice lambda phage cDNA library (ABF1)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhoI, Leaf was dried for 2hrs. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was prepared from ABA-responsive

Query Match 0.4%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 633 GCCTGTCA 639
||| |||||
8 GCCTGTCA 2

Db

RESULT 137
CF305141
LOCUS

DEFINITION CF305141 8 bp mRNA linear EST 15-AUG-2003
ABF1--06-009.g1 ABF3-overexpressing transgenic rice lambda phage cDNA library (ABF1) Oryza sativa (japonica cultivar-group) cDNA clone ABF1--06-009, mRNA sequence.

ACCESSION CF305141
VERSION CF305141.1 GI:33676902
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 8)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source location/Qualifiers
1..8
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF1-06-009"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="ABF3-overexpressing transgenic rice lambda phage cDNA library (ABF1)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhoI, Leaf was dried for 2hrs. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was prepared from ABA-responsive

element binding transcription factor 3 overexpression line."

Query Match 0.4%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1303 CACGAGG 1309
Db 2 CACGAGG 8

RESULT 138
CF306116 8 bp mRNA linear EST 15-AUG-2003
LOCUS HDAl--02-L22.g1 OSHDAC1-overexpressing transgenic rice lambda phage
DEFINITION cDNA library I (HDAl) Oryza sativa (japonica cultivar-group) cDNA
clone HDAl--02-L22, mRNA sequence.
CF306116
ACCESSION CF306116.1 GI:33677877
VERSION EST.
KEYWORDS Oryza sativa (japonica cultivar-group)
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 8)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source 1..8
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HDAl--02-L22"
/cissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OSHDA1-overexpressing transgenic rice lambda
phage cDNA library I (HDAl)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Callus was treated with ABA(20um) for 1hour. cDNA
was inserted into lambda Uni-ZAP XR vector at 5' end with
EcoRI and 3' end with XhoI site. mRNA was derived from
rice Histone Deacetylase overexpression line."

Query Match 0.4%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1303 CACGAGG 1309
Db 2 CACGAGG 8

RESULT 139
CF306762 8 bp mRNA linear EST 15-AUG-2003
LOCUS HDAl--04-M13.g1 OSHDAC1-overexpressing transgenic rice lambda phage
DEFINITION cDNA library I (HDAl) Oryza sativa (japonica cultivar-group) cDNA
clone HDAl--04-M13, mRNA sequence.
CF306762
ACCESSION CF306762.1 GI:33678523
VERSION

KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 8)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source 1..8
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HDAl--04-M13"
/cissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OSHDA1-overexpressing transgenic rice lambda
phage cDNA library I (HDAl)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Callus was treated with ABA(20um) for 1hour. cDNA
was inserted into lambda Uni-ZAP XR vector at 5' end with
EcoRI and 3' end with XhoI site. mRNA was derived from
rice Histone Deacetylase overexpression line."

Query Match 0.4%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1303 CACGAGG 1309
Db 2 CACGAGG 8

RESULT 140
CF322514 8 bp mRNA linear EST 18-AUG-2003
LOCUS HDN--01-E13.g1 OSHDAC1-overexpressing transgenic rice lambda phage
DEFINITION cDNA library II (HDN) Oryza sativa (japonica cultivar-group) cDNA
clone HDN--01-E13, mRNA sequence.
CF322514
ACCESSION CF322514.1 GI:33793267
VERSION EST.
KEYWORDS Oryza sativa (japonica cultivar-group)
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 8)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source 1..8
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HDN--01-E13"
/cissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OSHDA1-overexpressing transgenic rice lambda
phage cDNA library II (HDN)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Callus was treated with ABA(20um) for 1hour. cDNA
was inserted into lambda Uni-ZAP XR vector at 5' end with
EcoRI and 3' end with XhoI site. mRNA was derived from
rice Histone Deacetylase overexpression line."

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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HDN--01-B13"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OshDAC1-overexpressing transgenic rice lambda
phage cDNA library II (HDN)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."

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Query Match 0.4%; Score 7; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1303 CACGAGG 1309
 Db 2 CACGAGG 8

RESULT 141

LOCUS CF322653 8 bp mRNA linear EST 18-AUG-2003
 DEFINITION HDN--01-K24.g1 OshDAC1-overexpressing transgenic rice lambda phage
 cDNA library II (HDN) Oryza sativa (japonica cultivar-group) cDNA
 clone HDN--01-K24, mRNA sequence.

ACCESSION CF322653
 VERSION CF322653.1 GI:33793540

SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

JOURNAL Large-scale Sequencing Analysis of Rice ESTs
 COMMENT Unpublished (2003)

CONTACT Nahm B.H.

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Yongin, Kyonggi, Korea
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Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

location/Qualifiers

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1..8
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HDN--01-K24"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OshDAC1-overexpressing transgenic rice lambda
phage cDNA library II (HDN)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."

```

Query Match 0.4%; Score 7; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1303 CACGAGG 1309
 Db 2 CACGAGG 8

RESULT 142

LOCUS CF323889 8 bp mRNA linear EST 18-AUG-2003
 DEFINITION HDN--05-A16.g1 OshDAC1-overexpressing transgenic rice lambda phage
 cDNA library II (HDN) Oryza sativa (japonica cultivar-group) cDNA
 clone HDN--05-A16, mRNA sequence.

ACCESSION CF323889
 VERSION CF323889.1 GI:33796043

SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

JOURNAL Large-scale Sequencing Analysis of Rice ESTs
 COMMENT Unpublished (2003)

CONTACT Nahm B.H.
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 of Bioscience and Bioinformatics, Myongji University

Yongin, Kyonggi, Korea
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Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

location/Qualifiers

```

1..8
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HDN--05-A16"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OshDAC1-overexpressing transgenic rice lambda
phage cDNA library II (HDN)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."

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Query Match 0.4%; Score 7; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1303 CACGAGG 1309
 Db 2 CACGAGG 8

RESULT 143

LOCUS CF324406 8 bp mRNA linear EST 18-AUG-2003
 DEFINITION HDN--06-H05.g1 OshDAC1-overexpressing transgenic rice lambda phage
 cDNA library II (HDN) Oryza sativa (japonica cultivar-group) cDNA
 clone HDN--06-H05, mRNA sequence.

ACCESSION CF324406
 VERSION CF324406.1 GI:33797080

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

JOURNAL Large-scale Sequencing Analysis of Rice ESTs
 COMMENT Unpublished (2003)

CONTACT Nahm B.H.

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 of Bioscience and Bioinformatics, Myongji University

Yongin, Kyonggi, Korea
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Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,O.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HDN-06-H05"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OshDA1-overexpressing transgenic rice lambda
phage cDNA library II (HDN)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.4%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1303 CACGAGG 1309
|||||
2 CACGAGG 8

Db

RESULT 144
CF325379 8 bp mRNA linear EST 18-AUG-2003
LOCUS JMT1--03-B08.g1 AtUMT-overexpressing transgenic rice lambda phage
DEFINITION cDNA library (JMT1) Oryza sativa (japonica cultivar-group) cDNA
clone JMT1--03-B08, mRNA sequence.
ACCESSION CF325379.1 GI:33799039
VERSION CF325379.1
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 8)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source
1..8
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT1--03-B08"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="AtUMT-overexpressing transgenic rice lambda
phage cDNA library (JMT1)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site. mRNA was
prepared from Arabidopsis jasmonate Carboxyl
methyltransferase overexpression line."

/lab_host="E.coli SOLR"
/clone_lib="AtUMT-overexpressing transgenic rice lambda
phage cDNA library (JMT1)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site. mRNA was
prepared from Arabidopsis jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 0.4%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1303 CACGAGG 1309
|||||
2 CACGAGG 8

Db

RESULT 145
CF325469 8 bp mRNA linear EST 18-AUG-2003
LOCUS JMT1--03-F06.g1 AtUMT-overexpressing transgenic rice lambda phage
DEFINITION cDNA library (JMT1) Oryza sativa (japonica cultivar-group) cDNA
clone JMT1--03-F06, mRNA sequence.
ACCESSION CF325469.1 GI:33799223
VERSION CF325469.1
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 8)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source
1..8
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT1--03-F06"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="AtUMT-overexpressing transgenic rice lambda
phage cDNA library (JMT1)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site. mRNA was
prepared from Arabidopsis jasmonate Carboxyl
methyltransferase overexpression line."

LOCUS CF325485 8 bp mRNA linear EST 18-AUG-2003
 DEFINITION JMT1--03-F22.g1 ActMT-overexpressing transgenic rice lambda phage
 cDNA library (JMT1) Oryza sativa (japonica cultivar-group) cDNA
 clone JMT1--03-F22, mRNA sequence.
 ACCESSION CF325485
 VERSION CF325485.1 GI:33799255
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep
 clade; Euhartioideae; Oryzaceae; Oryza.
 1 (bases 1 to 8)
 REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT Nahm B.H.
 COMMENT Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers
 1..8
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="JMT1--03-F22"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="ActMT-overexpressing transgenic rice lambda
 phage cDNA library (JMT1)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
 end with EcoRI and 3' end with XhoI site. mRNA was
 prepared from Arabidopsis thaliana Carboxyl
 methyltransferase overexpression line."

Query Match 0.4%; Score 7; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1303 CACGAGG 1309
 |||||
 Db 2 CACGAGG 8

RESULT 147
 CF330558 8 bp mRNA linear EST 18-AUG-2003
 LOCUS NACL--06-F04.g1 Rice callus plasmid cDNA library (NACL) Oryza
 DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--06-F04, mRNA
 sequence.
 ACCESSION CF330558
 VERSION CF330558.1 GI:33809354
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep
 clade; Euhartioideae; Oryzaceae; Oryza.
 1 (bases 1 to 8)
 REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT Nahm B.H.
 COMMENT Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers
 1..8
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="NACL--06-F04"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.4%; Score 7; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 633 GCTGTCA 639
 |||||
 Db 8 GCTGTCA 2

RESULT 148
 CF339091 8 bp mRNA linear EST 18-AUG-2003
 LOCUS RCL1--03-M05.g1 Regenerated callus lambda phage cDNA library (RCL1)
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone RCL1--03-M05,
 mRNA sequence.
 ACCESSION CF339091
 VERSION CF339091.1 GI:33826564
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep
 clade; Euhartioideae; Oryzaceae; Oryza.
 1 (bases 1 to 8)
 REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT Nahm B.H.
 COMMENT Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers
 1..8
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="RCL1--03-M05"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli SOLR"
 /clone_lib="Regenerated callus lambda phage cDNA library
 (RCL1)"
 /note="Vector: pBluescript SK(+); Site 1: SstI; Site 2:
 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
 end with SstI and 3' end with XhoI site. Callus was
 induced on 2N6 media for 30 days and cultured for 36hrs on
 regenerated media"

Query Match 0.4%; Score 7; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1096 AGCTCCA 1102
8 AGCTCCA 2

RESULT 149

CV933258 8 bp mRNA linear EST 25-JAN-2005
LOCUS CV933258
DEFINITION PMcsm_0140 mating of 88069 (A1) and 618 (A2) Phytophthora infestans
cDNA, mRNA sequence.

ACCESSION CV933258
VERSION CV933258.1 GI:58122873
KEYWORDS EST.

SOURCE Phytophthora infestans (potato late blight agent)
ORGANISM Eukaryota; Stramenopiles; Oomycetes; Peronosporales; Phytophthora.

REFERENCE 1 (bases 1 to 8)
Randall,T., Dwyer,R.A., Huitema,E., Beyer,K., Cvitanich,C.,
Kelkar,H., Fong,A.M., Gates,K., Roberts,S., Yatikan,E., Gaffney,T.,
Law,M., Testa,A., Torco-Alalibo,A., Zhang,M., Zheng,L., Mueller,E.,
Mindas,J., Binder,A., Birch,P.R.J., Gisi,U., Govers,F., Gow,N.A.,
Mauch,F., van West,P., Waugh,M.E., Yu,J., Boller,T., Kamoun,S.,
Lam,S.T. and Udelsom, H.S.
Large-scale gene discovery in the oomycete Phytophthora infestans
reveals likely components of phytopathogenicity shared with true
fungi

TITLE Mol. Plant-Microbe Interact. 18 (3), 229-243 (2005)
JOURNAL 15782637
PUBMED
COMMENT Contact: Judelson HS
Department of Plant Pathology
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Fax: 909 787 4234
Email: howard.judelson@ucr.edu.

FEATURES
source Location/Qualifiers

1..8
/organism="Phytophthora infestans"
/mol_type="mRNA"
/strain="88069 and 618"
/db_xref="taxon:4787"
/sex="A1 and A2"
/clone_lib="mating of 88069 (A1) and 618 (A2)"
/note="Vector: pSPORT1"

Query Match 0.4%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1688 ACCAGCT 1694
2 ACCAGCT 8

RESULT 150

CV933304 8 bp mRNA linear EST 25-JAN-2005
LOCUS CV933304
DEFINITION PMcsm_0589 mating of 88069 (A1) and 618 (A2) Phytophthora infestans
cDNA, mRNA sequence.

ACCESSION CV933304
VERSION CV933304.1 GI:58122919
KEYWORDS EST.

SOURCE Phytophthora infestans (potato late blight agent)
ORGANISM Eukaryota; Stramenopiles; Oomycetes; Peronosporales; Phytophthora.

REFERENCE 1 (bases 1 to 8)
Randall,T., Dwyer,R.A., Huitema,E., Beyer,K., Cvitanich,C.,
Kelkar,H., Fong,A.M., Gates,K., Roberts,S., Yatikan,E., Gaffney,T.,
Law,M., Testa,A., Torco-Alalibo,A., Zhang,M., Zheng,L., Mueller,E.,
Mindas,J., Binder,A., Birch,P.R.J., Gisi,U., Govers,F., Gow,N.A.,
Mauch,F., van West,P., Waugh,M.E., Yu,J., Boller,T., Kamoun,S.,
Lam,S.T. and Udelsom, H.S.
Large-scale gene discovery in the oomycete Phytophthora infestans
reveals likely components of phytopathogenicity shared with true
fungi

Mauch,F., van West,P., Waugh,M.E., Yu,J., Boller,T., Kamoun,S.,
Lam,S.T. and Udelsom, H.S.
Large-scale gene discovery in the oomycete Phytophthora infestans
reveals likely components of phytopathogenicity shared with true
fungi

TITLE Mol. Plant-Microbe Interact. 18 (3), 229-243 (2005)
JOURNAL 15782637
PUBMED
COMMENT Contact: Judelson HS
Department of Plant Pathology
University of California
Webster Hall, Riverside, CA 92521, USA
Tel: 909 787 4199
Fax: 909 787 4234
Email: howard.judelson@ucr.edu.

FEATURES
source Location/Qualifiers

1..8
/organism="Phytophthora infestans"
/mol_type="mRNA"
/strain="88069 and 618"
/db_xref="taxon:4787"
/sex="A1 and A2"
/clone_lib="mating of 88069 (A1) and 618 (A2)"
/note="Vector: pSPORT1"

Query Match 0.4%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1688 ACCAGCT 1694
2 ACCAGCT 8

RESULT 151

CVX001098 8 bp mRNA linear EST 03-DEC-2004
LOCUS CVX001098/c
DEFINITION i39b01.bl left Cardiac Ventricle (DOGST7) Canis familiaris cDNA,
mRNA sequence.

ACCESSION CVX001098
VERSION CVX001098.1 GI:56272514
KEYWORDS EST.

SOURCE Canis familiaris (dog)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butcheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.

REFERENCE 1 (bases 1 to 8)
Balija,V.S., Nascimento,L.U. and McCombie,W.R.
ESTs from Canis familiaris left cardiac ventricle (dog)
Unpublished (2004)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org.

FEATURES
source Location/Qualifiers

1..8
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
/tissue_type="Cardiac muscle"
/dev_stage="3 month old normal canine"
/lab_host="X110 Gold"
/clone_lib="Left Cardiac Ventricle (DOGST7)"
/note="Organ: Heart; Vector: pBluescript II SK; Site 1:
EcoRI, Site 2: XhoI; Library constructed using pBluescript
XR kit from Stratagene. Cloned cDNA was size selected
between 1-3 kb. Tissue supplied by Mark Haakins VMD, PhD,
Pathology and Medical Genetics, School of Veterinary
Medicine, University of Pennsylvania, 3800 Spruce Street,

Philadelphia, PA 19104-6051"

Query Match 0.4%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred.No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1303 CACGAGC 1309
Db 7 CACGAGG 1

RESULT 152
CX001172/c

LOCUS 8 bp mRNA linear EST 03-DEC-2004
DEFINITION i439e06.b1 Left Cardiac Ventricle (DOGE5T7) Canis familiaris cDNA,
mRNA sequence.

ACCESSION CX001172
VERSION CX001172.1 GI:56272588
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris

REFERENCE 1 (bases 1 to 8)
AUTHORS Balija,V.S., Nascimento,L.U. and McCombie,W.R.
TITLE ESTs from Canis familiaris left cardiac ventricle (dog)
JOURNAL Unpublished (2004)
COMMENT Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org.

FEATURES
source Location/Qualifiers

1..8
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
/tissue_type="Cardiac muscle"
/dev_stage="3 month old normal canine"
/lab_host="XL10 Gold"
/clone_lib="Left Cardiac Ventricle (DOGE5T7)"
/note="Organ: Heart; Vector: pBluescript II SK; Site_1:
ECORI; Site_2: XhoI; Library constructed using pBluescript
XR kit from Stratagene. Cloned cDNA was size selected
between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD,
Pathology and Medical Genetics, School of Veterinary
Medicine, University of Pennsylvania, 3800 Spruce Street,
Philadelphia, PA 19104-6051"

Query Match 0.4%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred.No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1296 GGGGGCC 1302
Db 7 GGGGGCC 1

RESULT 153
CX001200

LOCUS 8 bp mRNA linear EST 03-DEC-2004
DEFINITION i439f09.g1 Left Cardiac Ventricle (DOGE5T7) Canis familiaris cDNA,
mRNA sequence.

ACCESSION CX001200
VERSION CX001200.1 GI:56272616
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 8)
AUTHORS Balija,V.S., Nascimento,L.U. and McCombie,W.R.
TITLE ESTs from Canis familiaris left cardiac ventricle (dog)
JOURNAL Unpublished (2004)
COMMENT Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org.

FEATURES
source Location/Qualifiers

1..8
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
/tissue_type="Cardiac muscle"
/dev_stage="3 month old normal canine"
/lab_host="XL10 Gold"
/clone_lib="Left Cardiac Ventricle (DOGE5T7)"
/note="Organ: Heart; Vector: pBluescript II SK; Site_1:
ECORI; Site_2: XhoI; Library constructed using pBluescript
XR kit from Stratagene. Cloned cDNA was size selected
between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD,
Pathology and Medical Genetics, School of Veterinary
Medicine, University of Pennsylvania, 3800 Spruce Street,
Philadelphia, PA 19104-6051"

Query Match 0.4%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred.No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1303 CACGAGC 1309
Db 2 CACGAGG 8

RESULT 154
CX001601/c

LOCUS 8 bp mRNA linear EST 03-DEC-2004
DEFINITION i442a05.b1 Left Cardiac Ventricle (DOGE5T7) Canis familiaris cDNA,
mRNA sequence.

ACCESSION CX001601
VERSION CX001601.1 GI:56273017
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.

REFERENCE 1 (bases 1 to 8)
AUTHORS Balija,V.S., Nascimento,L.U. and McCombie,W.R.
TITLE ESTs from Canis familiaris left cardiac ventricle (dog)
JOURNAL Unpublished (2004)
COMMENT Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org.

FEATURES
source Location/Qualifiers

1..8
/organism="Canis familiaris"
/mol_type="mRNA"
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/sex="Unknown"
/tissue_type="Cardiac muscle"
/dev_stage="3 month old normal canine"
/lab_host="XL10 Gold"

/clone.lib="Left Cardiac Ventricle (DOGEST7)"
/note="Organ: Heart; Vector: pbluescript II SK; Site: 1;
ECORI; Site_2: XhoI; Library constructed using pbluescript
XR kit from Stratagene. Cloned cDNA was size selected
between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD,
Pathology and Medical Genetics, School of Veterinary
Medicine, University of Pennsylvania, 3800 Spruce Street,
Philadelphia, PA 19104-6051"

Query Match 0.4%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1296 GGGGGCC 1302
|||||
Db 7 GGGGGCC 1

RESULT 155
CX001811 8 bp mRNA linear EST 03-DEC-2004
LOCUS 1v43b1.g1 Left Cardiac Ventricle (DOGEST7) Canis familiaris cDNA,
DEFINITION mRNA sequence.
ACCESSION CX001811 GI:56273227
VERSION
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.

REFERENCE 1 (bases 1 to 8)
AUTHORS Balija,V.S., Nascimento,L.U. and McCombie,W.R.
TITLE ESTs from Canis familiaris left cardiac ventricle (dog)
JOURNAL Unpublished (2004)
COMMENT Contact: W. Richard McCombie
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Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org.
Location/Qualifiers

FEATURES
source
1..8
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
/tissue_type="Cardiac muscle"
/dev_stage="3 month old normal canine"
/lab_host="XL10 Gold"
/clone.lib="Left Cardiac Ventricle (DOGEST7)"
/note="Organ: Heart; Vector: pbluescript II SK; Site: 1;
ECORI; Site_2: XhoI; Library constructed using pbluescript
XR kit from Stratagene. Cloned cDNA was size selected
between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD,
Pathology and Medical Genetics, School of Veterinary
Medicine, University of Pennsylvania, 3800 Spruce Street,
Philadelphia, PA 19104-6051"

Query Match 0.4%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1303 CACGAGG 1309
|||||
Db 2 CACGAGG 8

RESULT 156
CX001864/C 8 bp mRNA linear EST 03-DEC-2004
LOCUS 1v43e04.bl Left Cardiac Ventricle (DOGEST7) Canis familiaris cDNA,
DEFINITION

mRNA sequence.
ACCESSION CX001864
VERSION CX001864.1 GI:56273280
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.

REFERENCE 1 (bases 1 to 8)
AUTHORS Balija,V.S., Nascimento,L.U. and McCombie,W.R.
TITLE ESTs from Canis familiaris left cardiac ventricle (dog)
JOURNAL Unpublished (2004)
COMMENT Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org.
Location/Qualifiers

FEATURES
source
1..8
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
/tissue_type="Cardiac muscle"
/dev_stage="3 month old normal canine"
/lab_host="XL10 Gold"
/clone.lib="Left Cardiac Ventricle (DOGEST7)"
/note="Organ: Heart; Vector: pbluescript II SK; Site: 1;
ECORI; Site_2: XhoI; Library constructed using pbluescript
XR kit from Stratagene. Cloned cDNA was size selected
between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD,
Pathology and Medical Genetics, School of Veterinary
Medicine, University of Pennsylvania, 3800 Spruce Street,
Philadelphia, PA 19104-6051"

Query Match 0.4%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1303 CACGAGG 1309
|||||
Db 7 CACGAGG 1

RESULT 157
CX001954 8 bp mRNA linear EST 03-DEC-2004
LOCUS 1v44a06.g1 Left Cardiac Ventricle (DOGEST7) Canis familiaris cDNA,
DEFINITION mRNA sequence.
ACCESSION CX001954
VERSION CX001954.1 GI:56273370
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.

REFERENCE 1 (bases 1 to 8)
AUTHORS Balija,V.S., Nascimento,L.U. and McCombie,W.R.
TITLE ESTs from Canis familiaris left cardiac ventricle (dog)
JOURNAL Unpublished (2004)
COMMENT Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org.
Location/Qualifiers

FEATURES
source
1..8

/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
/tissue_type="Cardiac muscle"
/dev_stage="3 month old normal canine"
/lab_host="X110 Gold"
/clone_lib="Left Cardiac Ventricle (DOGEST7)"
/note="Organ: Heart; Vector: pBluescript II SK; Site_1: EcotRI; Site_2: XhoI; Library constructed using pBluescript XR kit from Stratagene. Cloned cDNA was size selected between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD, Pathology and Medical Genetics, School of Veterinary Medicine, University of Pennsylvania, 3800 Spruce Street, Philadelphia, PA 19104-6051"

Query Match 0.4%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1303 CACGAG 1309
|||||

Db 2 CACGAG 8
|||||

RESULT 158
CX001980 8 bp mRNA linear EST 03-DEC-2004
LOCUS i144b07.g1 Left Cardiac Ventricle (DOGEST7) Canis familiaris CDNA,
DEFINITION mRNA sequence.
ACCESSION CX001980
VERSION CX001980.1 GI:56273396
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
1 (bases 1 to 8)
Baliya,V.S., Nascimento,L.U. and McCombie,W.R.
ESTs from Canis familiaris left cardiac ventricle (dog)
Unpublished (2004)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org.
Location/Qualifiers
1..8
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
/tissue_type="Cardiac muscle"
/dev_stage="3 month old normal canine"
/lab_host="X110 Gold"
/clone_lib="Left Cardiac Ventricle (DOGEST7)"
/note="Organ: Heart; Vector: pBluescript II SK; Site_1: EcotRI; Site_2: XhoI; Library constructed using pBluescript XR kit from Stratagene. Cloned cDNA was size selected between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD, Pathology and Medical Genetics, School of Veterinary Medicine, University of Pennsylvania, 3800 Spruce Street, Philadelphia, PA 19104-6051"

Query Match 0.4%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1303 CACGAG 1309
|||||

Db 2 CACGAG 8
|||||

REFERENCE
AUTHORS Baliya,V.S., Nascimento,L.U. and McCombie,W.R.
TITLES ESTs from Canis familiaris left cardiac ventricle (dog)
JOURNAL Unpublished (2004)
COMMENT Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org.
Location/Qualifiers
1..8
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
/tissue_type="Cardiac muscle"
/dev_stage="3 month old normal canine"
/lab_host="X110 Gold"
/clone_lib="Left Cardiac Ventricle (DOGEST7)"
/note="Organ: Heart; Vector: pBluescript II SK; Site_1: EcotRI; Site_2: XhoI; Library constructed using pBluescript XR kit from Stratagene. Cloned cDNA was size selected between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD, Pathology and Medical Genetics, School of Veterinary Medicine, University of Pennsylvania, 3800 Spruce Street, Philadelphia, PA 19104-6051"

FEATURES
source
1..8
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
/tissue_type="Cardiac muscle"
/dev_stage="3 month old normal canine"
/lab_host="X110 Gold"
/clone_lib="Left Cardiac Ventricle (DOGEST7)"
/note="Organ: Heart; Vector: pBluescript II SK; Site_1: EcotRI; Site_2: XhoI; Library constructed using pBluescript XR kit from Stratagene. Cloned cDNA was size selected between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD, Pathology and Medical Genetics, School of Veterinary Medicine, University of Pennsylvania, 3800 Spruce Street, Philadelphia, PA 19104-6051"

Query Match 0.4%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1303 CACGAG 1309
|||||

Db 2 CACGAG 8
|||||

RESULT 160
CX002747 8 bp mRNA linear EST 03-DEC-2004
LOCUS i13310.g1 Left Cardiac Ventricle (DOGEST7) Canis familiaris CDNA,
DEFINITION mRNA sequence.
ACCESSION CX002747
VERSION CX002747.1 GI:56274163
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
1 (bases 1 to 8)
Baliya,V.S., Nascimento,L.U. and McCombie,W.R.
ESTs from Canis familiaris left cardiac ventricle (dog)
Unpublished (2004)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center

Db 2 CACGAG 8
|||||

RESULT 159
CX002359 8 bp mRNA linear EST 03-DEC-2004
LOCUS i13102.g1 Left Cardiac Ventricle (DOGEST7) Canis familiaris CDNA,
DEFINITION mRNA sequence.
ACCESSION CX002359
VERSION CX002359.1 GI:56273775
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
1 (bases 1 to 8)
Baliya,V.S., Nascimento,L.U. and McCombie,W.R.
ESTs from Canis familiaris left cardiac ventricle (dog)
Unpublished (2004)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org.
Location/Qualifiers
1..8
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
/tissue_type="Cardiac muscle"
/dev_stage="3 month old normal canine"
/lab_host="X110 Gold"
/clone_lib="Left Cardiac Ventricle (DOGEST7)"
/note="Organ: Heart; Vector: pBluescript II SK; Site_1: EcotRI; Site_2: XhoI; Library constructed using pBluescript XR kit from Stratagene. Cloned cDNA was size selected between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD, Pathology and Medical Genetics, School of Veterinary Medicine, University of Pennsylvania, 3800 Spruce Street, Philadelphia, PA 19104-6051"

FEATURES
source
1..8
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
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/dev_stage="3 month old normal canine"
/lab_host="X110 Gold"
/clone_lib="Left Cardiac Ventricle (DOGEST7)"
/note="Organ: Heart; Vector: pBluescript II SK; Site_1: EcotRI; Site_2: XhoI; Library constructed using pBluescript XR kit from Stratagene. Cloned cDNA was size selected between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD, Pathology and Medical Genetics, School of Veterinary Medicine, University of Pennsylvania, 3800 Spruce Street, Philadelphia, PA 19104-6051"

Query Match 0.4%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1303 CACGAG 1309
|||||

Db 2 CACGAG 8
|||||

RESULT 160
CX002747 8 bp mRNA linear EST 03-DEC-2004
LOCUS i13310.g1 Left Cardiac Ventricle (DOGEST7) Canis familiaris CDNA,
DEFINITION mRNA sequence.
ACCESSION CX002747
VERSION CX002747.1 GI:56274163
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
1 (bases 1 to 8)
Baliya,V.S., Nascimento,L.U. and McCombie,W.R.
ESTs from Canis familiaris left cardiac ventricle (dog)
Unpublished (2004)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org

FEATURES

source

1..8
Location/Qualifiers
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
/tissue_type="Cardiac muscle"
/dev_stage="3 month old normal canine"
/lab_host="XL10 Gold"
/clone_id="Left Cardiac Ventricle (DOGEST7)"
/note="Organ: Heart; Vector: pBluescript II SK; Site 1; Escori; Site 2: XhoI; Library constructed using pBluescript XR kit from Stratagene. Cloned cDNA was size selected between 1-3 kb. Tissue supplied by Mark Haekins VMD, PhD, Pathology and Medical Genetics, School of Veterinary Medicine, University of Pennsylvania, 3800 Spruce Street, Philadelphia, PA 19104-6051"

Query Match 0.4%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Mismatches 0; Gaps 0;
Matches 7; Conservative 0; Indels 0

QY 1303 CACGAGG 1309

Db 2 CACGAGG 8

RESULT 161
LOCUS CX003296 8 bp mRNA linear EST 03-DEC-2004
DEFINITION i366f10.g1 left Cardiac Ventricle (DOGEST7) Canis familiaris cDNA,
mRNA sequence.
ACCESSION CX003296
VERSION CX003296.1 GI:56274712
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE 1 (bases 1 to 8)
AUTHORS Balija,V.S., Nascimbeno,L.U. and McCombie,W.R.
TITLE ESTs from Canis familiaris left cardiac ventricle (dog)
JOURNAL Unpublished (2004)
COMMENT Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org

FEATURES
source Location/Qualifiers

1..8
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
/tissue_type="Cardiac muscle"
/dev_stage="3 month old normal canine"
/lab_host="XL10 Gold"
/clone_id="Left Cardiac Ventricle (DOGEST7)"
/note="Organ: Heart; Vector: pBluescript II SK; Site 1; Escori; Site 2: XhoI; Library constructed using pBluescript XR kit from Stratagene. Cloned cDNA was size selected between 1-3 kb. Tissue supplied by Mark Haekins VMD, PhD, Pathology and Medical Genetics, School of Veterinary Medicine, University of Pennsylvania, 3800 Spruce Street, Philadelphia, PA 19104-6051"

Query Match 0.4%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Mismatches 0; Gaps 0;
Matches 7; Conservative 0; Indels 0

QY 1303 CACGAGG 1309

Db 2 CACGAGG 8

RESULT 162
LOCUS DR025726 8 bp mRNA linear EST 26-MAY-2005
DEFINITION Osmo00576 F. cylindrus osmotic stress library Fragiliariopsis
cylindrus cDNA clone Fcyl187a23h01.s1, mRNA sequence.
ACCESSION DR025726
VERSION DR025726.1 GI:66748089
KEYWORDS EST.
SOURCE Fragiliariopsis cylindrus
Fragiliariopsis cylindrus
Eukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae;
Bacillariophycidae; Bacillariales; Bacillariaceae; Fragiliariopsis.

REFERENCE 1 (bases 1 to 8)
AUTHORS Krell,A. and Gloeckner,G.
TITLE Analysis of an osmotic stress induced cDNA library of the
psychrophilic diatom Fragiliariopsis cylindrus
JOURNAL Unpublished (2004)
COMMENT Contact: Krell, Andreas; Gloeckner, Gernot
Biological Oceanography, Sea ice research; Genome Analysis
Alfred-Wegener-Institute for Polar and Marine Research; Institute
for Molecular Biotechnology
Am Handelshafen 12, D-27570 Bremerhaven, Germany; Beutenbergstr.
11, D-07745 Jena, Germany
Tel: ++49 471 48311812; ++49 3641 656440
Fax: ++49 471 48311425; ++49 3641 656255
Email: akrell@awi-bremerhaven.de; gernot@imb-jena.de

PCR Primers
FORWARD: 5'M13
BACKWARD: 3'M13
Seq primer: 5'GTAAACGACGCGCCAG 3'.
Location/Qualifiers

1..8
/organism="Fragiliariopsis cylindrus"
/mol_type="mRNA"
/db_xref="taxon:186039"
/clone_id="Fcyl187a23h01.s1"
/note="Samples for total RNA isolation were taken continuous for 5 days after a salt shock treatment increasing salinity from 34 to 60 PSU. Total RNA extraktion was performed with RNAqueous (Ambion) and mRNA purification with polyA Purist (Ambion). Further steps were carried out as described in the Clontecher Kit. cDNA size fractionation was carried out with CHROMA Spin-400 columns and additionally on a gel."

FEATURES
source Location/Qualifiers

QY 1593 AAAAATC 1599
Db 1 AAAAATC 7

Query Match 0.4%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Mismatches 0; Gaps 0;
Matches 7; Conservative 0; Indels 0

RESULT 163
LOCUS DT909735 8 bp mRNA linear EST 19-SEP-2005
DEFINITION BMSB16597 Hematopoietic stem cells Mus musculus cDNA, mRNA
sequence.
ACCESSION DT909735
VERSION DT909735.1 GI:75890216
KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 8)
Pritsker M., Doniger, T.T., Kramer, L.C., Westcott, S.E. and
Lemischka, I.R.
Diversification of Stem Cell Molecular Repertoire by Alternative
Splicing
Proc. Natl. Acad. Sci. U.S.A. (2005) In press

JOURNAL Contact: Pritsker M
Lab of Ihor Lemischka, Department of Molecular Biology
Princeton University
Princeton, NJ 08544, USA
Tel: 609 258 5657
Fax: 609 258 1704
Email: pritsker@molbio.princeton.edu.

COMMENT Location/Qualifiers

FEATURES

source 1..8
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/tissue_type="Hematopoietic stem cells"
/cell_type="Hematopoietic stem cells"
/clone_lib="Hematopoietic stem cells"
/note="cDNA library was made from FACS-purified
hematopoietic stem cells"

Query Match 0.4%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 160 GCTGCAG 166
|||||
1 GCTGCAG 7

Db

RESULT 164
LOCUS CL659535 8 bp DNA linear GSS 09-JUL-2004
DEFINITION PRI0134b.G05 - PRI0134b.B21 (8) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
CL659535
CL659535.1 GI:50143739
GSS.
Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 8)
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.U.
ApbAbD: an Acedb database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
14681447
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.

FEATURES

source 1..8
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"

REFERENCE 1 (bases 1 to 8)
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.U.
ApbAbD: an Acedb database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
14681447
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.

FEATURES

source 1..8
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"

Query Match 0.4%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 223 CTCCCGG 229
|||||
1 CTCCCGG 7

Db

RESULT 166
LOCUS CL676755 8 bp DNA linear GSS 09-JUL-2004
DEFINITION PRI0119c.A08_2 - PRI0119c.BR (8) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
CL676755
CL676755.1 GI:50182472
GSS.
Pristionchus pacificus

/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"

Query Match 0.4%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 815 TGCTGAT 821
|||||
2 TGCTGAT 8

Db

RESULT 165
LOCUS CL675700 8 bp DNA linear GSS 09-JUL-2004
DEFINITION PRI0115c.E10_2 - PRI0115c.BR (8) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
CL675700
CL675700.1 GI:50180435
GSS.
Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 8)
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.U.
ApbAbD: an Acedb database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
14681447
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.

FEATURES

source 1..8
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"

Query Match 0.4%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 223 CTCCCGG 229
|||||
1 CTCCCGG 7

Db

RESULT 166
LOCUS CL676755 8 bp DNA linear GSS 09-JUL-2004
DEFINITION PRI0119c.A08_2 - PRI0119c.BR (8) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
CL676755
CL676755.1 GI:50182472
GSS.
Pristionchus pacificus


```
ORGANISM      Pristionchus pacificus
REFERENCE      Eukaryote; Metazoa; Nematoda; Chromodorea; Diplogasterida;
AUTHORS        Noddiplogasteridae; Pristionchus.
TITLE          1 (bases 1 to 8)
JOURNAL        Srinivasan,J., Oltic,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
PUBMED         AppabD: an Acedb database for the nematode satelellite organism
COMMENT        Pristionchus pacificus
               Nucleic Acids Res. 32 (1), D421-D422 (2004)
               14681447
               Contact: Sommer RJ
               Evolutionary Biology
               Max-Planck-Institute for Developmental Biology
               Spemannstr. 37-39, Tuebingen D-72076, Germany
               Tel.: 00497071601371
               Fax: 00497071601498
               Email: ralf.sommer@tuebingen.mpg.de
               This library was generated at Caltech, Pasadena, USA and end
               sequenced at Vancouver, Canada.
               Seq primer: T7
               Class: fosmid ends.
               Location/Qualifiers
                 1..8
                 /organism="Pristionchus pacificus"
                 /mol_type="genomic DNA"
                 /strain="California"
                 /db_xref="taxon:54126"
                 /clone_1lb="Mixed stage fosmid library of P. pacificus
                 var. California"
                 /note="Vector: pBf1fos-5 Fosmid vector"

Query Match      0.4%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches          7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1480 CCTCCT 1486
Db      2 CCTCCT 8

RESULT 167
CL677992      8 bp      DNA      linear      GSS 09-JUL-2004
LOCUS         PRI0121d_B07_2 - PRI0121d.BR (8) Mixed stage fosmid library of P.
DEFINITION    pacificus var. California Pristionchus pacificus genomic, genomic
ACCESSION     CL677992
VERSION       CL677992.1 GI:50184054
KEYWORDS      GSS.
SOURCE        Pristionchus pacificus
ORGANISM      Eukaryote; Metazoa; Nematoda; Chromodorea; Diplogasterida;
               Noddiplogasteridae; Pristionchus.
REFERENCE      1 (bases 1 to 8)
AUTHORS        Srinivasan,J., Oltic,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE          AppabD: an Acedb database for the nematode satelellite organism
JOURNAL        Pristionchus pacificus
PUBMED         Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT        Contact: Sommer RJ
               Evolutionary Biology
               Max-Planck-Institute for Developmental Biology
               Spemannstr. 37-39, Tuebingen D-72076, Germany
               Tel.: 00497071601371
               Fax: 00497071601498
               Email: ralf.sommer@tuebingen.mpg.de
               This library was generated at Caltech, Pasadena, USA and end
               sequenced at Vancouver, Canada.
               Seq primer: T7
               Class: fosmid ends.
               Location/Qualifiers
                 1..8
                 /organism="Pristionchus pacificus"
                 /mol_type="genomic DNA"
                 /strain="California"
                 /db_xref="taxon:54126"
                 /clone_1lb="Mixed stage fosmid library of P. pacificus
                 var. California"
                 /note="Vector: pBf1fos-5 Fosmid vector"

Query Match      0.4%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches          7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1397 CAGAGAG 1403
Db      7 CAGAGAG 1

RESULT 169
CL682011/c    8 bp      DNA      linear      GSS 09-JUL-2004
LOCUS         PRI0133c_H05_2 - PRI0133c.BR (8) Mixed stage fosmid library of P.
DEFINITION    pacificus var. California Pristionchus pacificus genomic, genomic
ACCESSION     CL682011
VERSION       CL682011.1 GI:50189203
KEYWORDS      GSS.
SOURCE        Pristionchus pacificus
ORGANISM      Eukaryote; Metazoa; Nematoda; Chromodorea; Diplogasterida;
               Noddiplogasteridae; Pristionchus.
REFERENCE      1 (bases 1 to 8)
AUTHORS        Srinivasan,J., Oltic,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE          AppabD: an Acedb database for the nematode satelellite organism
JOURNAL        Pristionchus pacificus
PUBMED         Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT        Contact: Sommer RJ
               Evolutionary Biology
               Max-Planck-Institute for Developmental Biology
               Spemannstr. 37-39, Tuebingen D-72076, Germany
               Tel.: 00497071601371
               Fax: 00497071601498
               Email: ralf.sommer@tuebingen.mpg.de
               This library was generated at Caltech, Pasadena, USA and end
               sequenced at Vancouver, Canada.
               Seq primer: T7
               Class: fosmid ends.
               Location/Qualifiers
                 1..8
                 /organism="Pristionchus pacificus"
                 /mol_type="genomic DNA"
                 /strain="California"
                 /db_xref="taxon:54126"
                 /clone_1lb="Mixed stage fosmid library of P. pacificus
                 var. California"
                 /note="Vector: pBf1fos-5 Fosmid vector"

Query Match      0.4%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches          7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      975 CACCTTC 981
Db      1 CACCTTC 7

RESULT 168
CL681141/c    8 bp      DNA      linear      GSS 09-JUL-2004
LOCUS         PRI0130b_C04_2 - PRI0130b.BR (8) Mixed stage fosmid library of P.
DEFINITION    pacificus var. California Pristionchus pacificus genomic, genomic
ACCESSION     CL681141
VERSION       CL681141.1 GI:50188149
KEYWORDS      GSS.
SOURCE        Pristionchus pacificus
ORGANISM      Eukaryote; Metazoa; Nematoda; Chromodorea; Diplogasterida;
               Noddiplogasteridae; Pristionchus.
REFERENCE      1 (bases 1 to 8)
AUTHORS        Srinivasan,J., Oltic,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE          AppabD: an Acedb database for the nematode satelellite organism
JOURNAL        Pristionchus pacificus
PUBMED         Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT        Contact: Sommer RJ
               Evolutionary Biology
               Max-Planck-Institute for Developmental Biology
               Spemannstr. 37-39, Tuebingen D-72076, Germany
               Tel.: 00497071601371
               Fax: 00497071601498
               Email: ralf.sommer@tuebingen.mpg.de
               This library was generated at Caltech, Pasadena, USA and end
               sequenced at Vancouver, Canada.
               Seq primer: T7
               Class: fosmid ends.
               Location/Qualifiers
                 1..8
                 /organism="Pristionchus pacificus"
                 /mol_type="genomic DNA"
                 /strain="California"
                 /db_xref="taxon:54126"
                 /clone_1lb="Mixed stage fosmid library of P. pacificus
                 var. California"
                 /note="Vector: pBf1fos-5 Fosmid vector"

Query Match      0.4%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches          7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      975 CACCTTC 981
Db      1 CACCTTC 7
```

SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT

Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasteridae;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 8)
Srinivasan,J., Otto,G.W., Kahlow U., Geisler,R. and Sommer,R.J.
Appadri: an Acceda database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
14681447
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@uebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: 77
Class: fosmid ends.

FEATURES
source
1..8
Location/Qualifiers
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pBpifos-5 Fosmid vector"

Query Match
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Length 8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 74 AAAAAA 80
|||||
7 AAAAAA 1

RESULT 170
DUT53265
LOCUS
DEFINITION
AUTHORS
TITLE
JOURNAL
COMMENT

DUT53265 8 bp DNA linear GSS 27-JAN-2006
ASNP3048.b2 HF130_10-06-02 uncultured marine microorganism
HF130_10-06-02 genomic clone HF0130_044H09, genomic survey
sequence.
DUT53265
DUT53265.1 GI:85763101
GSS.
uncultured marine microorganism HF130_10-06-02
uncultured marine microorganism HF130_10-06-02
unclassified sequences; environmental samples.
1 (bases 1 to 8)
DeJong,E.F., Preston,C.M., Mincer,T., Rich,V., Hallam,S.J.,
Frigaard,N.U., Martinez,A., Sullivan,M., Edwards,R., Chisholm,S.W.
and Karl,D.M.
Comparative genomics reveals the ecological trends in stratified
microbial communities in the ocean's interior
Science (2006) In press
Contact: Susan Lucas, Alex Copeland, Sam Pittluck, Alla Lapidus,
Kerrie Barry, Tijana Glavinic, David Bruce, Paul Richardson
and Edward DeJong
US DOE Joint Genome Institute
2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA
Tel: 617-253-5271
Fax: 617-253-2679
Email: pkrichardson@lbl.gov; delong@mit.edu
North Pacific Subtropical Gyre (Hawaii) picoplankton genomic fosmid
DNA library prepared from marine picoplankton in the less than 1.6
um, greater than 0.22 um fraction. Sample Date: 10/6/2002
Coordinates: 22.45 N, 158 W Depth 130 m Temperature: 22.19 C
Salinity: 35.31 psu Oxygen: 204.9 umol/kg

Class: fosmid ends.
Location/Qualifiers

FEATURES
source
1..8
/organism="uncultured marine microorganism HF130_10-06-02"
/mol_type="genomic DNA"
/db_xref="taxon:361146"
/clone="HF0130_044H09"
/cell_type="marine picoplankton, less than 1.8 um, greater
than 0.22 um fraction"
/clone_lib="HF130_10-06-02"
/note="Vector: pCC1P0S; North Pacific Subtropical Gyre
(Hawaii) picoplankton genomic fosmid DNA library prepared
from marine picoplankton in the less than 1.6 um, greater
than 0.22 um fraction. Picoplankton collected at 130 m
depth on 10/6/2002. Coordinates: 22.45 N, 158 W. Sample
Date: 10/6/2002 Coordinates: 22.45 N, 158 W Depth 130 m
Temperature: 22.19 C Salinity: 35.31 psu Oxygen: 204.9
umol/kg"

Query Match
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Length 8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 245 CCCCCA 251
|||||
2 CCCCCA 8

RESULT 171
DX021589/c
LOCUS
DEFINITION
AUTHORS
TITLE
JOURNAL
COMMENT

DX021589 8 bp DNA linear GSS 10-JAN-2006
KBRB015G08 KBRB, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBRB015G08, genomic survey
sequence.
DX021589
DX021589.1 GI:84712826
GSS.
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 8)
Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
End sequence of Brassica rapa BamHI (KBRB) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-dong, Suwon, 441-707, Korea
Tel: +82-31-298-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBRB015G08
Seq primer: M13 Reverse
Class: BAC ends.

FEATURES
source
1..8
Location/Qualifiers
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBRB015G08"
/lab_host="R.coli DH10B"
/clone_lib="KBRB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp
pekinensis var. Chifu BAC library (KBRB BAC) is provided
by Yong-Pyo Lim (CNU)."

Query Match 0.4%; Score 7; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 941 GCAGGT 947
 |||||
 Db 7 GCAGGT 1

RESULT 172
 CNS06ESN 9 bp DNA linear GSS 17-JUN-2001
 LOCUS
 DEFINITION T3 end of clone AR0A018H04 of library AR0A from strain CBS 732 of
 Zygosaccharomyces rouxii, genomic survey sequence.
 ACCESSION AL394689
 VERSION AL394689.1 GI:12145788
 KEYWORDS
 SOURCE GSS.
 ORGANISM Zygosaccharomyces rouxii
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; Saccharomycetaceae; Zygosaccharomyces.

REFERENCE
 AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
 1 (bases 1 to 9)
 Bolotin-Fukuhara,M., Bon,E., Broctier,P., Casaregola,S.,
 de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
 Maupertuy,A., Neuvéglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
 Saurin,W., Tekaya,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
 Wincker,P. and Weissenbach,J.
 Genomic exploration of the hemiascomycetous yeasts: 1. A set of
 yeast species for molecular evolution studies
 JOURNAL FEMS Lett. 487 (1), 3-12 (2000)
 PUBMED 11152876

REFERENCE
 AUTHORS de Montigny,J., Straub,M., Potier,S., Tekaya,F., Dujon,B.,
 Wincker,P., Artiguenave,F. and Souciet,J.
 Genomic exploration of the hemiascomycetous yeasts: 8.
 Zygosaccharomyces rouxii
 JOURNAL FEMS Lett. 487 (1), 52-55 (2000)
 PUBMED 11152883

REFERENCE
 AUTHORS Genoscope.
 Direct Submission
 Submitted (06-SEP-2000) Genoscope - Centre National de Séquençage,
 2 rue Gaston Crémieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
 seqret@genoscope.cns.fr - Web : www.genoscope.cns.fr)
 TITLE This GSS is part of a random genomic sequencing program of thirteen
 yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
 ekebergii, Saccharomyces servazzii, Zygosaccharomyces rouxii,
 Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
 lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
 angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
 Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
 5 kb were prepared and both extremities were sequenced. See
 keywords for description of this sequence and for the sequence of
 the other extremity of this insert.

FEATURES

source
 1..9
 /organism="Zygosaccharomyces rouxii"
 /mol_type="genomic DNA"
 /strain="CBS 732"
 /db_xref="taxon:4956"
 /clone="AR0A018H04"
 /clone_11b="AR0A"
 /note="end : T3"

Query Match 0.4%; Score 7; DB 1; Length 9;
 Best Local Similarity 77.8%; Pred. No. 1.7e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 331 GTCAATTGTG 339
 |||||
 Db 9 GTCAATTGTG 1

RESULT 173
 CF307008 9 bp mRNA linear EST 15-AUG-2003
 LOCUS
 DEFINITION HDAL--05-H11.g1 OSHDAC1-overexpressing transgenic rice lambda phage
 cDNA library I (HDAL) Oryza sativa (japonica cultivar-group) cDNA
 clone HDAL--05-H11, mRNA sequence.

ACCESSION CF307008.1 GI:33678769
 VERSION
 KEYWORDS
 SOURCE EST.
 ORGANISM Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 9)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
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FEATURES

source
 1..9
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="HDAL--05-H11"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E. coli SOLR"
 /clone_11b="OSHDA1-overexpressing transgenic rice lambda
 phage cDNA library I (HDAL)"
 /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
 XhoI; Callus was treated with ABA(20um) for 1hour. cDNA
 was inserted into lambda Uni-ZAP XR vector at 5' end with
 EcoRI and 3' end with XhoI site. mRNA was derived from
 rice histone Deacetylase overexpression line."

Query Match 0.4%; Score 7; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1303 CACGAGG 1309
 |||||
 Db 2 CACGAGG 8

Search completed: June 12, 2006, 06:13:47
 Job time : 3 secs

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